evolution
2014

ABSTRACTS

Raleigh Convention Center, June 20 – 24, 2014

An annual meeting presented by the Society for the Study of Evolution (SSE),
the Society of Systematic Biologists (SSB), and the American Society of Naturalists (ASN)

Snails in Art and the Art of Snails

Steve Jones

0E_BalC-Stephen Jay Gould Award Lecture
Friday, June 20, 2014

Images of snails are everywhere in art, Some are literal - Matisse's paper cut-out version, or Guadi's sculptures on the spires of the Sagrada Familia in Barcelona - but many more are metaphorical, illustrating the philosophical, biological - and evolutionary - ideas of sex, age, death and resurrection. I will talk briefly about the meaning of some of these molluscan images, but at rather more length about my own work on the evolution and genetics of Cepaea snails (which themselves make an appearance in some famous paintings). These creatures are a reminder of the time, just fifty years ago, when - in stark contrast to today, it can uncover it was possible to study genetic diversity, the raw material of evolutionary change, in only a few creatures such as butterflies, Drosophila, and snails themselves. Now such animals have almost been abandoned as candidates for research in evolution investigation (as I sometimes say, I am one of the top six world experts on their population genetics, and the other five agree) but I will discuss a series of experiments on their individual experience of the environment in which they live whose results suggest that even in these technological times they have something to say about the machinery of Darwinian evolution and, most of all, about its central and largely unanswered question - why do so many creatures have so much genetic diversity?

Skull integration and modularity in five toad species of the Rhinella granulosa group

Monique Simon, *Gabriel Marroig*

1A_201-Morphology
Saturday, June 21, 2014 8:30 AM-8:45 AM

Morphological integration and modularity are related concepts that refer to the relative degrees of connectivity among morphological elements within a complex structure. Morphological integration theory states that integration/modularity patterns are explained by functional and/or developmental interactions among the elements. Integration patterns and modularity hypothesis were never assessed in adult toads. We worked with five closely related toad species - R. granulosa, R. merianae, R. mirandariberoi, R. pygmea and R. major – to compare phenotypic covariance and correlation structure of skull bones and its integration magnitudes. We also performed a modularity test in which we hypothesized three functional modules: neurocranium, snout and suspensorium, and a full integration hypothesis (three modules tested concomitantly). We scanned all skulls with a microtomography X-ray system and placed 42 landmarks in the 3D skulls by using the TINA-Landmark software. All individuals were measured twice to assess distance repeatability. Twenty-eight linear distances were calculated and covariance/correlation matrices were constructed. Matrix repeatability was calculated by bootstrapping. We compared species matrices with Krzanowski correlation. Integration magnitudes were calculated as the squared average correlation (r2) from the species correlation matrices and indicate the overall degree of connectivity among the distances. Since toads have indeterminate growth, size variation alone could ensure similarity among the species matrices, so we also compared them after removing size variation (residual matrices). The modularity test was done by correlating theoretical correlation matrices (which express the hypothetical functional modules) and the empirical matrices. Mean distance repeatability for all species was 0.98. Matrix repeatability ranged from 0.87 to 0.94. Covariance and correlation species matrices were highly similar both for raw (0.89 + 0.04 and 0.91 + 0.03, respectively) and residual matrices (0.87 + 0.05 and 0.93 + 0.05, respectively). Integration indexes r2 varied from 0.22 for R. pygmea to 0.43 for R. major, reflecting different percentages of variation explained by the PC1 (size related vector) of the covariance matrices (52% to 79%). Modularity tests detected the modules snout and suspensorium for all species, except R. pygmea, in which only the suspensorium appeared. The snout module was also detected in the residual matrices of all species, along with the full integration hypothesis in three species. Even though size variation is a major component of the individual species phenotypic morphospace, its removal did not change matrix similarity among the species. Thus, species matrix similarity must be a consequence of the alike modular organization of skull bones in distinct functional/developmental units.

Quantification of coiling patterns in gastropod shells and evaluation of functional traits

Koji Noshita

1A_201-Morphology
Saturday, June 21, 2014 8:45 AM-9:00 AM

The morphology of gastropod shells has been a focus of analyses in evolution. It has recently emerged as an important issue in developmental biology, thanks to recent advancements in molecular biological techniques. The growing tube model is a theoretical morphological model for describing various coiling patterns of molluscan shells. It is a useful tool to relate local tissue growth with global shell morphology. However, the growing tube model has hardly been adopted in empirical research owing to the difficulty in estimating the parameters from morphological data. In this talk, I attempt to solve this problem by developing methods of parameter estimation when 1) 3D Computed Tomography (CT) data are available and 2) only 2D image data (such as photographs) are available. When 3D CT data are available, the parameters can be estimated by fitting an analytical solution of the growing tube model to the data. When only 2D image data are available, we first fit Raup’s model to the 2D image data and then convert the parameters of Raup’s model to those of the growing tube model. Both methods work well, except when shells grow without coiling.

Moreover, I attempt to evaluate functional traits of gastropod shells. In this talk, I focus on defensive traits against invading predators (e.g. giant water bugs and larvae of firefly). I proposed three indexes to evaluate those; length of growing trajectory, change of curvature, and shapes of tube slices. These traits can be evaluated from either growing tube model or 3D CT data. I would like to discuss what kinds of traits are helpful to understand morphological diversity of gastropods and their shell forms.

Lizard scales in an adaptive radiation: variation of scale number follows climatic and structural habitat diversity in Anolis lizards

Johanna Wegener, Gabriel Gartner, Jonathan Losos

1A_201-Morphology
Saturday, June 21, 2014 9:00 AM-9:15 AM
p>Lizard scales vary in size, shape and texture among and within species. The overall function of scales in squamates is attributed to protection against abrasion, solar radiation and water loss. We quantified scale number of Anolis lizards across a large sample of species (142 species) and examined whether this variation was related either to structural or climatic habitat diversity. We found that species in arid environments have fewer and thus larger scales than species in humid ones. This is consistent with the hypothesis that scales reduce evaporative water loss through the skin.

In addition, scale number varied among groups of ecomorphs and specific aspects of the structural microhabitat (i.e. perch height and perch diameter). This was unexpected, because ecomorph groups are based on morphological features related to locomotion in different structural microhabitats. Body scales are not likely to play an important role in locomotion in lizards. The observed variation may relate to other features of the ecomorph niche and more work is needed to understand the putative adaptive basis of these patterns.

Taking many-to-one to the next level: decoupled evolution in an ultrafast prey capture mechanism

Philip Anderson, Sheila Patek

1A_201-Morphology
Saturday, June 21, 2014 9:15 AM-9:30 AM
Biomechanical systems are inherently multi-part, multi-level and interconnecting. Evolution may operate at individual levels independently, on the entire apparatus as a whole or both simultaneously. We examined the interconnecting lever and linkage mechanisms found in the fast raptorial appendages of mantis shrimp (Stomatopoda) both at the level of the individual mechanisms and the apparatus as a whole. The many-to-one mapping of biological mechanisms is a common framework for understanding evolution within mechanical systems such as 4-bar linkages, yet it is not clear whether an analogous process should occur for interconnecting mechanical systems. We tested the hypothesis that the individual mechanisms (levers and linkages) show the same basic pattern of evolution as the overall multi-part system. We measured a series of biomechanical metrics (e.g., kinematic transmission) and utilized landmark-based geometric morphometrics to characterize the mechanics and morphology of the raptorial appendage system. We used phylogenetic comparative methods to test the prediction that if the overall system is canalized towards a limited number of biomechanical profiles (as previously shown) then the individual mechanisms will likewise show constrained variation in morphology and mechanics. Contrary to this prediction, we find that different levels of the biomechanical system show differing evolutionary patterns of variability. The overall raptorial appendage shows strong canalization towards one of two biomechanical profiles, either force amplification or displacement amplification. However, the linkage mechanism underlying this system shows a greater variability of forms as expected from many-to-one mapping theory. These findings suggest that the evolutionary dynamics of coupled mechanical systems need not be coupled themselves. Multi-level systems can follow different evolutionary pathways depending on the level being examined.

Exceptional avian herbivores: Multiple origins of folivory in the bird order Anseriformes and its correlation with body mass

Aaron Olsen

1A_201-Morphology
Saturday, June 21, 2014 9:30 AM-9:45 AM
An herbivorous diet, or a diet consisting primarily of the fibrous parts of plants (leaves, stems and roots), has evolved repeatedly in multiple groups of vertebrates including lizards, fishes and mammals. Although herbivory has also evolved multiple times among birds, its origination is thought to be limited by its consequences for the cost of flight due to an associated increase in body mass. Species in the bird order Anseriformes, which includes ducks, geese, swans and mergansers, represent a great diversity of diets including granivory, piscivory and herbivory. I tested whether herbivory has evolved multiple times within Anseriformes using data from three different sources: diet, behavior and morphology. I compiled diet data from published stomach contents studies and handbook entries to create continuous dietary categories for over 95% of anseriform species. The major categories included animal matter, seeds, nuts, leaves, stems and roots. Feeding behavior was scored as presence or absence of dabbling based on published studies and videos of bird feeding behaviors archived on sites such as the Internet Bird Collection and Arkive.org. Lastly, I collected morphometric data on the 3D curvature of the beak (tomium and culmen) from skeletal specimens representing most anseriform genera. Dietary, behavioral and morphological data are consistent with at least six independent origins of a primarily herbivorous diet in Anseriformes from a less herbivorous, dabbling, duck-like ancestor. This is equal to the number of times herbivory has originated across all the rest of birds. Using body mass data obtained from published species averages, I also tested whether a more herbivorous diet correlates with a higher body mass. Surprisingly, a more herbivorous diet did not correlate significantly with an increase in body mass. These results raise the question of whether herbivory in birds necessarily implies an increase in body mass and why Anseriformes is exceptional among bird orders in the number of origins of herbivory.

Developmental Mechanisms for Novel Morphological Evolution: Origin and Diversification of the Avian Skull

Arkhat Abzhanov

1A_206-Avian Evolution
Saturday, June 21, 2014 8:30 AM-8:45 AM

Comprising 30 orders and over 10,000 species, birds are the most successful land vertebrates and much of their success can be attributed to beak shape variation. My group studies developmental mechanisms responsible for differences in shapes of avian beaks by taking advantage of the natural diversity of beak shapes of songbirds, including the iconic Darwin's Finches. Their highly diverse beak shapes represent a classic example of adaptive radiation, niche partitioning, and rapid morphological evolution. We recently mathematically modeled beak developmental evolution and uncovered developmental mechanisms that control beak development, which allow for extensive morphological variation in beak shapes but also place significant developmental constraints on what kind of variation can be produced. At the large-scale evolutionary level, all modern birds (Class Aves) are a crown group of division Archosauria (the "ruling reptiles"), a large clade of diapsid reptiles that appeared about 250 million years ago and which also includes more basal archosaurs. The bird face is profoundly modified compared to its non-avian reptilian antecedents. To understand the significance of bird-specific changes, we recently performed a morphometric analysis of skulls from basal archosaurs to theropod dinosaurs, to primitive and modern birds. Remarkably, such analyses already revealed an important role for heterochrony in the origin of the bird skulls from non-avian theropods. We hypothesized that such profound morphological changes in avian skull morphology were driven by alterations of their molecular patterning and investigated the origin of the avian skull combining geometric morphometrics, comparative developmental analysis and functional embryological tests. Our studies revealed the morphological distinctiveness of the bird rostrum as fused, elongate premaxillae and demonstrated a relatively simple regulatory molecular adjustment that produced the bird face, enabled avian jaw kinesis and allowed the beak to diversify as an independent module.

Neotenous feather replacement facilitates loss of flight in birds

Ryan Terrill

1A_206-Avian Evolution
Saturday, June 21, 2014 8:45 AM-9:00 AM

The ability to fly was a key adaptation for the evolution of modern birds and has allowed birds to radiate into a diverse array of habitats and evolve novel life-history strategies. However, maintaining the ability to fly is physiologically costly because of the energy required to maintain structures such as an extremely enlarged pectoralis muscle. Because of this, flight has been evolutionarily lost many times and in many groups of birds. The ancestral bird to crown Aves was likely volant, and so all extant flightless birds have lost flight. Some of the most charismatic flightless birds, such as ostriches or penguins, have lost flight deep in the past and have evolved life-history strategies that do not involve flight. Conversely, some groups, such as rails and ducks, have rapidly evolved a flightless lifestyle many times in the recent past. A common character shared by groups that have shown prolific recent losses of flight is that volant species in these families molt all their remiges simultaneously as adults, while most other groups of birds molt feathers simultaneously only as juveniles and sequentially as adults to maintain flight ability during the molt. Otherwise-volant species that molt their remiges simultaneously are thus left flightless during the molting period. I hypothesize that these lineages lose flight quickly and commonly because of preadaptions to a non-volant lifestyle facilitated by the ability to escape predators and forage for resources without the ability to fly. I suggest that simultaneous molt in adults birds is best viewed as a neotenous character, and that molt strategies should be examined within the context of heterochrony. Neoteny has been implicated as a facilitator of rapid morphological and ecological evolution in other groups because change in developmental timing can result in profound life-history alteration with relatively few physiological and morphological changes. I used a Bayesian approach to test the hypothesis that simultaneous molt has facilitated loss of flight in birds, by implementing a reversible-jump Markov-chain Monte Carlo method over a pseudo-posterior distribution of super trees of all birds to test whether a model in which the loss of flight is dependent upon simultaneous molt is more likely than a model of independent evolution. Preliminary analyses support a model of dependent evolution, in which a simultaneous molt strategy facilitates loss of flight.

A new island rule for birds: evolution towards flightlessness

Natalie Wright, Christopher Witt

1A_206-Avian Evolution
Saturday, June 21, 2014 9:00 AM-9:15 AM

Flightlessness has evolved in over one thousand bird lineages on islands with no land-based predators. This allows for decreased energetic demands by reducing the size of metabolically expensive flight muscles. The majority of island birds, however, retain flight despite sharing these low-predation island habitats. Are these flighted island birds evolving towards flightlessness as well? To answer this question, we examined flight musculature from over 700 species of birds, including populations from over 75 islands. Across the avian tree, island species have evolved smaller flight muscles than their continental relatives. Within island taxa, flight muscles and legs evolve in concert along a continuum from large flight muscles/short legs to small muscles/long legs. Small flight muscles and longer legs were best predicted by low island species richness. On small islands with few to no predators, most birds have evolved towards flightlessness, including those that must fly in order to forage (e.g., hummingbirds). These changes are likely driven by biotic interactions on islands, as they are best predicted by ecological factors rather than physical characteristics such as island size or location. Our findings suggest that flighted island birds have reduced escape and dispersal abilities. The susceptibility of island birds to introduced predators and human hunting may be due in part to their reduced flight muscles and thus reduced burst flight and escape ability.

Phylogeny and forelimb disparity in waterbirds

Xia Wang, Julia Clarke

1A_206-Avian Evolution
Saturday, June 21, 2014 9:15 AM-9:30 AM

Previous work has shown that the relative proportions of wing components (i.e., humerus, ulna, carpometacarpus) in birds are related to function and ecology, but these have rarely been investigated in a phylogenetic context. Waterbirds including “Pelecaniformes”, Ciconiiformes, Procellariiformes, Sphenisciformes and Gaviiformes form a highly supported clade and developed a great diversity of wing forms and foraging ecologies. In this study, forelimb disparity in the waterbird clade was assessed in a phylogenetic context. Phylogenetic signal was assessed via Pagel’s lambda, Blomberg’s K and permutation tests. We find that different waterbird clades are clearly separated based on forelimb component proportions, which are significantly correlated with phylogeny but not with flight style. Most of the traditional contents of “Pelecaniformes” (e.g., pelicans, cormorants and boobies) cluster with Ciconiiformes (herons and storks) and occupy a reduced morphospace. These taxa are closely related phylogenetically but exhibit a wide range of ecologies and flight styles. Procellariiformes (e.g. petrels, albatross, and shearwaters) occupy a wide range of morphospace, characterized primarily by variation in the relative length carpometacarpus and ulna. Gaviiformes (loons) surprisingly occupy a wing morphospace closest to diving petrels and penguins. Whether this result may reflect wing proportions plesiomorphic for the waterbird clade or a functional signal is unclear. A Bayesian approach detecting significant rate shifts across phylogeny recovered two such shifts. At the base of the two sister clades Sphenisciformes + Procellariiformes, a shift to an increase evolutionary rate of change is inferred for the ulna and carpometacarpus. Thus, changes in wing shape begin prior to the loss of flight in the wing-propelled diving clade. Several shifts to slower rate of change are recovered within stem penguins.

Late evolutionary origin of modern bird flight inferred from shoulder allometry

Daniel Field, Colton Lynner

1A_206-Avian Evolution
Saturday, June 21, 2014 9:30 AM-9:45 AM

The evolution of powered flight, defined as the capacity to sustain level aerial locomotion by flapping wings as in crown-clade birds, was a pivotal event in dinosaur evolution, and played a major role in the ascendancy of birds to their current position as the most diverse and widely distributed tetrapods. Understanding the pattern of powered flight acquisition has become a key goal in dinosaur paleobiology, with the flying potential of early avialans, such as Archaeopteryx, inspiring debate since the 19th Century. Understanding of powered flight capacity on the avian stem has, however, been limited by two primary factors: the uncritical application of poorly constrained mass estimates to Mesozoic stem birds, and the difficulty of identifying accurate osteological correlates of flying ability. Here, an analysis of shoulder joint dimensions and body mass in over 1,000 extant birds and several Mesozoic avialans appears to delineate functional flying and flightless zones, enabling explicit tests of flying potential in stem birds. By incorporating broad 95% prediction intervals on mass estimates for stem birds, this approach enables the incorporation of statistical uncertainty in inferences of flying ability. This approach casts doubt on the powered flying potential of early Mesozoic avialans such as Archaeopteryx and Confuciusornis, and indicates that the powered flying ability of modern birds arose considerably later than is often assumed. These data clarify the stepwise sequence by which flight-related modifications accrued on the avian stem (e.g., the evolution of asymmetrical pennaceous feathers and a pygostyle appear to predate the origin of powered flapping flight), and bring us closer to a more complete understanding of one of the great macroevolutionary transitions in the history of life.

Reef-specific patterns of osmotic response in larval and adult eastern oysters, Crassostrea virginica, from a single estuary

Laura Eierman, Matthew Hare

1A_301A-Genetics of Traits
Saturday, June 21, 2014 8:30 AM-8:45 AM

Differential fitness among genotypes in response to environmental variation results in natural selection, particularly beyond the limits of phenotypic plasticity. Understanding the interaction between selection and plasticity is important for predicting species’ persistence in rapidly changing environments. In species with sedentary adults, many traits typically show broad phenotypic plasticity. However, when coupled with high fecundity and widely dispersing offspring, there is an opportunity for selection to reshape the functional genetic composition of populations across fine-grained habitat heterogeneity every generation. We tested for this pattern of selection using RNA-seq methods to study functional genetic variation controlling gene expression in adult eastern oysters, Crassostrea virginica, from different reefs after acclimation to salinity in common gardens. We analyzed 24 adult oysters collected from high and low salinity source reefs within a single estuary after they were acclimated in common gardens at 10 and 30 salinity for 9 weeks. We modeled patterns of expression using reef source, treatment salinity and the reef-by-treatment interaction term as predictors. A total of 9,921 reference transcriptome contigs (reftigs; 23.6%) were significantly differentially expressed (DE), with 0.6% of all reftigs DE for the reef source, 18.9% DE for treatment salinity, and 13.9% DE for the reef-by-treatment factor. The reftigs responding to treatment and the reef-by-treatment factors demonstrate a genomically pervasive pattern of plastic gene expression in response to osmotic pressure. Additionally, the reef-specific reaction norms and abundant GxE patterns suggest that the history of selection at each source reef is generating different plastic responses after acclimation to the same osmotic condition. To further test the hypothesis of recurrent viability selection, we made within-reef pair crosses from low, intermediate and high salinity source oysters. Survival analyses of larvae over a ten day period, starting 48 hours after fertilization, indicated a significant parent reef source by larval salinity treatment interaction. This result indicates that differences in plasticity in oysters from different reef sources are heritable. Overall, we conclude that reef-specific patterns of gene expression and larval survival indicate that oyster responses to habitat heterogeneity are shaped both by phenotypic plasticity and recurrent selection on each generation of migrants. Studies on the interaction between plasticity and evolutionary responses typically classify these two mechanisms as acting within and between generations, respectively. We suggest that for many high dispersal species with type III survivorship, intra-generational selection molds patterns of plasticity across habitats such that the interaction between these two processes expands the niche margin.

Environmental effects on genetic covariances

Corlett Wood, Butch Brodie

1A_301A-Genetics of Traits
Saturday, June 21, 2014 8:45 AM-9:00 AM

No trait exists in isolation: organisms are composed of integrated suites of correlated traits that evolve together. Because selection on one trait results in an indirect response to selection in correlated traits, trait correlations act as evolutionary constraints, interfering with evolutionary response in the direction favored by selection. However, the degree to which patterns of trait correlation—and thus their role in evolutionary constraint—are sensitive to the environment remains poorly understood.

The relationships among correlated traits are described by the genetic variance-covariance (G) matrix. This matrix contains the genetic variance of each trait along the diagonal and the strength and sign of trait covariances in the off-diagonal elements. The genetic variances affect the magnitude of the response to selection, and the genetic covariances, the degree to which traits respond independently to conflicting selection pressures.

Many environmental variables—most notably stress, quality, and novelty—have been shown to affect genetic variances, suggesting that a trait's capacity to respond to selection depends on the environment in which it is expressed. By contrast, environmental effects on genetic covariances remain understudied, in spite of the fact that the same mechanisms that drive differences in genetic variances (differences in the underlying loci or in the allelic effects among environments) should affect genetic covariances as well. Although a number of studies have estimated the G matrix in multiple environments, few have examined whether there are any general patterns that emerge across taxa. Strong environmental effects on patterns of genetic covariance would suggest that the role of constraint may be highly dependent on the local environment.

We conducted a meta-analysis on studies that have estimated the G matrix in multiple environments. We examine whether the environment affects the magnitude of genetic covariances and the direction of the major axes of genetic variation. We discuss the implications of our results in the context of environmental effects on evolutionary constraint in natural populations.

Breaking the mold: the effects of mutations on phenotypic covariation in the fruit fly wing

Annat Haber, William Pitchers, Ian Dworkin

1A_301A-Genetics of Traits
Saturday, June 21, 2014 9:00 AM-9:15 AM

The study of character covariation can yield important insights into the interplay between genetic architecture and selection in determining evolutionary trajectories. However, the implication of covariation for evolution depends on its stability relative to the evolution of the population mean. In order to better understand the potential of integration to change due to segregating variation or fixation of alleles, we used 12 mutant strains of Drosophila melanogaster, as well as 12 inbred strains derived from natural populations. All mutant strains were backcrossed into the Samarkand wild type (Sam). All mutations were associated with either the EGFR or TGF-b pathways, known to affect adult wing shape. All individuals within genotype are genetically identical, and therefore their covariance matrix reflects environmental factors only. We extracted 48 landmarks and semi-landmarks from the wing, and superimposed them using Procrustes superimposition. In addition, we used LORY, a recently developed method for evaluating local shape variables as the determinant of the Jacobian matrix of local deformations. This method translates the multidimensionality of the Procrustes coordinates into a multivariate dataset that is amenable to conventional multivariate analyses and therefore more suitable for quantifying covariation. All analyses were repeated for both datasets, as well as two different interpolation functions for evaluating local shape variation, the thin plate and elastic body splines. We calculated the covariance matrix and mean shape for each genotype and estimated their differences in terms of total variance, matrix eccentricity, matrix pattern, and mean shape.

We found that the Jacobian-based data using Elastic Body Splines as an interpolation model provided the best representation of mean shape and covariance differences. Mutants that differed more from Sam in their mean shape also had a greater total variance among individuals, suggesting an association between shape change and the level of phenotypic decanalization. Most mutants, however, had a lower variance – i.e., were more canalized – than Sam and the natural wild types. Most mutations do not alter the eccentricity of the matrix, and there is no relationship between shape changes and eccentricity. Most natural wild types have significantly higher eccentricity than Sam, yet no association with shape differences from Sam. Differences in covariance pattern, measured as differences in average response to random skewers, correlate positively with shape differences. These results suggest a complex non-linear relationship between development and phenotypic variation, and indicate that different aspects of the covariation structure can be associated differently with shape changes.

C. elegans harbors pervasive cryptic genetic variation for embryogenesis

Annalise Paaby, Matthew Rockman

1A_301A-Genetics of Traits
Saturday, June 21, 2014 9:15 AM-9:30 AM

Conditionally functional mutations represent an important class of natural genetic variation, yet little is known about their prevalence in natural populations. Here, we describe a vast reserve of cryptic genetic variation, alleles that are normally silent but which become penetrant when other genes are knocked down, in the gene networks of C. elegans embryogenesis. The discovery of this variation represents identification of penetrance modifiers and indicates that the generally invariant, canalized process of early development can be destabilized to produce heritable differences in network function. The cryptic genetic variation we uncovered demonstrates low developmental pleiotropy, in that specific, rather than general, perturbations are required to reveal it. Our findings emphasize the importance of genetic background in characterizing gene function and provide insight into the phenomenon of developmental system drift, in which the genetic mechanisms of development change over evolutionary time.

Genetic architecture of rapid and extreme body size evolution in an island population of house mice

Melissa Gray, Michelle Parmenter, Caley Hogan, Irene Ford, Richard Cuthbert, Peter Ryan

1A_301A-Genetics of Traits
Saturday, June 21, 2014 9:30 AM-9:45 AM
Organisms on islands routinely evolve unusual body sizes over short time periods, but the genetic mechanisms underlying this evolutionary pattern remain poorly understood. As successful colonizers of islands across the globe and the targets of intense genetic study, house mice provide a model system for dissecting the genetics of island evolution. In this study, we examined the evolution of body size in the largest wild house mice in the world, which inhabit Gough Island (GI). These mice (belonging to Mus musculus domesticus) are twice the mass of their mainland counterparts, a difference that evolved during the last 100 years. To dissect the genetic architecture of gigantism in Gough Island mice, we conducted a large F2 intercross between GI mice and a smaller bodied strain (WSB). By weighing mice weekly at 16 time points, we reconstructed the growth curves of individual F2s. Mice were genotyped at more than 3,000 informative SNPs. We identified a suite of quantitative trait loci (QTL) associated with body weight. QTL ranged in phenotypic effect sizes, including a large-effect locus on chromosome 10. Most QTL had additive effects on body weight and acted at multiple, contiguous ages. The GI allele increased body weight at all QTL, consistent with natural selection driving size evolution. Our results provide a rare genetic dissection of extreme body size on islands, and pave the way for identification of the mechanisms responsible for rapid evolution of size.

Functional analysis of the B gene homolog PISTILLATA reveals novel regulatory interactions controlling stamen identity in Aquilegia coerulea

Bharti Sharma, Elena Kramer

1A_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 8:30 AM-8:45 AM
Within the context of the ABC model for floral organ identity determination, the canonical function of the B gene PISTILLATA (PI) is establishment and maintenance of petal and stamen organ identity. Down-regulation of PI homologs in diverse model plant systems such as Arabidopsis and Antirrhinum results in homeotic conversion of petals to sepals and stamens to carpels. However, in Aquilegia coerulea, which bears four to seven whorls of stamens, down-regulation of AqPI results in homeotic transformation of outer stamens to sepals and inner stamens to sepal-carpel or stamen-carpel chimeras. These results suggest, first, that expression of the C gene homologs, which normally promote stamen and carpel identity, may be dependent on B gene function, and second, that outer and inner stamens differ in their sensitivities to both B and C gene expression. Interestingly, similar studies of other Ranunculid model systems have revealed some parallels, indicating that this novel regulatory interaction between the B and C class gene homologs may be more broadly conserved. The present study opens new avenues for further evolutionary developmental and genetic studies to better understand how varying in floral morphology, such as the production of a wide domain of stamens, may correlate with changes in regulatory interactions among the floral organ identity genes.

Conserved core genes are under positive selection in a long-term Escherichia coli evolution experiment

Rohan Maddamsetti, Phil Hatcher, Barry Williams, Richard Lenski

1A_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 8:45 AM-9:00 AM
In this study, we ask whether those genes that are evolving fastest in a long-term E. coli evolution experiment also tend to be evolving faster in nature than typical genes, or alternatively, whether the genes targeted in that evolution experiment are in nature more slowly evolving—i.e. more conserved--than typical genes. To this end, we computed a set of 1968 panorthologs: single copy genes found in the ancestral strain REL606 as well as 59 published E. coli genomes. These published sequences include lab strains, pathogens, commensals, and a few environmental isolates. We found that beneficial mutations in the long-term lines tend to occur in genes that are strongly conserved in E. coli as well as in more diverged bacterial species. Further, we found that non-synonymous mutations tend to fall more often in panorthologs than in the rest of the genome. Although panorthologs make up 48% of coding sequence in REL606, 109 out of 161 non-synonymous mutations fall into this set (p-value E. coli evolution, even though they are very simple and seemingly unremarkable given their culturing conditions in a minimal salts medium with limiting glucose at 37C. We speculate that what may be most novel, however, is the constancy of the environment, its biophysical simplicity, and the absence of microbial competitors and parasites.

Comparative genomics sheds light on the evolution and function of the Highly Iterative Palindrome -1 motif in Cyanobacteria

Minli Xu, Jeffrey Lawrence, Dannie Durand

1A_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 9:00 AM-9:15 AM
The Highly Iterative Palindrome-1 (HIP1), an octamer palindromic motif (GTCATCGC), is highly abundant in a wide range of cyanobacterial genomes from various habitats. HIP1 frequency can be as high as one occurrence per 350 nucleotides, which is rather

astonishing considering that at this frequency, on average, every gene in that genome will be associated with more than one HIP1 motif. HIP1 was first identified in the early 1990s, yet its functional and molecular roles are still not understood. No mechanism or biological system has been identified that explains this level of prevalence. More discouraging, it is still not clear whether HIP1 has a function, or whether HIP1 abundance is an artifact of some neutral process, such as DNA repair or transposition.

Here we present results from genome scale analyses that provide the first evidence that HIP1 motifs are under selection, which further demonstrates that HIP1 motifs are functional. We estimate the expected HIP1motif frequency, taking into account the background tri-nucleotide frequency in the genome, and showed that observed HIP1 frequencies are as much as 100 times higher than expected. This HIP1 motif enrichment is observed in both coding and non-coding regions. Analyses of alignments of genomes with Ks values ranging from 0.02 to 0.59 further showed HIP1 motif conservation in homologous sequences. The level of HIP1 conservation is significantly higher than the conservation of control motifs, i.e., other octamer palindromes with the same GC content. To show that such conservation is not merely a result of codon usage, we demonstrated that codons in HIP1 motifs are more conserved than the same codons found outside HIP1 motifs. Our results, taken together, are consistent with the hypothesis that HIP1 motifs are under selection, which proves that the abundance of HIP1 motifs is related to biological functions, rather than to some neutral process.

Invade, co-opt, and swap: Evolution of G1/S cell cycle control in Fungi and other eukaryotes

Edgar Medina, Jan Skotheim, Nicolas Buchler

1A_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 9:15 AM-9:30 AM

The core eukaryotic cell cycle is believed to have emerged before the last common ancestor of plants, fungi, and animals. The structure of the G1–S regulatory network that regulates cell cycle entry and its dynamic properties are highly similar in budding yeast and mammals despite lack of sequence homology between many G1/S regulators (cyclins, transcription factors, and inhibitors). This is all the more striking because plant and animal G1/S regulators (Cyclin D, E2F/DP, Rb) have much higher sequence homology even though fungi and animals are more closely related. This suggests that plants and animals have conserved both the components and the network structure of the ancestral G1/S network, while more dramatic cell cycle evolution occurred in Fungi.

To investigate cell cycle evolution, we have constructed a eukaryotic phylogeny of the G1/S cyclin, CDK, inhibitor, and transcription factor superfamily anchored on Saccharomyces cerevisiae, Homo sapiens, and Arabidopsis thaliana. We show that the last eukaryotic common ancestor likely had complex cell cycle regulation involving at least one cell cycle Cdk, multiple cyclin families, activator and inhibitory E2F transcription factors, and pRb-family pocket proteins. Basal Fungi are characterized by the emergence of novel Whi5 inhibitor and novel SBF/MBF transcription factors followed by the eventual loss of their Rb inhibitor and E2F/DP transcription factors during the transition to dikarya. The SBF/MBF DNA-binding domain has sequence homology to a domain of viral origin. It appears that these new regulators were able to acquire, maintain, and eventually usurp the function and dynamics of the original G1-S regulatory network following the formation of a hybrid network.

Intragenic epistasis on adaptive dynamics at the gene couch potato

Emily Behrman, Alan Bergland, Dmitri Petrov, Paul Schmidt

1A_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 9:30 AM-9:45 AM

Epistasis is a fundamental component of natural selection and adaptation in natural populations. It is not clear if the alleles that segregate in the wild act independently or if they associate to have non-additive effects on fitness. Previous mapping in Drosophila melanogaster has identified that the couch potato gene is involved with climate adaptation by controlling the propensity to express a reproductive diapause needed to overwinter in temperate climates. A screen of clinal and seasonal wild populations of Drosophila identified multiple SNPs that vary predictably with climate. Three SNPs in the couch potato gene exhibit independent clines, however, certain multi-SNP combinations vary non-randomly with geographic location. This suggests that there are epistatic interactions between independent SNPs in the couch potato gene and these non-additive interactions influence performance and fitness phenotypes that underlie adaptation to climate. Here, this hypothesis is tested using DGRP inbred lines to create seven populations that are each constant for one of the three-SNP couch potato allele combinations to test these alleles in a randomized genetic background. The performance and fitness of these multi-locus alleles is assessed using a comprehensive phenotypic screen, which includes assays for stress tolerance, fecundity, development, aging, body size, diapause, immunity, learning and behavior. There is significant variation for all traits investigated and epistasis is pervasive among SNPs for these traits. There are emergent properties associated with combinations of SNPs that lead to an adaptive pattern; the northern haplotype has non-additive effects in traits associated with a cold climate life history strategy while traits involved with the warm weather life history syndrome are overexpressed for the southern haplotype. The changes in life history phenotypes correspond with differential expression patterns of cpo among the haplotypes. These epistatic interactions result in higher frequency of the northern and southern allele combinations in wild populations, demonstrating how emergent properties of combinations of SNPs underlie adaptive life history evolution in natural populations.

When field experiments yield unexpected results: lessons learned from measuring selection in White Sands lizards

Kayla Hardwick, Luke Harmon, Erica Rosenblum

1A_302A-Adaptation
Saturday, June 21, 2014 8:30 AM-8:45 AM

Determining the adaptive significance of phenotypic traits is key for understanding evolution and diversification in natural populations. However, evolutionary biologists have an incomplete understanding of how specific traits affect fitness in most populations. The White Sands system provides an opportunity to study the adaptive significance of traits in an experimental context. Blanched color evolved recently in three species of lizards inhabiting the gypsum dunes of White Sands, and is likely an adaptation to avoid predation. To determine whether there is a relationship between color and susceptibility to predation in White Sands lizards, we conducted enclosure experiments, quantifying survivorship of lizards exhibiting substrate-matched and substrate-mismatched phenotypes. Lizards in our study experienced strong predation. Color did not have a significant effect on survival, but we found several unexpected relationships including variation in predation over small spatial and temporal scales. In addition, we detected a marginally significant interaction between sex and color, suggesting selection for substrate matching may be stronger for males than females. We use our results as a case study to examine six major challenges frequently encountered in field-based studies of natural selection, and suggest that insight into the complexities of selection often results when experiments turn out differently than expected.

Survival in a cutthroat world: experimental estimation of natural selection on stickleback armor.

Diana Rennison, Seth Rudman, Dolph Schluter

1A_302A-Adaptation
Saturday, June 21, 2014 8:45 AM-9:00 AM

While there has been longstanding interest in competition as a source of divergent natural selection, predation has received far less attention, especially experimentally. In threespine stickleback (Gasterosteus aculeatus) differential predation by cutthroat trout (Oncorhynchus clarki) is thought to be involved in armor divergence between sympatric benthic and limnetic species. To test this hypothesis we have undertaken a multi-generation experiment of selection on armor in variable populations (hybrids between benthic and limnetic stickleback) undergoing natural breeding and development in ponds. In five ponds only stickleback were introduced (no-predator treatment; insect and avian predators were not manipulated) and in five other ponds cutthroat trout as well as stickleback were introduced (predator treatment). Using samples of stickleback taken every four months over two years we found evidence of strong selection on multiple armor traits, including dorsal and pelvic spines. The strength and direction of selection was temporally variable, sometimes favoring reduced spine length regardless of the presence of the predator. This study provides the first experimental evidence that vertebrate predation favors increased armor in threespine stickleback. This study also suggests that cutthroat trout may indeed play a role in the divergence of benthic and limnetic species, favoring more armor in the open-water species than in the littoral species.

Increased egg viability, male mating ability and mating frequency evolve in populations of D. melanogaster selected for resistance to cold shock

Karan Singh, N.G PRASAD

1A_302A-Adaptation
Saturday, June 21, 2014 9:00 AM-9:15 AM

Abstract

Ability to resist temperature shock is an important component of fitness of insects and other ectotherms. We selected replicate populations of Drosophila melanogaster for resistance to cold shock. We then investigated the evolution of larval survivorship, adult mortality, fecundity, egg viability and reproductive behaviour in these populations. Larval survivorship, adult mortality and fecundity post cold shock was not significantly different between selected and control populations. However, compared to the control populations, the selected populations laid significantly higher percentage of fertile eggs (egg viability) 24 hours post cold shock. Interestingly, the selected populations had higher mating frequency both with and without cold shock. After being subjected to cold shock, males from the selected populations successfully mated with significantly more number of non-virgin females and sired significantly more number of progeny compared to control males. Thus, our results, document the evolution of reproductive behaviour and egg viability in response to selection for cold shock resistance in D. melanogaster.

The evolution of fur colour: a marsupial perspective

Sarah Kerr

1A_302A-Adaptation
Saturday, June 21, 2014 9:15 AM-9:30 AM

Fur colour is critical in allowing mammals to camouflage themselves, and as such is subject to strong natural selective pressures. Mammals may also rely on their fur color to signal status, and to assist thermoregulation. Yet there has been very little quantification of fur coloration, and the few research studies of fur color and its evolution have largely overlooked the marsupials. This large group of mammals, which includes well-known species such as the red kangaroo and koala, offers some valuable opportunities to better understand the evolution of fur colour due to both their divergence from eutherian mammals approximately 160 million years ago, and because of some unusual ecological trends of the group. For example, most marsupial species are nocturnal, and they occur across a diverse range of environments, with many marsupial species inhabiting thermally extreme conditions. Some of the more interesting case studies include a species with olive-green fur colour; the green ringtail possum, and some populations of common brushtail possum that may have their fur colour determined by maternal diet.

Is it time to abandon the holey fitness landscape metaphor?

Bjørn Østman, Christoph Adami

1A_302A-Adaptation
Saturday, June 21, 2014 9:30 AM-9:45 AM

A holey fitness landscape consists of network of genotypes that has a fitness of one, and where all other genotypes have a fitness of zero. The metaphor of the holey fitness landscape has had success catching the imagination of many people, especially in the light of the success of Kimura's neutral theory of molecular evolution. Researchers and philosophers have embraced holey landscapes as an approximation for what is really going on with evolutionary dynamics and speciation, and have further suggested that it heralded the end of the adaptive landscape metaphor altogether.

The basic premise of the holey landscape model is that when the dimensionality is very high a neutral network appears on which populations can traverse wide areas of genotype space. Genotypes that have fitness lower than this neutral network can be assigned a fitness of zero, and the claim is that this approximation does not change the dynamics of adaptive evolution and speciation. Here we will explain why we think this conclusion is unwarranted. First, the original mathematical argument rests upon an assumption about the structure of fitness landscapes that has later been shown to be inaccurate. Second, we present some simple models that demonstrate that evolutionary dynamics of evolving populations in holey landscapes and rugged landscapes with peaks separated by valleys of intermediate fitness do not resemble each other. The ease with which populations can cross even very deep valleys in the fitness landscape, and the frequency at which populations will take this path rather than relying on a sparse neutral network, renders the holey landscape approximation tenuous. We therefore suggest that rather than abandoning the metaphor of fitness landscapes and the intuitions they afford us about evolutionary dynamics, we should relinquish the holey fitness landscape model.

Differential gene expression in ovarian tissue of sexual vs. asexual freshwater snails

Kyle McElroy, Deanna Soper, Laura Bankers, Jeffrey Boore, John Logsdon, Maurine Neiman

1A_302B-Sexual selection
Saturday, June 21, 2014 8:30 AM-8:45 AM

The rate of production of successful new asexual lineages from sexual ancestors is a primary determinant of the threat that sexual populations face from asexual invaders. As such, understanding the maintenance of sexual reproduction in natural populations requires characterization of the largely unstudied proximate mechanisms that underlie transitions to asexual reproduction in otherwise obligately sexual taxa. Here, we make initial strides towards identifying these mechanisms in Potamopyrgus antipodarum, an ancestrally sexual New Zealand freshwater snail distinguished by frequent transitions to asexual reproduction. The coexistence of phenotypically similar and closely related sexual and asexual P. antipodarum allows for powerful direct comparisons between sexual and asexual lineages without the potentially confounding effects of genetic background or population of origin. We used RNA-Seq to compare patterns of gene expression in ovarian transcriptomes from a diverse set of reproductively active sexual and asexual Potamopyrgus antipodarum. By characterizing gene expression differences between sexuals and asexuals we can identify candidate loci that are likely involved in and/or influenced by transitions to asexuality. Our initial analyses reveal extensive variation in gene expression and hundreds of transcripts expressed in consistently different ways between sexual and asexual P. antipodarum. We also found larger sets of differentially expressed transcripts between asexual lineages than between sexual lineages. Greater variability in expression profiles among asexual lineages may reflect a relaxation of expression demands in the absence of sexual reproduction and/or different sets of genetic factors involved with each transition to asexuality in P. antipodarum. We are currently annotating and performing gene ontology enrichment analyses to identify candidate genes for transitions to asexual reproduction. Identifying sets of genes associated with reproductive mode will help illuminate the proximate mechanisms that facilitate frequent transitions to asexual reproduction in P. antipodarum and provide a useful set of genomic resources for other researchers studying the maintenance of sex and evolution of asexuality in natural systems.

The multifaceted role of mating system on genome evolution.

Peter Harrison, Rebecca Dean, Alison Wright, Fabian Zimmer, Stephen Montgomery, Marie Pointer

1A_302B-Sexual selection
Saturday, June 21, 2014 8:45 AM-9:00 AM

Males and females in most vertebrates share nearly identical genomes. This shared genome produces sexually dimorphic phenotypes through sex-specific variation in gene expression levels. The genome-wide analysis of sex-biased genes makes it possible to connect phenotypic sexual dimorphism, the sexually antagonistic selection pressures that shape them, and the regions of the genome that encode them. To assess the link between complex phenotypic sexual dimorphism and global gene expression differences between males and females, we assembled and analysed transcriptomes from six species of birds that range from sexual monomorphism to extreme sexual dimorphism. This gradient of sexual dimorphism within a single clade makes it possible to directly test how sexual selection affects genome evolution and examine how sexually dimorphic phenotypes are encoded.

Congruent phenotypic and transcriptomic responses to testosterone in both sexes:implications for the evolution of endocrine-mediated sexual dimorphism

Christian L Cox, Daren Card, Audra Andrew, Todd Castoe, Robert Cox

1A_302B-Sexual selection
Saturday, June 21, 2014 9:00 AM-9:15 AM

Understanding how different phenotypes are produced from the same underlying genome is an important goal of evolutionary biology. Males and females share an autosomal genome, which may constrain the evolution of sexual dimorphism. Sex steroids, which are secreted in sex-specific fashion, can facilitate the development of sexual dimorphism by differentially regulating the expression of shared autosomal loci. However, it is generally unknown whether the evolution of endocrine-mediated sexual dimorphism is achieved primarily through sex differences in circulating hormones, or also through sex-specific tissue sensitivity to these hormones. We tested the effect of the sex steroid testosterone (T) on whole-organism growth and tissue-specific gene expression of the liver (a major integrator of energetics and growth) in males and females of a lizard (Anolis sagrei) with pronounced male-biased sexual size dimorphism. In two separate experiments on captive lizards, we administered either testosterone or placebo implants to (1) intact males and females at the age (5-6 mo) when sexual dimorphism first becomes pronounced, and (2) intact females and castrated males at an age (10-11 mo) when developmental trajectories are highly divergent between the sexes. T shifted both sexes toward a male-specific pattern of development by stimulating growth, bone elongation, resting metabolic rate, and utilization of fat reserves. The transcriptome of the liver was similarly impacted by T, which shifted both sexes towards a male-specific pattern of gene expression that included upregulation of insulin-like growth factor (IGF-1). Our results suggest that the evolution of endrocrine-mediated sexual dimorphism in growth and body size is achieved primarily through sex differences in circulating androgen levels, rather than through a reduction in sensitivity of females to androgens.

Can intralocus sexual conflict explain the maintenance of alternative reproductive tactics?

Agata Plesnar-Bielak, Anna Skrzynecka, Krzysztof Miler, Jacek Radwan

1A_302B-Sexual selection
Saturday, June 21, 2014 9:15 AM-9:30 AM
Intralocus sexual conflict (IASC) arises when fitness optima for a shared trait differ between the sexes; such conflict may help maintain genetic variation within populations. Sex-limited expression of sexually antagonistic traits may help resolve the conflict, but the extent of this resolution remains a subject of debate. In species with alternative male reproductive tactics, unresolved conflict should manifest more in a more sexually dimorphic male phenotype. We tested this prediction in the bulb mite (Rhizoglyphus robini), a species in which aggressive fighters, which possess sharply terminated and thickened legs used to combat other males, coexist with benign scramblers, which have unmodified, female-like legs. To do this, we established replicated lines in which we increased the proportion of each of the alternative male morphs using artificial selection.

After approximately 40 generations, the proportion of fighters and scramblers stabilized at >0.9 in fighter- and scrambler-selected lines, respectively. We then measured several female fitness components. As predicted by IASC theory, female fecundity and longevity was lower in lines selected for fighters and higher in lines selected for scramblers. This finding indicates that sexually selected phenotypes are associated with an ontogenetic conflict that is not easily resolved. Furthermore, we suggest that IASC may be an important mechanism contributing to the maintenance of genetic variation in the expression of alternative reproductive tactics.

Genetics of polymorphic male-male copulatory behavior in C. elegans

Matthew Rockman

1A_302B-Sexual selection
Saturday, June 21, 2014 9:30 AM-9:45 AM
We investigated a natural model for sexually antagonistic pleiotropy, male sexual behavior in the nematode C. elegans. In this species, the recent origin of hermaphroditism has relaxed selection on male function, allowing for the evolution of traits that are beneficial for hermaphrodites but detrimental to male fitness. We find substantial genetic variation for male-male sexual behavior in C. elegans. In some strains, males copulate with one another and deposit copulatory plugs on one another's excretory pores. We find that this phenotype is genetically complex but strongly influenced by a QTL that has a large effect in particular backgrounds. We mapped the major-effect locus to a single nucleotide polymorphism in a previously uncharacterized gene. This loss-of-function allele increases the attractiveness of the male excretory pore to other males. The affected gene is expressed in the one-cell renal system of both males and hermaphrodites, suggesting that its effect on males may be countered by an effect on hermaphrodite fitness.

How to train your symbionts: antagonistic coevolution and the evolution of transmission mode

Devin Drown, Michael Wade

1A_302C-Antagonistic Coevolution
Saturday, June 21, 2014 8:30 AM-8:45 AM
Here we develop a general theory for the coevolution of transmission mode and virulence in host-symbiont interactions. The fidelity of an interaction, determined by transmission mode, has a direct effect on the efficiency of selection. This new theory will combine models to understand the mechanisms of virulence evolution in structured populations. We find that interaction of virulence and genetic structure determines the balance between hosts escaping virulent pathogens and host-symbiont coevolution reducing virulence.

Examining the presence of a geographic mosaic of coevolution in the walnut aphid biological control system

Jeremy Andersen, Nicholas Mills

1A_302C-Antagonistic Coevolution
Saturday, June 21, 2014 8:45 AM-9:00 AM
The introduction of Trioxys pallidus to the walnut growing regions of California led to the successful control of the walnut aphid (Chromaphis juglandicola), which was once a primary pest. However, in recent years, spray treatments are again being used in mid-late summer. Central to the sustainability of classical biological control programs is the concept that co-evolutionary forces will provide permanent and sustainable control after a pest is reunited with its natural enemies. The geographic mosaic theory of co-evolution predicts a patchy landscape to exist, both with “hot-spots” where co-evolutionary forces are strong, and “cold-spots” where they are weak. This patchy landscape matches patterns observed in the walnut orchards of California, where some orchards require pesticide treatments and others do not. Using a population genomics approach to investigating the geographic mosaic of co-evolution (as per Vermeer et al. 2011) we have genotyped individuals of T. pallidus and C. juglandicola from geographically distinct parts of the walnut growing region of California. Our results indicate that Fst values for examined microsatellite loci vary by location as predicted by the geographic mosaic theory. With these results we plan to address what role the geographic mosaic of co-evolution may have in providing sustainable biological control services in the walnut aphid-T. pallidus system.

How Nonadditivity of Fitness Impacts Alters Selection for Resistance in a Multiple-Herbivore Community

Michael Wise

1A_302C-Antagonistic Coevolution
Saturday, June 21, 2014 9:00 AM-9:15 AM

Organisms in nature are simultaneously or sequentially subjected to multiple stresses with which they must cope to survive and reproduce. Can ecological and evolutionary responses to the stresses be sufficiently understood from looking at one stressor at a time? This question has been of particular interest in the field of plant-herbivore coevolution. Specifically, if the fitness impacts of two herbivores combine nonadditively (i.e., the total impact is not equal to the sum of the individual impacts), then any coevolution between the host plant and herbivores would be considered "diffuse." This supposition that nonadditivity of impact necessarily leads to diffuse coevolution has recently been questioned, however, which has resulted in a diminishing focus on how impacts of herbivores combine—even though it is recognized that most plants are attacked by a diverse community of multiple herbivores.

Here, I show with simple models how nonadditivity of herbivore impacts necessarily leads to diffuse selection on host-plant resistance. The models make three main predictions: 1) If two herbivores affect the same plant resource (e.g., they are both leaf chewers), then their effect will be additive if that resource was the one limiting plant fitness; 2) If two herbivores affect the same plant resource, but it takes damage by both herbivores to cause this resource to become limiting, then the impacts will combine synergistically (i.e., greater than additively); 3) If two herbivores affect different resources (e.g., one is a flower feeder and the other is a leaf feeder), then the impacts will combine antagonistically (i.e., less than additively).

I tested the third prediction in a field experiment using the herbivore community of the native herbaceous weed horsenettle (Solanum carolinense). Four levels of leaf damage (controlled with insecticide) were factorially crossed with five levels of simulated weevil damage to flower buds, and seed production was recorded. The fitness impact of the two types of damage combined significantly antagonistically. Specifically, the fitness impact of floral damage was greatest when foliar damage was minimal, and the fitness impact of leaf damage was greatest when floral damage was minimal. The results also suggest that selection for resistance against flower feeding would be negligible when leaf feeders are common, and vice versa. Such antagonistic impacts may explain why multiple herbivores may exist on a host plant, even though selection would favor increased resistance if any of the herbivore species fed alone on the plant.

Evolving virulence and defense in a symbiotic community.

Paul Nelson

1A_302C-Antagonistic Coevolution
Saturday, June 21, 2014 9:15 AM-9:30 AM

Symbiotic organisms are ubiquitous and can be integral to the survival, fitness, and development of their hosts. These relationships are not limited to microbial symbionts and their multicellular hosts, but can be extended to multiple multicellular organisms that rely on each other for resources, protection, or reproduction. Furthermore, interactions between a symbiont and its host are carried out in the context of the community of other symbionts affecting that host. These between symbiont interactions can range from facilitating to excluding other symbionts from the host. From fungi inhabiting plants to bacteria living in our guts, symbionts have been shown to protect their hosts against other, more damaging symbionts. Here we put forth a model which examines the evolution of two traits in a symbiont. First, the effect of a symbiont on host mortality, and second, the effect of a symbiont on other symbionts interacting with a host.

We make three key assumptions in this model. First, we assume that symbionts receive a reproductive payoff for harming their host. This tradeoff leads to an evolutionary stable level of virulence. Second, we assume that symbionts coinfecting a host share the costs of each other virulence. These shares costs can cause the evolutionary stable level of virulence to increase. Third, we assume that in defending a host a symbiont pays a reproductive cost while decreasing the impact of the shared costs of virulence on themselves. Together these three assumptions allow for the coevolution of two traits, virulence and defense, in multiple species of symbionts infecting the same host species.

The terms "defensive" and "mutualist" are often used synonymously, however examples exist of symbionts that inflict a high toll on the hosts they defend. Thus we pose the question: If virulence and defense are independent traits, does defense necessarily lead to mutualism? Additionally, we examine the role that defense plays in the stability of evolutionary stable levels of virulence when the levels of coinfection vary. We show that, while the evolution of defense does not necessarily lead to mutualism, defensive traits can temper selection for increased virulence due to multiple infections. This model shows that virulence and defense of the host must be looked at as two separate traits, and that defense can be a powerful moderator of virulence in a symbiotic community.

Experimental evolution of reduced antagonism: a role for host-parasite coevolution

Amanda Gibson, Kayla Mitman, Ian Gelarden, Curt Lively, Levi Morran

1A_302C-Antagonistic Coevolution
Saturday, June 21, 2014 9:30 AM-9:45 AM

Symbiotic relationships vary in nature from parasitism to mutualism, with shifts in degrees of antagonism occurring readily, even between populations of the same symbiont species. Ecological factors driving these shifts have been the subject of recent studies, which have demonstrated a need for further investigation of the genetic and evolutionary processes at play in the variation underlying symbioses. In the present study, we selected for reduced antagonism between the nematode Caenorhabditis elegans and its virulent bacteria Serratia marcescens. Infection by S. marcescens typically results in rapid mortality of C. elegans. We selected for a rare infection phenotype in which hosts survive and reproduce while hosting bacteria that are neither cleared nor lethal to the host. Our passaging scheme allowed the evolution of reduced antagonism to be compared under conditions of reciprocal symbiont evolution (coevolution) vs. independent evolution of both symbionts, in which selection on one partner was performed with a non-evolving partner population. Quantification of infected host fecundity after 20 generations of selection demonstrates that reduced antagonism between host and bacteria did evolve. This was true, however, only for symbionts selected under conditions permitting coevolution. Selection on either partner alone, with a non-evolving partner population, did not increase fitness of infected hosts relative to the ancestor. Our results implicate coevolution, in which interacting partners reciprocally evolve, as a key process driving reductions in antagonism between hosts and parasites.

Life-history, Selection and Effective Population Size shaping Evolution during Colonization – Lessons from Drosophila melanogaster.

Marta Santos

1A_303-Life History
Saturday, June 21, 2014 8:30 AM-8:45 AM

Consider the scenario where a population migrates to a new environment: it encounters qualitatively novel nutrition (possibly including periods in which it starves) and its effective population size is reduced in the course of migration or as a result of an initial lack of adaptation. How will the population's life history evolve and how will effective population size affect its evolutionary response to this new environment? If this population survives and its descendants migrate back to their ancestral environment, how will this preceding period of adaptation to a new environment affect its initial life history, upon return to ancestral conditions? To tackle these issues we used a highly replicated system of Drosophila melanogaster populations of known differentiated histories on which selection (both forward and reverse) was imposed with contrasting population sizes.

Genetic basis of ageing evolution under differential extrinsic mortality in a nematode

Bjorn Rogell, Hwei-yen Chen, Severin Uebbing, Alexei Maklakov

1A_303-Life History
Saturday, June 21, 2014 8:45 AM-9:00 AM

Ageing evolves ultimately because the force of natural selection declines with age. On the proximate level, ancient nutrient-sensing signaling pathway insulin/insulin-like pathway (IIS) and stress response pathway SKN-1/Nrf2 have been shown to play a key role in ageing, longevity and stress response: down-regulated IIS signaling and up-regulated SKN-1 expression increase longevity and stress resistance. While the importance of these pathways in regulation of longevity and stress resistance has been strongly supported by knockdown and mutant single-gene studies, their role in evolutionary response to selection on ageing and stress resistance remains unclear because these pathways affect multiple physiological and life-history traits that interact and tradeoff with each other. Here we combine experimental evolution approach in a nematode Caenorhabditis remanei with genome-wide next-generation RNA sequencing to show simultaneous evolution of up-regulated gene expression in both IIS and SKN-1 pathways in long-lived lines that also have high fecundity and increased stress resistance. We recently showed experimentally that populations of C. remanei evolved to live shorter under high extrinsic mortality, but only when mortality was applied haphazardly. On the contrary, when extrinsic mortality was condition-dependent (caused by heat-shock), populations experiencing the same high mortality rate evolved greater longevities. Remarkably, stress-resistant and long-lived worms were also more fecund. Our current data shows that an unusual combination of concerted constitutive up-regulation of IIS and SKN-1 pathways underlines the evolution of "superworms". These results suggest that evolution of gene expression in signaling pathways that control key life-history traits, such as longevity and fecundity, involves a fine balance between expression of genes that increase fecundity and those that increase stress resistance and intrinsic longevity. We discuss several possibilities that could constrain evolution of such "superworms" in nature.

Genomic response to 30-years of selection for increased lifespan reveals increased immunity as correlated trait

Daniel Fabian, Peter Klepsatel, Martin Kapun, Bruno Lemaitre, Robert Arking, Christian Schlötterer

1A_303-Life History
Saturday, June 21, 2014 9:00 AM-9:15 AM

Evolutionary theory posits that aging evolves by mutation accumulation and/or antagonistic pleiotropy. However, to date, the precise identity of the genes and molecular polymorphisms that underlie the evolution of aging and longevity remains poorly understood. Here, we have analyzed the genomic basis of the evolution of longevity in Drosophila melanogaster by applying whole-genome next-generation resequencing to a set of longevity selection and control lines initiated by Leo Luckinbill and Bob Arking about 30 years ago. Using population genetic and statistical tools, we have identified candidate genes whose patterns of differentiation have most likely been shaped by selection. Interestingly, among the candidates, we found strong evidence for a functional enrichment of immunity genes, particularly those involved in the defense response to fungi. To test whether this pattern is functionally relevant and real, we measured survival of selected and control flies upon pathogenic challenge with the fungus B. bassiana, the gram-positive bacterium E. faecalis, and the gram-negative bacterium E. carotovora. We found that long-lived lines are indeed significantly more resistant to all three pathogenic infections than controls. As predicted, the age-dependent decline in survival upon infection with B. bassiana and E. faecalis was much steeper in control flies than in long-lived selected flies. Moreover, RT-qPCR results further indicated that selection and control lines differ in their age-dependent expression for several immunity genes, including antimicrobial peptides, again confirming functional differentiation between selection and control lines for immunity. Our results thus establish a causal link between the evolution of longevity and improved immune function at old age.

EVOLUTION OF INCREASED ADULT LONGEVITY IN DROSOPHILA MELANOGASTER POPULATIONS AS CORRELATED RESPONSE FOR ADAPTATION TO LARVAL CROWDING

Vinesh Shenoi, N.G PRASAD

1A_303-Life History
Saturday, June 21, 2014 9:15 AM-9:30 AM
For holometabolous animals, such as fruit flies, larval crowding is one of the most important stress factors, which in-turn induces both nutritional limitation and increased exposure to toxic waste products during development. Larval crowding has been shown to be capable of selecting for a wide range of traits, including larval tolerance to toxic waste products, pre-adult development time, survival rate, adult body size, fecundity etc. It also affects patterns of resource allocation to reproduction versus somatic maintenance. Hence it is very likely that adaptation to larval crowing could potentially affect rates of aging through correlated selection for environmental stress resistance and/or its effects on adult body size. We addressed this issue by studying a set of large, out-bred populations of Drosophila melanogaster, experimentally evolved for adaptation to larval crowding for more than 85 generations in the laboratory conditions. We looked at the adult longevity of flies from both selected and un-selected populations when they were grown at different levels of larval density. We found that the selected populations have evolved increased longevity when compared to the control populations, when they were grown in crowded condition but had comparable longevity, when grown under non-crowded conditions. Our results indicate the evolution of plasticity of resource allocation to life-history traits, such as longevity.

Jumping genes and life history: De novo transposable element insertions respond to selection for accelerated and delayed development times

Kate Hertweck, Mira Han, Lee Greer, Mark Phillips, Michael Rose, Joseph Graves

1A_303-Life History
Saturday, June 21, 2014 9:30 AM-9:45 AM
A wealth of scientific literature has speculated on the response of both the genome and organism to proliferation of transposable elements (TEs, or jumping genes). In particular, the relationship between TEs and aging has been addressed by both theory and empirical studies. Theory suggests TEs may contribute to life history features such as aging, by introducing detrimental somatic mutation. However, a comparison TEs between organisms indicate the number of copies may increase, decrease, or have no effect on lifespan, depending on the model system and type of TE investigated. Long-term studies in experimental evolution allow explicit testing of such hypothesis using replicated populations. Our data represent pooled population genome-wide resequencing from Drosophila selected for both delayed and accelerated reproduction times and development. Our previous results indicate that insertion frequencies of ancestral TEs (i.e., annotated in the fully sequenced reference genome) respond fairly consistently to selection. For the present study, we use two independent approaches (PoPoolation TE and RelocaTE) to identify de novo TE insertions. We find that the magnitude of TE proliferation varies among multiple families of LTRs, LINEs, and DNA transposons. We present methodological considerations for interpreting such results.

Exploring patterns of symbiont diversity in natural pea aphid populations

Andrew Smith, Kerry Oliver, Jacob Russell

1A_304-Symbiosis
Saturday, June 21, 2014 8:30 AM-8:45 AM
Symbioses that involve maternally transmitted bacteria have proven to be highly prevalent in the natural world and serve as important sources of adaptive novelty. Many of these symbionts are facultative, found at intermediate levels within host populations and confer unique host-level phenotypes that favor both the host and bacterium under certain conditions. High levels of symbiont diversity in some host populations in nature are likely maintained by a heterogeneous environment over space and time. Understanding adaptive evolution will require identification of the environmental forces that shape symbiont-, and by extension, phenotypic- variation in the wild. The pea aphid, Acyrthosiphon pisum, and its diverse microbiome serve as a model to study the dynamics and diversity of heritable symbiosis. All seven symbionts have been implicated, to some extent, in defense against natural enemies. Recent surveys reveal that the frequencies of these symbiont species differ in relation to host plant, geography and, to some extent, fluctuating natural enemy pressures. Yet multiple strain variants exist for several symbiont species, and the known variation in effects conferred by different strains, suggest a need to track symbiont genotype along with species prevalence. Toward this end we have begun to investigate the genetic variation of Hamiltonella defensa and its associated bacteriophage over several scales, spanning multiple years, regions, and host race populations. Our findings reveal variation in strain types across regions and, potentially, seasons. They also show non-random associations between H. defensa/bacteriophage strains and other co-infecting species, suggesting the potential for symbiont-symbiont mutualisms or beneficial effects of specific co-infections at the host level. Finer-scale tracking currently underway will allow us to correlate symbiont strain diversity with natural enemy pressure, providing unprecedented insight into the natural dynamics of defensive symbiosis.

Environmental context matters: the impact of microbial symbiont on invasive insect host Megacopta cribraria is mediated by host plant

Jannelle Couret, Lynn Huynh-Griffin, Ivan Antolic-Soban, Tarik Acevedo, Nicole Gerardo

1A_304-Symbiosis
Saturday, June 21, 2014 8:45 AM-9:00 AM
Host-microbe interactions are ubiquitous and occur on a sliding scale from parasitic to mutualistic. The costs and benefits of maintaining symbioses can be altered by environmental and ecological context. The impact of contextual factors remains unknown for most symbioses, especially during range expansion or invasion. In such cases, microbes may enhance or constrain the use of novel resources by hosts. We sought to test the hypothesis that

the impacts of a microbial symbiont on its host are contingent on the environmental and ecological context of plant diet. We examined sap-feeding insect, Megacopta cribraria, which in 2009 invaded North America through Atlanta, Georgia. Since this time the range of M. cribraria has dramatically expanded throughout the southeastern United States. M. cribraria harbors an obligate bacterial symbiont in its gut that can be experimentally removed to assess the impact on host life-history traits. In the native range, it has been shown that without these symbionts, insect host development is delayed. We assessed host life-history traits, including development time, survival, and size, of these newly invaded M. cribraria under two potential host plants in field and laboratory experiments. We found life-history trait differences in insects reared with and without microbial symbionts were mediated by the host plant context. Our results support the hypothesis that the host-microbe interaction is environmentally contingent. These findings have broad implications for our understanding of the nature of symbiosis.

Holarctic biogeography of a widespread host-symbiont association

Bronwyn Williams, Frank Anderson

1A_304-Symbiosis
Saturday, June 21, 2014 9:00 AM-9:15 AM
Cophylogenetic analyses of host-symbiont communities provide insight into the history of the association as well as patterns and processes of evolution within each taxonomic component. Unfortunately, challenges arise when a robust phylogeny or fossil evidence is lacking for either host or symbiont. In such cases, cross-validation of host and symbiont phylogenies in a biogeographic framework may provide valuable resolution to coevolutionary patterns. Astacoidean crayfishes are ecologically important and highly visible components of freshwater habitats across much of the Holarctic. Despite numerous studies on astacoidean phylogeny, several deeper relationships remain unclear. Astacoidean crayfishes are host to a group of obligate ectosymbiotic clitellate annelids called branchiobdellidans (crayfish worms). The obligate nature of the symbiosis suggests a shared evolutionary history between host and symbiont. Our objective is to reconstruct cophylogenetic relationships of astacoidean crayfishes and branchiobdellidans to elucidate the evolutionary history of both host and symbiont, as well as the evolutionary history of the symbiosis. We used a supermatrix approach incorporating publicly available data and fossil evidence to estimate a time-calibrated crayfish phylogeny, and a combination of four genes (COI, 16S, 28S, and 18S) and transcriptome data to reconstruct the branchiobdellidan phylogeny. We employed maximum-likelihood and Bayesian methods (Lagrange, BioGeoBears) to reconstruct the historical biogeography of the crayfish and approximate Bayesian computation (Coala) to infer the coevolutionary history of the crayfish/branchiobdellidan symbiosis. Preliminary results show that our well-supported branchiobdellidan phylogeny provides valuable insight to the biogeography of their crayfish hosts.

Host evolution and ecology govern community assembly of the gut microbiome in lemurs

Erin McKenney, Allen Rodrigo, Anne Yoder

1A_304-Symbiosis
Saturday, June 21, 2014 9:15 AM-9:30 AM
Host evolution and ecology govern community assembly of the gut microbiome in lemurs Nearly every aspect of mammalian life is linked in some way to microbes. Bacteria promote tissue development, train the immune system, and affect host behavior. In addition, gut microbes facilitate fiber digestion—thereby not only impacting nutrition across an individual's lifespan, but also driving mammalian speciation by enabling novel adaptive feeding strategies. Yet little is known of the ecological rules that govern the trillions of microbial symbionts that impact host fitness. We examined the relationship between host factors and gut microbiota characteristics in three lemur species (frugivorous Varecia variegata, generalist Lemur catta, and folivorous Propithecus coquereli) to determine to what extent host lineage, diet, and life stage shape gut community membership. Fecal samples were collected from captive lemur mothers and infants at 6 life stages from birth to weaning. DNA was extracted and a region of bacterial 16S rDNA was sequenced on the Illumina MiSeq platform using protocols from the Earth Microbiome Project. We found that gut colonization proceeds differently in lemur species with differing dietary and ecological profiles: successional trajectories proceed at rates that correspond with infant precocity in each species. Specifically, leave-eating P. coquereli infants' gut microbiota composition resembles the adult climax community at an earlier life stage (the introduction of solid foods) compared to L. catta and V. variegata infants (whose communities do not stabilize until they consume solid foods on a daily basis). Radiation within specific bacterial lineages further implies that gut microbial communities have evolved in response to, or in conjunction with, specific lemur feeding strategies.

Interactions between host phylogeny and biogeography structure sponge-associated microbial communities

Bob Thacker, Cole Easson

1A_304-Symbiosis
Saturday, June 21, 2014 9:30 AM-9:45 AM
Sponges (phylum Porifera) can host diverse and abundant communities of microbial symbionts that make critical contributions to host metabolism. Although observations suggest that these communities may be transferred among hosts through a combination of vertical and horizontal transmission, direct evidence of transmission is rare for most symbiotic taxa. On large scales, we predicted that vertical transmission would be correlated with host phylogeny, while horizontal transmission would be correlated with geographic location. In collaboration with the Earth Microbiome Project (EMP), we investigated whether host phylogeny, geographic location, or interactions between these factors impact symbiotic microbial community structure. We used high-throughput pyrosequencing of the V4 region of the 16S ribosomal RNA gene to assess community structure in 90 specimens representing 20 sponge species. As expected, the richness of operational taxonomic units varied significantly among

host species. A significant interaction between host phylogeny and geography explained 62% of the observed variance in microbial community dissimilarity and 69% of the observed variance in microbial phylogenetic dissimilarity, suggesting that interactions between vertical and horizontal transmission play a major role in structuring these symbiotic communities.

Genetic basis of alkaloid resistance in harlequin toads and poison frogs

Rebecca Tarvin, Juan Santos, Lauren O'Connell, Harold Zakon, David Cannatella

1A_305A-Toxins
Saturday, June 21, 2014 8:30 AM-8:45 AM
Chemical defense using alkaloids has evolved multiple times in amphibians, including newts (Cynops, Taricha), toads (Atelopus, Melanophryniscus), and poison frogs (Mantella, Dendrobatidae). Tetrodotoxin (TTX, in Taricha, Cynops, and Atelopus) and diverse lipophilic alkaloids (e.g. pumiliotoxin, PTX, in many dendrobatids and mantellids) bind to and disrupt the function of voltage-gated sodium channels, a family of genes that encode proteins responsible for muscle and nerve function. Explaining alkaloid resistance is important because some predators evolve resistance to prey alkaloids, and prey organisms must be resistant to their own alkaloids. Alkaloid resistance can be traced directly to amino acid (AA) substitutions in sodium channels at sites where the alkaloids bin--d. AA substitutions that contribute different levels of TTX resistance have been identified in garter snakes (exposed to TTX when consuming Taricha newts) and in pufferfish (exposed to their own TTX defenses). Using Next Generation Sequencing we found AA substitutions at homologous sites in two sodium channels of Atelopus, as well as at a novel site unknown in other TTX-defended organisms. Convergence in the mechanism of alkaloid resistance suggests that the binding sites of alkaloids such as PTX can be identified by phylogenetic analysis of AA substitutions in alkaloid-defended and non-defended clades. We are analyzing sequences of several species of poison frogs to locate the binding site of PTX (currently unknown) as well as AA substitutions that may contribute to PTX resistance.

Auto-toxicity and the evolution of the muscular voltage-gated sodium channel in Phyllobates poison frogs

Roberto Márquez, Adolfo Amézquita

1A_305A-Toxins
Saturday, June 21, 2014 8:45 AM-9:00 AM
The genetic basis and origin of phenotypic changes are among main drivers of a lineage's ability to respond to selection pressures. Do these changes arise from de novo mutation, or does natural selection favor preexisting variants (i.e. standing variation) that become beneficial under new selective regimes? Toxic organisms must evolve mechanisms to avoid self intoxication, however, these mechanisms usually have costs. For instance, resistance to neurotoxins many times involves modifications of ion-transport proteins, which often negatively influence the performance of such proteins. Hence, although preexisting toxin-resistant variants can allow for a faster response to changes in selective regimes, they are expected to have lower probabilities of persistence in a population before changes in selective regimes make them beneficial, due to their deleterious effects. Here, we examine the evolution of resistance to auto-toxicity in Phyllobates poison frogs, bearers of batrachotoxin (BTX), possibly the most potent known neurotoxin of natural origin, which covalently binds to voltage-gated sodium channels, rendering neurons useless. We sequenced regions of the muscular voltage-gated sodium channel involved in BTX binding for several Phyllobates and closely related species, and found four amino acid substitutions at BTX binding sites present in Phyllobates species. Three of these originated simultaneously with BTX bearing, while the remaining one originated before BTX, suggesting that standing variation and de novo origination have contributed to batrachotoxin resistance in Phyllobates frogs.

A native root herbivore drives the evolution of defensive latex metabolites in nature

Meret Huber, Daniella Triebwasser-Freese, Michael Reichelt, Christian Schulze-Gronover, Jonathan Gershenzon, Matthias Erb

1A_305A-Toxins
Saturday, June 21, 2014 9:00 AM-9:15 AM
Roots produce an enormous diversity of secondary compounds with potential activity against below ground herbivores. Yet, evidence that root feeding insects can drive the evolution of defensive metabolites in nature is lacking. We studied the interaction of the common dandelion (Taraxacum sect. Ruderalia) and its native root herbivore, the white grub Melolontha melolontha, by i) measuring the abundance of defensive latex secondary metabolites in dandelion populations under different root herbivore pressure in nature, ii) testing the observed patterns under controlled conditions in the glasshouse and a common garden and iii) using a reverse genetic approach to verify the importance of latex secondary metabolites for root herbivore resistance. We found that taraxinic acid glucoside (TA-G), a sesquiterpene lactone glycoside, is highly enriched in the dandelion latex. Natural dandelion populations growing under high M. melolontha density in the field produced more TA-G than local and regional controls under low root herbivore pressure. The concentration of TA-G among different dandelion genotypes was positively correlated to plant performance upon root herbivory and negatively correlated with larval growth under controlled conditions. Silencing of germacrene-A synthase, a key biosynthesis step of sesquiterpene lactones by RNA interference (RNAi) strongly reduced TA-G levels in the plant, and we are currently testing whether these lines are less resistant against M. melolontha. Taken together, our results provide first evidence that a native root herbivore may have the potential to drive the evolution of defensive metabolites in nature.

Transcriptome phylogeny and evolution of host chemical sequestration within the lichen moths (Insecta: Lepidoptera: Erebidae)

Clare Scott, Susan Weller, Jennifer Zaspel

1A_305A-Toxins
Saturday, June 21, 2014 9:15 AM-9:30 AM
The lichen moths are a diverse and cosmopolitan tribe (Lepidoptera: Erebidae: Arctiinae: Lithosiini) composed of over

3,000 described species. Their common name arises from the hypothesized larval host: lichens. Lithosiini is the most diverse lineage of lichen feeding Lepidoptera, and the only one known to be able to sequester toxic lichen phenolics. It is hypothesized that the lichen moths use these chemicals to defend the larval, pupal, and adult stages from predators and parasitoids. However, the origin of this defensive strategy within the tribe is unknown. Further study of the evolution of chemical sequestration in this charismatic group has been hindered by the lack of a resolved tribal phylogeny. Studies examining the relationships among the genera of Lithosiini using either morphological or molecular data have been unable to recover the deeper relationships of the tribe. Here we present the first use of next generation sequencing data (transcriptomes) within Lithosiini to construct a phylogenetic hypothesis. This phylogeny is used to assess the evolutionary relationships among the genera and the monophyly of 4 of the 7 subtribes and one generic group. In addition, the metabolic profiles of taxa represented in the phylogeny are surveyed for the presence of lichen phenolics using LC-MS. A hypothesis of the evolution of chemical sequestration and lichen feeding in Lithosiini is formed based on these data.

Sea slugs have their cake and eat it too: a phylogenetic analysis of sponge-eating nudibranchs and the defense chemicals they take and reuse

Shayle Matsuda, Terrence Gosliner

1A_305A-Toxins
Saturday, June 21, 2014 9:30 AM-9:45 AM
Brightly colored sea slugs that live in the most biodiverse and threatened coral reefs on the planet have evolved the ability to take their prey's toxic chemical compounds and use them for their own defense. Glossodoris nudibranchs (Mollusca: Gastropoda: Opisthobranchia: Chromodorididae) feed on sponges that synthesize sesterterpenoid defensive chemical compounds. Sesterterpenoid compounds exhibit a wide range of biological properties that aid in organism defense and have biomedical potential, including cytotoxicity, antimicrobial, ichthyotoxicity, antitumor, and anti-HIV. Nudibranch tooth morphology has traditionally been used for classification and sponge prey from many species has been well documented, but with recent advances in molecular systematics, many of these relationships have changed. A recent mitochondrial phylogeny of the Chromodorididae revealed many misplaced Glossodoris. While chemical compound data remains accurate for species, conclusions drawn about the types of compounds found within the genus as a whole contain inaccuracies. These discrepancies emphasize the necessity of a well-resolved phylogeny prior to the examination of chemical sequestration in nudibranchs. In this study, 50 individuals comprising 18 taxa were used to build a more robust phylogenetic tree of Glossodoris. Molecular phylogenetic analyses were performed on two mitochondrial genes (COI and 16s) and one nuclear gene (28s), and maximum likelihood and Bayesian statistical analyses were conducted to support the hypothesized evolutionary relationships within Glossodoris. Additionally we examine preexisting chemical profiles for current and previously identified Glossodoris based on morphological data alone. Because nudibranchs are stenophagus feeders, we hypothesize that Glossodoris nudibranchs that are more closely related with similar prey species will share similarities in tooth morphology and chemical profile. These results will provide insight into the evolution of chemical defense sequestering in nudibranchs, allow for a deeper understanding of coevolution and prey choice of Glossodoris nudibranchs, and aid in prospecting promising chemical compounds for biomedical applications.

How does pollination mutualism affect the evolution of prior self-fertilization? A model

Clotilde Lepers, Mathilde Dufay, Sylvain Billiard

1A_305B-Plant Mating Systems
Saturday, June 21, 2014 8:30 AM-8:45 AM
The mode of pollination is often neglected regarding the evolution of selfing. Yet the distribution of mating systems seems to depend on the mode of pollination, and pollinators are likely to interfere with selfing evolution, since they can cause strong selective pressures on floral traits. Most selfing species reduce their investment in reproduction, and display smaller flowers, with less nectar and scents (referred to as selfing syndrome). We model the evolution of prior selfing when selfing rate affects both the demography of plants and pollinators and the investment of plants in pollination. Including the selfing syndrome in the model allows to predict several outcomes. According to inbreeding depression and selfing syndrome kinetic, plants can evolve either towards complete outcrossing, complete selfing, or to a stable mixed-mating system, even when inbreeding depression is high. We predict that the evolution to high selfing rates could lead to evolutionary suicides, highlighting the importance of merging demography and evolution in models. The consequence of the selfing syndrome on plant-pollinator interactions could be a widespread mechanism driving the evolution of selfing in animal-pollinated taxa.

Does separation between sexual organs affect mating? A case study from the alpine primrose Primula halleri

Lirui Zhang, Michael Nowak, Jurriaan de Vos, Elena Conti

1A_305B-Plant Mating Systems
Saturday, June 21, 2014 8:45 AM-9:00 AM
Bankground: Floral design profoundly affects reproductive strategies. In self-compatible plants, variation in the distance between sexual organs, either within or between individuals, can enable a mixed mating strategy. The ability to reproduce via both outcrossing and selfing is thought to be beneficial for reproductive success and species survival under variable ecological conditions, such as those experienced by alpine plants. In the alpine, self-compatible Primula halleri, anther-stigma separation (herkogamy) decreases during floral development and differs between the mature flowers of distinct individuals. We investigate the relationship between herkogamy and mating system by comparing outcrossing rates among plants with different herkogamy levels in mature flowers. Methods: Levels of separation between male and female sexual organs of mature flowers were measured in the field for four populations of P. halleri from Switzerland by assigning each plant to one of two herkogamy classes: 0-1 mm or >1 mm. Eleven

microsatellite loci were used to estimate outcrossing rates with both population-structure and progeny-array approaches. The latter also allowed us to infer individual-level outcrossing rates. Finally, we statistically compared outcrossing rates among plants with different herkogamy levels. Results: At the population level, outcrossing rates (t) range from 0.690 to 0.750, based on the population-structure approach, and from 0.684 to 0.718, based on the progeny-array approach. At the individual level, multilocus outcrossing rates (tm) range from 0.017 to 1 across all populations, with values of 0.017 to 1 in the low-herkogamy group (0-1 mm) and 0.462 to 1 in the high-herkogamy group (>1 mm). Three out of four populations show significantly broader variation of outcrossing rate in the low-herkogamy group compared to the high herkogamy group. Conclusions: The results show that all studied populations exhibit intermediate outcrossing rates (0.2 P. halleri. The low-herkogamy group has more individuals with low outcrossing rates (tm

Is self-pollination an evolutionary dead end? The evolution of mating systems in Erythranthe section Paradantha (Phrymaceae)

Naomi Fraga

1A_305B-Plant Mating Systems
Saturday, June 21, 2014 9:00 AM-9:15 AM

Erythranthe section Paradantha (Phrymaceae) has a tremendous amount of floral diversity among a small number of closely related species. The section includes species that exhibit bicolored floral patterns, flower color polymorphisms, and variation in corolla size, degree of herkogamy, and nectar guide patterns. Twelve species included in the study have large showy flowers that have strong bilateral symmetry, complex nectar guide patterns, and are inferred to be primarily outcrossing. Four species included in the study are inferred to be primarily self-pollinating based on flowering time, size of reproductive parts, flower duration, and observations of self pollination. These four putatively self-pollinating species (Erythranthe androsacea, E. calcicola, E. rubella, and E. suksdorfii) have relatively large range sizes when compared with the remaining taxa included in the study. In this study I expand previous sampling, and utilize sequence data from nuclear ribosomal ITS and three non-coding regions from the chloroplast genome (petA-psbJ, psbD-trnT, rpl32-trnL) to examine the evolution of mating systems and its implications on diversification and range size for species in Erythranthe section Paradantha.

The breakdown of self-incompatibility in a range expansion

Francisco Encinas-Viso, John Pannell, Andrew Young

1A_305B-Plant Mating Systems
Saturday, June 21, 2014 9:15 AM-9:30 AM

Self-incompatibility (SI) is a crucial and effective mechanism to avoid self-fertilization in flowering plants. It helps to prevent the negative effects of inbreeding and it has evolved several times. The SI mating recognition system is usually encoded by one locus (the S locus) with numerous alleles that are maintained by negative frequency-dependent selection. Inbreeding depression is probably the main factor avoiding the invasion of self-compatibility (SC), given that selfers have an automatic advantage over outcrossers. Previous theoretical studies have shown that a reduction of inbreeding depression and mate availability (i.e. low number of S alleles) will facilitate the breakdown of SI and therefore the invasion of SC. During a range expansion (a series of founder events) we could expect that SC might be favoured by increasing selection for reproductive assurance. However, we still do not know what ecological and evolutionary conditions are needed for the breakdown of SI in a range expansion. Here, we develop a spatially explict individual-based simulation model of a 2D range expansions to explore this and other questions related to the breakdown of SI and the roles of purifying and balancing selection on the evolution of plant mating systems.

Diversification and Speciation in the Ethiopian Highlands: Insights from a Radiation of Endemic Frogs

Xenia Freilich, Marc Tollis, Stephane Boissinot

1A_306A-Biodiversity
Saturday, June 21, 2014 8:30 AM-8:45 AM

Ethiopia contains the most extensive continuous complex of mountainous habitats of Africa. The fauna and flora found in the Ethiopian highlands is unique and, for this reason, Ethiopia is considered one of the planet's biodiversity hotspots. The highest level of endemism is found in anurans, with 40% of the Ethiopian species being endemic to this country. The Ethiopian highlands are split in two uneven halves by the Great Rift Valley. Presently the valley floor is a very hot dry land and, as such, acts as a dispersal barrier for highland species. In spite of the general assumption that the Great Rift Valley has played a major role in shaping the biodiversity of the county, its impact on the evolutionary history of Ethiopian taxa it is not fully understood. We decided to examine the timing of anuran diversification in Ethiopia as well as the role geomorphological features, such as the Great Rift Valley, have played in the diversification of Ethiopian anurans. Frogs of the genus Ptychadena have experienced an evolutionary radiation in these highlands. Thus, this group provides an excellent opportunity to study the process of speciation in this important biogeographic area. Two mitochondrial and four nuclear genes were sequenced in more than 300 frogs collected across Ethiopia. Using a Bayesian species delimitation approach, we identified 8 genetically isolated populations which may represent separate cryptic species. We resolved the phylogeny of Ethiopian highland Ptychadena using a species tree approach and determined that species group on the phylogeny according to their habitat preference. We propose that the diversity of Ethiopian Ptychadena results from an early phase of specialization to distinct elevations followed by a phase of ecological diversification within each elevational range. We estimated that the early phase of diversification of Ethiopian Ptychadena probably occurred in the late Miocene and the most recent speciation events in the late-Pliocene or Pleistocene. Our analysis suggests that the south-eastern highlands and the tropical forests of the south-west have acted as speciation centers. From these centers, some Ptychadena species have recently spread across the Great Rift Valley, resulting in trans-Rift distributions, while others have remained limited to one side of the Valley, possibly because of their specialization to high elevations.

The tangled evolutionary histories of Madagascar's small mammals

Kathryn Everson, Sharon Jansa, Steven Goodman, Link Olson

1A_306A-Biodiversity
Saturday, June 21, 2014 8:45 AM-9:00 AM

Madagascar is a natural model system for studying evolution and diversification. It has a long history of isolation (88 million years) and supports remarkable levels of both species richness and endemism, including 100% endemism of its native non-volant mammals. This striking degree of endemism can be explained by infrequent, asynchronous colonization events followed by adaptive radiation. Madagascar's two small mammal lineages, tenrecs (Tenrecidae) and nesomyine rodents (Nesomyinae), each originated from a single common ancestor between 18-65 MYA and have since undergone spectacular diversification. Tenrecs include semiaquatic, semifossorial, and scansorial ecomorphologies; heterotherms as well as homeotherms; velvety pelage to stout, barbed, detachable spines; and body sizes spanning three orders of magnitude (2-2000 grams). Similarly, nesomyine rodents vary widely in size and morphology and have radiated to occupy arboreal, terrestrial, and semifossorial niches. Because tenrecs colonized Madagascar about 10 million years before nesomyines, it has been hypothesized that their adaptive radiation constrained the subsequent diversification of nesomyines. We tested this by comparing rates of diversification in the most speciose genus of tenrec (Microgale spp.) and nesomyine (Eliurus spp.) based on multiple unlinked molecular markers. Our results reveal a complex historical relationship between the two taxa and improve our understanding of small mammal evolution on Madagascar.

Zoogeography of genus Salvelinus in Kamchatka Peninsula

Ekaterina Bocharova, Evgeny Esin, Grigory Markevich, Nikolai Mugue

1A_306A-Biodiversity
Saturday, June 21, 2014 9:00 AM-9:15 AM

Dolly Varden Charr is known to have a continuous distribution range from Beringia to the Amur mouth. At the same time, distribution area of Arctic Charr is divided by Kamchatka peninsula. Ways of Kamchatka lake colonization are obviously associated with invasion of the anadromous form of charrs to the South of the peninsula by the end of Pleistocene last glacial period. We assumed that Arctic Charr could colonize Kamchatka peninsula by two possible ways: from the Arctic Ocean through Beringia and from the northern part of the Okhotsk Sea. Charrs were able to reach the Okhotsk Sea from the Arctic basin by the temporary water path, which was formed during glacier melting in the Kolima and the Indigirka River headwaters.

Six postglacial Kamchatka lakes were selected for the study of charrs fauna. These lakes are located along the both sides of Kamchatka peninsula ridge at the length of 720 km. Recently the Arctic morphotype local populations were described in the two neighbor lakes at the southern part of Kamchatka and fauna of the other four lakes was not previously studied. D-loop and Cytochrome B region sequences of the charrs were analyzed to clarify their taxonomic positions.

Lacustrine charrs were found to be divided into 2 groups using morphometric and meristic characters in all the lakes. The first group individuals were associated with Arctic charr and had a greater number of gill rakers and pyloric caeca, as well as increased antedorsal and anteventral distances. The second group was associated with common Kamchatka Dolly Varden. Salvelinus species were probably isolated during all the period of sympatric habitation in these lakes.

MtDNA analysis showed that the fishes inhabiting the Dal'nee Lake, the Nachikinskoe Lake, the Dvuchjurtochnoe Lake, and the Ayaogitgyn Lake are phylogenetically close to Arctic charr from Chukotka and Alaska or to common Dolly Varden. Also we revealed the mtDNA introgression between Dolly Varden and Arctic charr in the Sokoch Lake and the Kopil'ye Lake.

Findings of Arctic Charr in the south of the peninsula and the complete lack of intermediate population at the both coasts of Kamchatka is a mysterious zoogeographical incident, which confirms that this area of mountain lakes in Kamchatka is yet underexplored.

The total inventory of Cuatro Ciénegas (Coahuila, Mexico): Patterns and evolutionary causes of high diversity of an oligotrophic aquatic ecosystem

Valeria Souza, Luis Enrique Eguiarte

1A_306A-Biodiversity
Saturday, June 21, 2014 9:15 AM-9:30 AM

Cuatro Ciénegas (CC) Basin is a very diverse and unique site, despite its high nutrient limitations. Previous metagenomic studies compared the taxonomical and functional diversity of microorganisms in four sites within the basin, finding large and distinct diversity in each site, suggesting that it is precisely the oligotrophic nature of the site the reason underlying such diversity. We believe that low P can enforce reproductive isolation and nutrient recycling promotes community cohesion, and that effective migration and establishment of newcomers to such communities is extremely rare due to a series of competitive mechanisms and negative interactions, and to the fact that external source of DNA is an important source of P in these populations. Herein we give the first glimpse of the total inventories of Churince, an enclosed hydrological system within the CC Basin, where bacterial, micro-eukarionts, virus, fungi, invertebrates, animals and plants have been surveyed for 3 years in different seasons, using molecular ecology and evolutionary methods. We found an extraordinary diversity, even at the local level (in a scale of few meters) and a very large heterogeneity between sites at the different taxonomical levels. We believe that this system has evolved so many species due to the fact that local interactions have split the niche in very small bits and that the lack of bacterial sex and effective migration keeps microevolution at the local level.

Why is Madagascar special? Diversification patterns in pelican spiders (Archaeidae)

Hannah Wood, Rosemary Gillespie, Charles Griswold, Peter Wainwright

1A_306A-Biodiversity
Saturday, June 21, 2014 9:30 AM-9:45 AM

Madagascar is known for its remarkably high species richness and high endemism. Archaeids (pelican spiders) are an ancient group with unusual predatory behaviors and spectacular trophic morphology that likely have been on Madagascar since Pangaean times. We examine whether Madagascan archaeids are undergoing adaptive radiation compared to lineages in the only other areas where extant species exist, Australia and South Africa. We also examine the relationship between distribution and adaptive divergence on Madagascar. Using a fossil-calibrated phylogeny we find that there are increased rates of habitat and trait diversification in the Madagascar archaeids, and that there is a significant correlation between habitat and morphology, suggestive of an adaptive radiation. We also find that montane areas, rainforest refugia and the evolution of different ecogeographic regions are important for species accumulation; however, this diversification is due to ancient events. Possibly archaeid evolution in Madagascar reflects the influence of more ancient climatic events compared to the history of other archaeids from Australia and Africa, which have not radiated. These ancient events possibly allowed for cycles of forest contraction and expansion, providing a landscape and temporal change that allowed greater rates of diversification.

Recent divergence in fungal populations

Sara Branco, John Taylor, Tom Bruns

1A_306B-Divergence
Saturday, June 21, 2014 8:30 AM-8:45 AM

Genetic differentiation between populations, signaling the effects of reduced gene flow and adaptation that are the main drivers of speciation, is essential to understanding biodiversity. Very little is currently known about how fungal populations differentiate in nature. Here, we investigate the divergence of a coastal and a mountain population of Suillus brevipes, a widespread mycorrhizal fungus associated with pine forests. Whole genome assembly and resequencing of 28 S. brevipes individuals revealed 567,192 shared SNPs that supported two recently diverged populations, each with low genetic diversity. As expected, mean genome-wide Fst is very low, indicating little overall population differentiation. However, genome-wide scans for regions of high differentiation using 5kb windows, reveal several highly differentiated regions, that harbor eight genes coding for five known proteins associated with cellular processes and signaling. Demographic inference suggests the two populations are isolated, with no migration between the coast and mountain. Population genetic differentiation and adaptation can occur by natural selection or genetic drift. Tests of the ratio of non-synonymous to synonymous mutations and identity of genes in the highly diverged regions may provide evidence of natural selection and suggest modes of adaptation. Further research including other mountain and coastal S. brevipes populations will be needed to identify the sources of the highly diverged regions.

An intraspecific gradient from C3 to C4 photosynthesis

Marjorie Lundgren, Pascal-Antoine Christin, Colin Osborne

1A_306B-Divergence
Saturday, June 21, 2014 8:45 AM-9:00 AM

During the diversification of flowering plants, C4 photosynthesis evolved independently from C3 ancestors more than 60 times, but the details of how this happened remain poorly understood. Studies to decipher the transition from C3 to C4 photosynthesis often infer the nature of these changes across distantly related species, differing by many traits, which subsequently can only evaluate a limited number of steps during the C3 to C4 transition. Here, we analyze the variation in C4-related traits that exists within a single species, the grass Alloteropsis semialata. Some populations of this species use C3 photosynthesis, while others use the C4 pathway. Intriguing reports in the literature point to intermediate states, but these have never been confirmed nor extensively characterised. We developed a multidisciplinary research program to understand the causes and consequences of this variation, toward an elucidation of the processes that lead to novel ecological adaptations. First, 13C isotope data for 300 individuals across the species' range show the C3 and C4 physiological states are not discrete but form a continuum between pathways, suggesting the existence of C3-C4 intermediacy. Physiological data were combined with immunolocalization results to decipher the degree of this intermediacy. The 13C continuum was analyzed in a spatio-ecological context. Populations using C3 and C4 photosynthesis inhabit different, but overlapping, geographic ranges and the intermediate populations are only found in the overlapping region. Analyses of markers from chloroplast and nuclear genomes show that the C3 and C4 clades form two ancient and well-diversified sister groups and intermediates are nested in several places within the C3 clade, suggesting multiple transitions to C3-C4 intermediate photosynthesis from the pool of C3 ancestors, possibly via hybridization. Leaf anatomy measurements show some traits (e.g., mesophyll cell abundance) change abruptly across the 13C spectrum, while others (e.g., interveinal distance) form a continuum and the environmental drivers behind this variation are presented. Additionally, the environmental inducibility of each anatomical trait is described to confirm the degree to which plasticity may be influencing the evolution of photosynthesis in this species. The anatomical and physiological continua are discussed in light of the species phylogeography and plasticity for C4 anatomy, shedding new light on C4 evolution among populations of the same species. By comparing such closely related individuals that represent a continuum of photosynthetic states, we illustrate the small changes that accumulate over time to generate C4 photosynthesis, one of the most successful ecological innovations in flowering plants.

Genomic divergence of putatively adaptive genes along an altitudinal gradient in the common yellow monkeyflower, Mimulus guttatus.

Vanessa Koelling

1A_306B-Divergence
Saturday, June 21, 2014 9:00 AM-9:15 AM

A major goal of research in evolutionary genetics is to determine the genes responsible for local adaptation to different environmental conditions in natural populations. One way to identify putative genes underlying local adaptation is to use a genome scan approach to associate changes in allele frequencies with environmental variables. Here, I present data from an investigation of genomic divergence in the evolutionary model plant Mimulus guttatus along an altitudinal gradient. Loci were constructed from reduced-representation libraries of RAD-tagged DNA sequenced from 24 populations using the Illumina platform. I used multiple methods to identify outlier loci associated with changes in altitude and other environmental variables. These loci may play a role in local adaptation to climate in Mimulus guttatus.

Mechanisms for the evolution of seasonal timing in incipient species of Ostrinia moths

Crista Wadsworth, *Erik Dopman*

1A_306B-Divergence
Saturday, June 21, 2014 9:15 AM-9:30 AM

Dormancy is an environmentally induced developmental process that results in arrested development and is a nearly universal life-history strategy for animals and plants living in seasonal environments. The ability to synchronize dormant life-stages with adverse climatic conditions, and active stages with favorable ones, is a key adaptive strategy for organisms living in variable environments. In insects, evolution of in the timing of dormancy termination has been reported to lead to ecologically relevant shifts in seasonal timing and may be a critical component to both long-term persistence and speciation. Although there has been increasing focus on the correlation of particular genes or pathways with this transition period, the majority of identified genes are most likely downstream of the initial switch that triggers evolutionary divergence in dormancy program. Comparisons across taxonomic groups to identify long-term evolutionary trends in the dormancy termination is also lacking. To understand the evolution of seasonality we use two sympatrically speciating strains of the European Corn Borer (Ostrinia nubilalis) that differ in emergence timing due to a shift in the timing of dormancy termination. Using whole transcriptome sequencing we, 1) identify 51 candidate genes for seasonal timing based on location within the mapped QTL and differential expression or amino acid changes between strains, 2) identify shifts in stress, metabolic, and endocrine regulation pathways that define dormancy termination vs. maintenance, and 3) observe convergence in transcriptional profiles across taxa (flies vs. moths) at developmental stages that define dormancy termination. We therefore nominate molecular mechanisms that drive initial evolutionary divergence and long-term convergence in dormancy termination.

Multi-trait divergence driven by predation environment causes immigrant inviability in Brachyrhaphis fishes

Spencer Ingley

1A_306B-Divergence
Saturday, June 21, 2014 9:30 AM-9:45 AM

Natural selection often results in profound differences among populations from divergent selective environments. Predation is a well-studied driver of divergence, with predators having a strong effect on the evolution of prey body shape and behavior, especially for traits related to predator escape. Comparative studies, both at the population level and between species, show that the presence or absence of predators can alter these phenotypic traits. Although this pattern is well documented in various species or population pairs, few studies have tested for the resulting effects on fitness. Here, I examine divergence in morphology, behavior, performance (burst speed and endurance swimming ability), and fitness (survival in the presence of a predator) associated with predation environment in sister species of the livebearing fish genus Brachyrhaphis that occur in divergent predation environments (predator-present: B. roseni; predator-absent: B. terrabensis). First, I found compelling evidence that personality traits diverge species from different predation environments such that populations that experience predation are more bold, active, and prone to explore than those that do not experience predation. Second, I found significant differences in body shape between predation environments, consistent with the hypothesis that locomotor function is optimized for either steady swimming (predator-absent) or escape behavior (predator-present). Third, body shape is highly correlated with swimming ability, with fish exhibiting more 'high-predation' like body shapes also having faster burst speed swimming responses. Likewise, endurance swimming ability significantly differed between species, with B. terrabensis outperforming B. roseni nearly ten-told, suggesting a strong trade-off between burst speed and endurance swimming ability. This likely results in strong selection against habitat switching. Finally, using a predator mesocosm experiment and path analysis I demonstrate that burst-speed swimming ability strongly predicted survival in the presence of a predator, providing strong evidence for predator driven immigrant inviability in this group. I discuss the implications of the observed predator driven divergence on speciation within this group.

Invasion and hybridization of the highly aggressive introduced reed, Phragmites australis, in the York River watershed

Laura Murray, *Carrie Wu*

1A_306C-Hybridization and Speciation
Saturday, June 21, 2014 8:30 AM-8:45 AM

An introduced lineage of the common reed, Phragmites australis, has been aggressively invading estuarine habitats throughout North America, often replacing native Phragmites populations with dense monocultures that drastically alter ecosystem functioning. Because relatively few relic native P. australis populations are known to remain in the mid-Atlantic region, the ability to confidently distinguish between the invasive and native forms has important implications for management practices. In collaboration with the Virginia Department of Conservation and Recreation, we have used morphological and genetic analyses to determine the extent of Phragmites invasion in the York River watershed, and identify remnant native stands that warrant conservation. Unlike throughout much of the Atlantic coast, our genetic analyses indicate that native P. australis populations do persist in the greater York River, although introduced P. australis is relatively widespread. Additionally, we have evidence that the potential for natural hybridization between the lineages may present a serious concern for land managers. This ongoing collaboration has successfully immersed introductory biology students in service learning that has immediate impacts for the local community.

What is the link between transmission ratio distortion and sterility in Mimulus hybrids?

Andrea Sweigart

1A_306C-Hybridization and Speciation
Saturday, June 21, 2014 8:45 AM-9:00 AM

Recent work has provided insight into the molecular functions and evolutionary histories of genes involved in hybrid dysfunction, but we have yet to answer what might be the key question for speciation: which population genetic forces and selective agents drive the initial substitutions within species that lead to incompatibilities between species? Here I focus on a simple genetic incompatibility that causes nearly complete male sterility and partial female sterility in hybrids between two closely related yellow monkeyflower species: Mimulus guttatus and M. nasutus. I have mapped the two major incompatibility loci – hybrid male sterility 1 (hms1) and hybrid male sterility 2 (hms2) – to small nuclear genomic regions that contain only a handful of genes and include strong candidates. In addition to causing hybrid sterility, these same two regions show strong transmission ratio distortion in hybrids. To investigate the connection between these hybrid phenotypes and determine whether distortion occurs through male or female gametes, I performed a crossing experiment using nearly isogenic lines that segregate only at hms1 and hms2. I also tested whether transmission ratio distortion at these loci occurs exclusively in hybrid genetic backgrounds or also occurs within species. The latter would provide direct evidence that intragenomic conflict plays a role in the evolution of hybrid incompatibilities.

Paternal learning of a phenotype-matching trait promotes speciation at secondary contact, but not the spread of a new local adaptation

Douhan Yeh, Maria Servedio

1A_306C-Hybridization and Speciation
Saturday, June 21, 2014 9:00 AM-9:15 AM

Assortative mating can be an essential component of speciation with gene flow because it reduces genetic exchange between groups with different mating preferences. Assortative mating traits and/or preferences have been found to be affected by learning across a wide range of animal taxa, yet how differences in the template for learning affect speciation has been largely overlooked. We investigate how migration, the template for learning, assortative mating strength, and divergent selection affect the divergence of a trait that can be affected by learning, and is used as a cue for mate choice by self-referent phenotype matching. We found that oblique and maternal learning masks sexual selection and therefore does not facilitate the maintenance of divergence. Paternal learning can maintain divergence at a level higher than does genetic inheritance. The establishment of divergence through the spread of novel adaptations is however hindered by paternal learning. This is because paternal learning enhances positive frequency-dependent sexual selection, which makes it easier to lose polymorphism.

Mechanical Transgressive Segregation and the Rapid Origin of Trophic Novelty

Darrin Hulsey

1A_306C-Hybridization and Speciation
Saturday, June 21, 2014 9:15 AM-9:30 AM

Hybrid phenotypes often fall within the parental range. However, when traits are complex, hybridization can also generate novel phenotypes. For instance, even when the morphologies of individual musculo-skeletal components do not segregate outside the parental range in hybrid offspring, complex functional systems can exhibit emergent phenotypes whose mechanics do exceed the parental values. Within this context, we examined three functional systems in the trophic apparatus of Lake Malawi cichlids. We used these systems to determine how the evolutionary divergence of parental species influences the frequency that hybridization produces mechanics that transgress the parental range. Unlike what has generally been found when genetic mechanisms underlie transgressive segregation of linear phenotypes, the complex mechanical systems of the cichlid trophic apparatus often exhibited greater transgression in crosses between more recently diverged cichlid species. Because hybridization is known to take place in the hundreds of co-occurring cichlid species and virtually every lineage we studied has the theoretical capacity to produce hybrids with transgressive mechanics, mechanical transgressive segregation has likely helped shape the exceptional trophic diversity of the Lake Malawi cichlid radiation.

Life history and behavior in a primate hybrid zone

Susan Alberts, Jeanne Altmann, Jenny Tung

1A_306C-Hybridization and Speciation
Saturday, June 21, 2014 9:30 AM-9:45 AM

Hybridization in nature has potentially profound effects on evolutionary processes; it can create either evolutionary dead ends or evolutionary opportunities for the organisms experiencing it. Recent studies of hybridization have been enhanced by the advent of genetic marker-based techniques for inferring the degree of admixture occurring within individuals. We conducted a genetic marker-based analysis of hybridization in a large-bodied, long-lived mammal over multiple generations. Specifically, we analyzed patterns of hybridization between yellow baboons (Papio cynocephalus) and anubis baboons (P. anubis) in a well-studied natural population in Amboseli National Park, Kenya, using genetic samples from more than 700 individuals born over 40 years. We assigned genetic hybrid scores based on genotypes at 14 microsatellite loci using the clustering algorithm implemented in Structure 2.0, and assessed the robustness of these scores by comparison to pedigree information and through simulation. The proportion of hybrids in the Amboseli population has grown over time, but the average proportion of anubis ancestry within hybrids is gradually decreasing. We found that both dispersal and maturation occurred earlier in individual male baboons that were more admixed. Hybrid females, too, reached menarche slightly earlier than non-hybrid females, but maternal dominance rank and the presence of maternal relatives had larger effects on female maturation than genetic background. We also identified novel effects of genetic background on mating patterns, including a mating advantage for admixed males, and weakly assortative mating among both yellow-like and anubis-like pairs. These genetic effects acted alongside behavioral and demographic effects to produce highly nonrandom mating patterns. Our results suggest that this population may be undergoing admixture-related evolutionary change, driven in part by life history differences between yellow and hybrid individuals, and in part by nonrandom mating driven by differences in genetic background.

The Dark Side of Phylogenetic Comparative Methods

Natalie Cooper

1A_402-SSB Symposium: The "dark side" of phylogenetic comparative methods
Saturday, June 21, 2014 8:15 AM-8:45 AM
Phylogenetic Comparative Methods (PCMs) make numerous assumptions and suffer from biases in the same way as any statistical method, but these issues are often inadequately assessed in empirical studies. Such issues are the responsibility of end users but also of methods developers: the tools and approaches used to fit models are often far more user-friendly and better documented than the methods used to to assess whether that model fit is reasonable. To address these issues, speakers in this symposium will discuss issues in both classical and recent PCMs, along with new research on detecting for these issues and accounting for them. We hope that this will both increase awareness of these problems and encourage further research and careful thought in the area, along with better dialogue between method developers and method users.

The unsolved challenge to phylogenetic correlation tests for categorical characters

Wayne Maddison, *Richard FitzJohn*

1A_402-SSB Symposium: The "dark side" of phylogenetic comparative methods
Saturday, June 21, 2014 8:45 AM-9:15 AM
When testing whether traits have a correlated distribution among species, we know to consider phylogenetic relationships to avoid the pseudoreplication resulting from the shared history of species. Even Darwin realized this, noting that when two traits happen to characterize a single clade (e.g., fur and milk in mammals), we should not infer they are “in some necessary manner correlated” — they could have arisen independently and simply been co-inherited. No interesting functional or adaptive link between the characters, direct or indirect, can be inferred from their distribution alone. Similarly, when a single clade shows a higher rate of change in a character (the "unreplicated burst"), we cannot associate this with any particular synapomorphy of the clade, as any of the possibly-hundreds of its other synapomorphies could be responsible. Despite such admonitions, several correlation tests for categorical characters report a significant association in both Darwin's Scenario and the unreplicated burst, including Pagel's (1994) likelihood method. This serious issue applies also to diversification tests like BiSSE. We argue that this problem cannot be properly solved by vigilantly filtering the problem cases. We agree with suggestions in the literature that the problem arises from the methods' standard Markovian treatment of each small branch segment as independent, but we suggest non-random sampling of characters may also be at fault. We have no solution; it is possible that a solution may require fundamental changes to how we model trait evolution. This problem has been in the literature for two decades but has been largely ignored, which makes us concerned that we have not succeeded in grasping phylogenetic independence nearly as well as we had thought. It seems that comparative biology’s transition to a phylogenetic paradigm, as profound as cosmology's transition to a relativistic view of space-time, may be difficult and as yet incomplete.

Modeling Character Evolution with Phylogenetic Uncertainty

April Wright, *Kathleen Lyons*

1A_402-SSB Symposium: The "dark side" of phylogenetic comparative methods
Saturday, June 21, 2014 9:15 AM-9:45 AM
Phylogenetic comparative methods can only be relied upon to the extent that the underlying tree is reliable. Performing model fitting and parameter estimation on random samples of trees from the posterior set of trees from a Bayesian phylogenetic analysis is a common way to quantify this uncertainty. This, however, may not be practical for extremely large trees. Here, I re-examine previously published data on the evolution of viviparity among squamates. Many squamate taxa exhibit viviparity, and the number of evolutionary transitions to and from viviparity is contentious. Using samples from the bootstrap replicates from a likelihood analysis of 4161 squamate species, I reestimate the ancestral states and examine the relationship between parity mode and diversification rate. Results presented will show the effect of topological uncertainty on the estimation of the evolutionary history of parity mode in squamates.

Clade dynamics in size/shape space: Diversity, duration, and extinction risk

Shan Huang, *Kaustuv Roy, David Jablonski*

1B_201-Morphology
Saturday, June 21, 2014 10:15 AM-10:30 AM
Members of a clade are not randomly distributed in morphospace – a multi-dimensional space constructed using morphological traits. Previous studies on various biological systems have shown that the species richness and evolutionary durations of subclades can vary with position in morphospace. However, mechanisms behind these patterns are poorly understood. Here, we investigate the patterns of morphospace occupancy in a macroecological/macroevolutionary model system, the marine bivalves, to elucidate the underlying mechanisms.

For each bivalve family separately, we defined the center of a simple morphospace based on shell size and shape, and examined the composition of the species assemblages in central versus peripheral zones of family morphospaces to test three hypotheses. 1) Species belonging to species-rich genera are more concentrated near the center than expected by chance, leaving the species from species-poor genera mostly at the periphery. 2) Species belonging to older genera are more concentrated near the center than expected by chance, leaving the species from young genera mostly at the periphery. To investigate the link between morphospace occupancy and extinction as a possible mechanism for hypotheses 1) and 2), we use geographic range size as an indicator of extinction risk, and test the hypothesis that 3) geographically widespread species are more concentrated near the center than expected by chance.

Our results support all three of our hypotheses, suggesting that the center of a family's morphospace represents a location where diversity is maximized, most likely because of lower extinction rates. However, within the most diverse living family (Veneridae), where we have the morphologies of the earliest fossil member of each living genus (n = 51), genera did not move through morphospace in a manner suggesting that the center of the morphospace is an adaptive peak or evolutionary attractor at the species level. Therefore, the apparent preference for the central morphospace does not appear to be the outcome of the dynamics (or trajectory) of morphospace occupancy within individual genera, but seems to be a product of differential survivorship among species and genera (e.g. clade-level effects of geographic range or species richness).

Ecomorphological evolution in the Liolaemus darwinii species group (Squamata: Liolaemini): adaptive diversification to climatic niches

Arley Camargo, Jack W. Sites, Mariana Morando, Luciano Avila

1B_201-Morphology
Saturday, June 21, 2014 10:30 AM-10:45 AM
Patterns of diversification at the macroevolutionary level can be due to adaptation processes or simple random divergence. In turn, adaptive divergence can be driven by natural selection in response to ecological factors. In this work, we evaluated diversification models in the L. darwinii species group using comparative phylogenetic methods. We took seven morphometric measurements in males of 18 species and we obtained climatic data from georeferenced localities. First, we compared the fit of Brownian vs. adaptive models of diversification based on the morphological variation among species and a phylogeny for the group using the R packages 'picante' and 'geiger'. Second, we evaluated the evolutionary correlation between the morphological variation and the climatic niches using a phylogenetic canonical correlation analysis with the R package 'phytools'. Third, we fitted Ornstein-Uhlenbeck (OU) models of adaptive evolution to randomly evolving predictor (climatic) variables using the R script 'slouch'. Three morphometric traits showed phylogenetic signal and fitted a model of adaptive optima better than a Brownian model. Taking into account phylogeny, the morphological variation among species is highly and significantly correlated with the variation in climatic niches. OU models show that phylogenetic signal of several morphometic traits is the result of adaptive change to climatic variation instead of phylogenetic inertia. These results suggest that adaptive diversification in the L. darwinii group took place as a response to divergent climatic niches in the wide, latitudinal and altitudinal gradients of the Monte Desert in west-central Argentina.

A comparison of mammalian skull morphological integration throughout ontogeny

Alex Hubbe, Harley Sebastião, Guilherme Garcia, Gabriel Marroig

1B_201-Morphology
Saturday, June 21, 2014 10:45 AM-11:00 AM
Mammalian skull is frequently used to study evolutionary processes. Under the evolutionary quantitative genetics framework, G or P-matrices are usually estimated for adult individuals of the populations and then they are used to study micro and/or macroevolutionary processes. Implicitly it is assumed in these analyses that the G or P-matrices remained relatively constant throughout the ontogeny. Although cross-sectional and longitudinal studies suggest that these matrices are not strictly identical or proportional during ontogeny, up to date it has not been addressed how similar these matrices are and to what extent the differences may affect evolutionary studies within and between populations throughout the ontogeny. We explored this question analyzing both the structure and the overall magnitude of integration of mammalian cranium P-matrices (as surrogates to their G-matrices). We determined cranium P-matrices based on 35 linear distances for 13 genera of Didelphimorphia (Mammalia) at up to eight dental age classes encompassing from the first months of life after birth to adulthood and for Calomys (Rodentia, Mammalia) at seven age classes ranging from 20 days after birth (around weaning) to 400 days after birth. Structural similarity among matrices was evaluated within genus and between genera using the Random Skewers (RS) and the Krzanowski Projection (KP). The overall magnitude of integration for each dental age class and genus was determined for the correlation matrices by calculating the scale-independent coefficient of determination (r2). RS and KP results were most often > 0.7, even in the comparisons between Didelphimorphia and Rodentia. The smallest r2 was 0.13 and the largest 0.58. For Didelphimorphia, some genera presented relatively larger r2 for the first three dental age classes in comparison to the other dental age classes. The r2 between age classes for Calomys are relatively similar. These results show a highly conserved structure of the P-matrices within and between Didelphimorphia and Calomys throughout their post-natal ontogeny. The r2 varied more markedly than the structure of the P-matrices both between genera and age classes, suggesting that the intensity of inter-trait relationships varies more than the pattern of these relationships. Nevertheless, RS results suggest that independently of the variation in the r2, responses to selection tend to be similarly oriented. Thus the assumption that the G or P-matrices remained relatively similar throughout the ontogeny are supported for the taxa analyzed. Moreover, their phylogenetic

distance suggest that this interpretation can be extended to all therian mammals.

Phenotypic evolution of bat skulls, and its relationship with speciation

Jeff Shi, Dan Rabosky

1B_201-Morphology
Saturday, June 21, 2014 11:00 AM-11:15 AM

Diversity is unevenly distributed across the tree of life, without regards to scale: clades can be highly speciose or species-poor, have high disparity or be morphologically conserved, and be ecologically diverse or ecologically constrained. These patterns are produced by variable rates and types of evolution, thereby intertwining processes of diversification, phenotypic evolution, and adaptation. Understanding how these different processes are related, then, and the possible causes of rate variability has become a central issue in the field of macroevolution. Here, we present an analysis on diversification and phenotypic evolution in bats, a highly speciose clade with strong ties between ecologically diversity and morphological disparity. We focus on the evolution of the skull, considering its strong ties to feeding ecology and behavior across bats. Our analyses are based on the BAMM platform, a Bayesian rjMCMC program for modeling macroevolutionary dynamics of diversification and phenotypic evolution. Though we find evidence for family-level variability in both rates of diversification and phenotypic evolution, they are not well-correlated, and sometimes associate inversely. As such, we hypothesize that bursts of bat speciation have not always been associated with rapid phenotypic evolution, as predicted by classical models of adaptive radiations.

Ultraconserved Elements Yield New Insights Into the Exceptional Morphological Radiation of Neotropical Headstanding Fishes

Brian Sidlauskas, Michael Alfaro, Michael Burns, Casey Dillman, Brant Faircloth, Benjamin Frable, Kendra Hoekzema, Bruno Melo, Claudio Oliveira, Richard Vari

1B_201-Morphology
Saturday, June 21, 2014 11:15 AM-11:30 AM

The approximately 300 species of headstanding fishes (and their close relatives) in superfamily Anostomoidea represent one of the most ecomorphologically diverse and economically important components of the Neotropical fauna, but no one has yet proposed a comprehensive molecular phylogeny for them. Using a new ostariophysan-specific library of 1500 ultraconserved elements (UCEs) in juxtaposition with a morphological database approaching 500 characters, we are reconstructing their evolutionary history and investigating why some anostomoid clades have diversified greatly in oral jaw shape and coloration, while others seem to have diversified internally. We will present an UCE-based phylogeny for 69 ingroup and six outgroup taxa, discuss its extensive congruence with a prior morphological hypothesis and highlight the macroevolutionary implications of a few critical topological conflicts. The most surprising conflict involves a novel and well-supported interfamilial relationship that implies substantial convergence or reversal in osteological and myological features associated with the gill arches, pharyngeal apparatus, quadrate, hyomandibular and various ligaments. Our next steps involve further investigation of these morphological characters and comparative phylogenetic analysis of morphometric and lineage diversification on an expanded molecular dataset that will exceed 70% taxon sampling. Our results illustrate the capacity of UCE-based phylogenetics to sample extensively across the genome and provide robust estimates of relationships that can in turn spark new discoveries about diversification, ecomorphology and character evolution.

Testing the Effects of Oxidative Stress on Genomic Recombination in the Honey Bee, Apis mellifera

Kurt Langberg, Olav Rueppell, Matthew Phillips

1B_206-Honey Bee Evolution
Saturday, June 21, 2014 10:15 AM-10:30 AM

It has become increasingly evident that genomic recombination is an evolved trait that varies between and within species. The honey bee has an extremely high genomic recombination rate but the responsible mechanisms have not been studied. Based on the hypothesis that meiotic recombination and DNA damage repair share common mechanisms in honey bees, we predict that oxidative stress leads to a further increase in recombination rate. This prediction can be directly tested by subjecting honey bee queens to oxidative stress by paraquat injection and measuring the rates of genomic recombination in select genome intervals of their offspring before and after injection. We report on the outcomes of this experiment and will discuss the results' implications for the understanding of the evolution of excessive recombination rates, as shown in honey bees.

Exceptional Levels of Genome-Wide Recombination Extends to Novel Species in the Genus Apis

Olav Rueppell, Ryan Kuster, Katelyn Miller, Mananya Phaincharoen, Salim Tingek, Nikolaus Koeniger

1B_206-Honey Bee Evolution
Saturday, June 21, 2014 10:30 AM-10:45 AM

With about 20cM/Mb, the Western honey bee, Apis mellifera, exhibits an excessive rate of genome-wide recombination, which has attracted significant scientific attention. A recent linkage map in the closely related A. cerana has found similarly high recombination rates and the same conclusion was reached for the more distantly related A. florea, based on limited data from two chromosomes. Here, we report on two complete linkage maps in this genus, extending existing genome-wide linkage maps to all three major honey bee clades. Based on genotyped SNPs identified by RAD-tag sequencing in single-family mapping populations, we present genome-wide recombination maps of A. florea and A. dorsata. The results suggest that the high recombination rate is a genus-wide trait and Apis mellifera is not the unique, which may be taken as evidence for a single evolutionary transition. However, the maintenance of these high recombination rates also suggest in these divergent species suggests some long-term selection on this trait.

Fine-scale analysis of a genome-wide linkage map to examine meiotic recombination in the honey bee, Apis mellifera.

Katelyn Miller, Caitlin Ross, Corbin Jones, Olav Rueppell

1B_206-Honey Bee Evolution
Saturday, June 21, 2014 10:45 AM-11:00 AM

The western honey bee, Apis mellifera, has an exceptionally high rate of genomic recombination, but the fine-scale patterns that may allow a mechanistic explanation of this phenomenon are unclear. Specifically, the high overall recombination rate may be due to a higher background rate or due to more and/or hotter hotspots. The red queen explanation of the hotspot paradox predicts that honey bee hotspots, if existent, turn over much faster than in other species. Previous research has been unable to illuminate these predictions. Therefore, we combined a large sample size with genome re-sequencing to produce a fine-scale recombination map. This map will be used to describe the fine-scale patterns of honey bee recombination and search for sequence features that characterize genome regions with high recombination rates. These findings will be discussed in the context of honey bee genome evolution and the evolution of recombination in general.

Flexible decision-making in a variable environment: when do foraging honeybees rob nectar?

Jessica Barker, Judith Bronstein

1B_206-Honey Bee Evolution
Saturday, June 21, 2014 11:00 AM-11:15 AM

A behavior that is optimal in one environment may not be so in another. A key question is how individuals make optimal behavioral decisions when the environment is variable. It may be costly to assess environmental variation and switch behaviors; accordingly, fixed behaviors, rather than the ability to respond to variation in environmental conditions, might be expected to evolve. Alternatively, it may be costly to adopt a behavior that is not well-matched to a given environment; in that case, flexibility should evolve, with individuals changing behavior as the environment varies. We tested these predictions in an observational study of honeybee foraging. On manzanita (Arctostaphylos pungens) flowers in southern Arizona, honeybees must make two foraging decisions: first, whether to collect nectar through the openings of flowers (i.e., to legitimately forage) versus to rob nectar through holes chewed by primary nectar robbers (i.e., to secondarily rob); and second, if legitimately foraging, whether to visit robbed versus intact flowers. As there is variation across plants in the frequency of flowers with holes, as well as variation in flowers' nectar volume (flowers with holes on average contain less nectar), we predicted that 1) the frequency of secondary robbing would increase as the frequency of flowers with holes increases (flexible behavior); and 2) legitimate visitors would disproportionately visit intact flowers (fixed behavior), but would do so less as the frequency of flowers with holes increases (a flexible component). Contrary to the first prediction, the frequency of secondary robbing peaked on plants exhibiting an intermediate frequency of holes. In partial support of the second prediction, legitimate visitors disproportionately visited intact flowers, but did so mostly on plants exhibiting both low and high frequencies of holes. We suggest that the discrepancy between these observations and the predictions may arise because plants bearing many flowers with holes had so little nectar per flower that they were not worth visiting. This study suggests that honeybees' foraging strategies show both fixed and flexible aspects, and that it may be beneficial to respond to environmental variation unless the cost of switching behaviors is high.

Balancing selection and the recognition system of the honey bees

Brock Harpur, Amro Zayed

1B_206-Honey Bee Evolution
Saturday, June 21, 2014 11:15 AM-11:30 AM

Recognition systems are almost universally under balancing selection where diversity of a recognition signal allows for accurate discrimination of self vs non-self, or kin vs non-kin. In many social insect colonies, members are able to discriminate from non-members using differences in the cuticular hydrocarbon (CH) profile each individual expresses. In honey bees, each member of a colony expresses a heritable, colony-specify coating of hydrocarbons, derived in part from comb wax. The genes underlying variation in hydrocarbon have recently been identified, and include genes known in Drosophila to be responsible for hydrocarbon synthesis and desaturation. Here, I investigate the role balancing selection has on recognition systems in the honey bee using a full genome scans of 40 honey bees. I scanned the genome for shared polymorphisms between Apis mellifera and its sister species A. cerana; such variants are highly unlikely by chance alone and are candidates for balancing selection. The resulting map of selection across the genome yielded evidence of balancing selection acting on genes known to be involved in the development of the honey bee's CH profile. These data are the first empirical demonstration of balancing selection on a social insect and add credence to the fact that recognition genes are among the most diverse in the genome of many organisms.

GBS in Cornus florida L reveals co- divergence in genetic structure and foliar fungal communities along environmental gradients.

Andrew Pais, Jenny Xiang, William Hoffman, Ross Whetten

1B_301A-Genetics of Traits
Saturday, June 21, 2014 10:15 AM-10:30 AM

Understanding the molecular basis of ecological adaptation is a fundamental question in evolutionary ecology. Recent advances in DNA sequencing technology permit rapid generation of a large number of molecular markers for population genetic study, facilitating identification of genes or DNA markers associated with ecological adaptation. We employ the Genotyping by Sequencing (GBS) method for a study of Cornus florida L. (the flowering dogwood tree). Natural populations of the species are severely threatened by dogwood anthracnose and powdery mildew diseases. Thus, evaluating the genetic diversity and how environmental factors have shaped the genetic structure and associated fungal communities in the species is crucial to conservation management. We genotyped 180 plants using the GBS method for six populations occurring in three different ecological habitats and measured environmental conditions along with functional traits from each site. Site measurements include mineral and macronutrient analysis of soils (quantifying N, P, Na, cation exchange, etc.), visual measurement of canopy afflicted by disease (leaf blotting, spotting, or branch dieback), and leaf osmotic potential . The objectives are to test whether differences in abiotic environmental conditions have resulted in local ecological adaptation, genetic differentiation, and differences in associated fungal communities and to identify loci associated with the ecological adaptation. Our measurements of environment conditions at sites generally corroborate records of environmental differences, and measurements of disease severity support findings that mountain populations are plagued more by dogwood anthracnose. Preliminary analyses of GBS data identified on an average approximately 1090 SNPs per individual. Results from analyses of the data suggest genetic grouping of populations corresponding to an environmental gradient. Estimation of Fst per locus found approximately 300 potential outlier loci with high Fst values between populations from different environments. Blast of GBS data to fungal genomic databases identified fungal communities associated with the leaves of each population. The distribution and abundance of fungal taxa in the six populations exhibit correlation with environmental gradients. The data suggest that GBS is a valuable method for population genomics and metagenomic analysis of plant pathogens. The preliminary results further suggest that lower disease severity in coastal populations is likely a consequence of local adaption to different environment conditions favoring different kinds of pathogens and fungi communities. Healthy plants in pathogen prevalent (e.g., mountains) and rare (e.g., coast) environments may have a genetic basis for resistance. This will be tested with more detailed analysis of the data on genotype-phenotype association.

Genetic architecture of developmental traits in populations of male gypsy moths

Christopher Friedline, Kristine Dattelbaum, Erin Hobson, Brandon Lind, Rodney Dyer, Dylan Parry

1B_301A-Genetics of Traits
Saturday, June 21, 2014 10:30 AM-10:45 AM

Local adaptation, characterisic of increased relative fitness of a population of a particular genoytpe over genotypes originating from other habitats, is an important consequence of natural selection operating on fine spatial scales. In this study, we examine the pattern and process of local adaptation and genetic architecture of developmental traits potentially influencing dispersal capacity (larval mass, pupal duration, and developmental time) in male gypsy moths (Lymantria dispar L.), a particularly damaging, non-native, invasive species. A common garden was established in VA from a local population in addition six other populations from different regions of Virginia, North Carolina, and New York as well as sites in Canada; a fully-factorial design is currently under development. In this talk, I present results from a single reference assembly derived from a single individual, created from a paired-end sequencing run on an Illumina HiSeq 2500 instrument. To this assembly, 192 barcoded individuals, from the common garden (differing in source population) were mapped resulting in an individual-genotype matrix containing thousands of reliable SNPs. Bayesian Variable Selection Regression (BVSR) as well as standard linear mixed-model approaches were employed to explore the relationship between these complex phenotypes and the underlying genetic variation across populations. Understanding the genetic architecture of these characters can serve to inform the control of gypsy moth spread as well as increase understanding of the role of selective forces on invasive species.

The hunt for quantitative trait nucleotides: a near-isogenic line approach in C. elegans

Max Bernstein, Matthew Rockman

1B_301A-Genetics of Traits
Saturday, June 21, 2014 10:45 AM-11:00 AM

The individual nucleotides responsible for phenotypic diversity have been very difficult to isolate. Many known causal variants that affect traits in wild populations are of very large effect and variation in these traits tends to be explained by few genetic loci. There are many confounding elements that can explain the relative lack of causal variants, or quantitative trait nucleotides (QTNs), for more complex phenotypes, particularly alleles of small effect, limited marker density and sample size, and epistatic interactions. One way to elucidate quantitative trait loci (QTLs) is through the creation of near-isogenic lines (NILs), where the majority of the genome (>95%) is of one genomic background. NILs have previously been created for the nematode C. elegans and identified QTLs across the genome for several phenotypes. Starting with a NIL that harbors a ~1.5 Mb segment on Chromosome X originating from the Hawaiian isolate CB4856 in an otherwise N2 (lab strain) background, we have created a series of more than 1000 nested sub-NILs that break up this segment into smaller regions by recombination. 960 of these sub-NILs were genotyped at 278 single nucleotide polymorphisms (SNPs) using the Illumina GoldenGate platform. We are currently phenotyping the parental strains for a number of behavioral and fitness measures. Preliminary results suggest that these parental strains have different locomotory patterns. The large number of recombinant lines combined with the high-throughput phenotyping approaches that we are employing should provide the power to resolve individual nucleotides contributing to trait variation within this genomic interval.

Genetic architecture of skeletal evolution in unusually large house mice from Gough Island

Michelle Parmenter, Melissa Gray, Caley Hogan, Irene Ford, Karl Broman, Chris Vinyard, Richard Cuthbert, Peter Ryan, Bret Payseur

1B_301A-Genetics of Traits
Saturday, June 21, 2014 11:00 AM-11:15 AM

The skeleton provides a scaffold for both form and function, and its evolution has played a crucial role in shaping the vertebrate body plan. In mammals, much has been learned about the genetics of skeletal variation from laboratory mice, but the genetic basis of skeletal evolution in natural populations remains poorly understood. Gough Island (GI) mice are the largest wild house mice (Mus musculus domesticus) in the world, with body masses twice those of their mainland relatives. We used X-ray images to identify

16 skeletal dimensions that are enlarged in GI mice relative to a mainland reference strain (WSB). Historical records and population genetic results suggest that mice colonized Gough Island only 100 years ago, pointing to rapid skeletal evolution. To reveal the genetic basis of these skeletal changes, we measured the 16 skeletal traits in 840 F2 mice generated by an intercross between GI and WSB. Measurements were collected at three postnatal time points for each mouse to provide an ontogenetic perspective. F2s were genotyped at more than 3,000 informative single nucleotide polymorphisms (SNPs) across the mouse genome. Among the 16 measurements, 14 were associated with multiple quantitative trait loci (QTL). Some of the QTL, including a large effect locus on chromosome 10, were also connected to body weight in the same cross. Other QTL were unique to particular bone measurements. These results indicate that the genetic mechanisms controlling the evolution of bone size act both globally and locally, and lay the foundation for genetic studies of adaptation to island life in mice.

A systematic approach to investigate allele-specific gene function in the North American gray wolf

Rachel Johnston, Pauline Charruau, Dan Stahler, Noah Snyder-Mackler, Amanda Lea, Jenny Tung

1B_301A-Genetics of Traits
Saturday, June 21, 2014 11:15 AM-11:30 AM
A principal objective in biology is to connect ecologically important traits to their genetic underpinnings. Discovering such genotype-phenotype associations in natural populations is important for answering fundamental evolutionary questions, yet few associations have been identified in non-model species. We are studying the role of a coding sequence deletion in the canine beta-defensin 3 (CBD103) gene, which is known to result in black coat color and has undergone a selective sweep in North American gray wolves (Canis lupus). We hypothesize that the CBD103 deletion also affects immune defense, as population modeling supports allele-specific fitness effects that are independent of coat color. We have established and are utilizing wolf cell lines to experimentally test allele-specific functions of CBD103, as in vivo studies are not feasible for this species. Cell lines were successfully established from skin samples from ten North American wolves, and additional tissues were collected from a CBD103 wildtype wolf for gene expression analyses. CBD103 is lowly expressed in fibroblasts but highly expressed in keratinocytes and epithelial tissues, suggesting that CBD103 plays a role in immune defense. Our cell lines afford the opportunity to experimentally manipulate allele-specific expression of CBD103 and will provide proof of concept for using cell culture to test functions of candidate genes in other non-model species.

Theory of identity-by-descent in sequentially Markov coalescent models

Peter Wilton, Shai Carmi, Pier Palamara

1B_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 10:15 AM-10:30 AM
Identity by descent (IBD) is a central concept in the study of genetic variation. IBD is analyzed for a variety of purposes, ranging from genotype imputation and heritibility estimation to pedigree reconstruction and demographic inference. I will discuss new theoretical results related to gene IBD, which considers contiguous segments of a chromosome inherited from a single common ancestor. These results are obtained by considering two sequentially Markov coalescent models (SMC and SMC'). Under these models, I calculate the marginal distribution of IBD segment lengths. I also calculate the distribution of IBD segment ages conditional on segment length, and I use this distribution to show that the age of IBD segments of lengths typically analyzed in recent studies is too ancient to reflect any features particular to the pedigree of the individuals from which the chromosomes were sampled. Finally, I investigate the process of mutation along IBD segments and calculate the probability of true mutational identity for gene IBD segments of different lengths. I find that the number of mutations along a segment quickly converges to a Negative Binomial distribution as the IBD segment length increases, and I show that the shortest segments of gene IBD have the greatest probability of being entirely identical, despite the fact that short IBD segments tend to be older than long IBD segments. Throughout, I find that predictions made with SMC' model are indistinguishable from the results of simulations of the ancestral recombination graph. Potential applications to inference of mutation rate and demography will also be discussed.

Parallel evolution as a tool for understanding what limits the rate of adaptation.

Peter Andolfatto, Molly Schumer, Matthew Aardema, Ying Zhen, Dario Ghersi, Edgar Medina

1B_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 10:30 AM-10:45 AM
Ecological communities undergoing parallel evolution to a common selection pressure are naturally occurring “chemostats” that allow us to study the dynamics and genetic underpinnings of repeated rounds of adaptation to a common environment. Notably, these systems allow us to understand the number of permissible paths that lead to the same adaptation. To this end, we surveyed the transcriptomes of numerous specialist insects that have independently evolved the ability to feed on plants that produce toxic secondary compounds (cardenolides) that they often sequester for use in their defense. A specific target of these toxins is Na(+),K(+)-ATPase, a large ubiquitously expressed protein involved in a number of vital functions. Despite the large number of potential targets for modulating cardenolide sensitivity, amino acid substitutions associated with host-plant specialization are highly clustered, with many parallel substitutions. Additionally, we document four independent duplications of the gene with convergent tissue-specific expression patterns. We find that unique substitutions are disproportionately associated with recent duplications relative to parallel substitutions. Together, these findings strongly implicate negative pleiotropy as a major factor limiting the rate of adaptation of cardenolide tolerance. More generally, our approach illustrates how evolutionary parallelism can be probed in a diverse set of non-model organisms and ecological contexts to learn about the dynamics of adaptation.

Evolutionary trends in consolidated human biological pathways

Frida Belinky, Noam Nativ, Gil Stelzer, Shahar Zimmerman, Simon Fishilevich, Marilyn Safran

1B_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 10:45 AM-11:00 AM
Comparing biological pathways is an important tool for studies of evolution. To this end, we defined SuperPaths, clusters of human biological pathways that are similar in gene content, thus reducing the redundancy found in diverse pathway databases. We clustered human biological pathways from 12 sources into a collection of 1043 SuperPaths each containing 1-66 pathways and 1-1973 genes. For evolutionary analyses, we assigned an evolutionary age for every SuperPath. This was done by identifying for each constituent gene for the earliest appearance across 12 time points that include all domains of life: Bacteria, Archaea, Eukarya, Unikonta, Opisthokonta, Metazoa, Bilateria, Vertebrata, Amniota, Mammalia, Euarchontoglires, and Primates. This was based on orthology relations from GeneCards (www.genecards.org). For every SuperPath we constructed an evolutionary vector, conveying the number of genes originating at different time points. For 52% of the SuperPaths we were able to define an evolutionary age as that at which >50% of the contained genes originated. The most highly populated SuperPaths origins were Bacteria (16%), Eukarya (63%) and Metazoa (14%). It is noteworthy that >50% of the SuperPath show distinct origins, stemming from the observation that a majority of their genes originate in a narrow evolutionary window, suggesting that the rise of biological pathways is highly synchronized. Utilizing top-level KEGG ontology terms for genes we assigned a functional category to each SuperPath, based on the most prevalent term among its contained genes. Interestingly, metabolic pathways are significantly enriched in bacterial origin, while signal transduction pathways are enriched in Eukaryotic and Metazoan origin. Utilizing an algorithm for assessing a SuperPath’s RNAseq-based expression pattern across 16 tissues, we show that SuperPaths differentially expressed in liver are significantly correlated with enrichment in Bacterial origin, while those differentially expressed in testes have Archeal enrichment.

Genome-wide scans for signals of molecular adaptation in polar bear

Charlotte Lindqvist, Andreanna Welch, Oscar Bedoya-Reina, Lorenzo Carretero-Paulet, Michael Brannick, Enrique Ibarra-Laclette, Tianying Lan, Webb Miller, Aakrosh Ratan, Karyn Rode

1B_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 11:00 AM-11:15 AM
The development of high-throughput sequencing technology has facilitated an increase in genome-level analyses of domesticated animals and non-model species. These analyses have included identification of candidate genes associated with economic and ecological traits to help understanding the genetic underpinnings of species diversification and adaptive evolution. The polar bear is a prime example of adaptive evolution in response to the extremes of life in the high Arctic. These adaptations include mechanisms that allow them to maintain homeostasis under low temperatures and during times of fasting, and extend from evident morphological features to more subtle physiological traits. The polar bear and its closest relative, the lower-latitude brown bear, diverged relatively recently and open questions remain whether candidate genes and positive selection played a significant impact in the evolution of the polar bear. We are using different approaches to examine the polar, brown and black bear nuclear genomes to identify candidate genes involved in adaptation to life in the Arctic environment. Based on enrichment of functional categories in genes with fixed variants in polar bears, we recently found evidence for adaptations related to cellular respiration. Expanded scans for positive selection comparing the polar bear genome with genomes of panda and dog have identified >2000 genes, and when including draft genomes of brown and black bear, 26 candidate genes are found to be under positive selection in polar bear. With more targeted analyses of selected, candidate genes associated with lipid metabolism, hibernation, and pigmentation we have identified possible genes of importance in the functional divergence of the polar bear. This study highlights that genome-wide scans can be limited in statistical power and accuracy due to recent speciation, the lack of high-quality, annotated genomes and incomplete gene models when relying on large-scale analyses and automated construction of alignments of large numbers of homologous gene families. Careful sampling and curation of alignments in analyses of de-novo, non-model draft genomes is imperative.

Gene family evolution and functional plasticity following whole genome duplication events in plants

Daniel Ilut, Michael Gore, John Dyer

1B_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 11:15 AM-11:30 AM
Polyploidy (whole genome duplication) in plants is well documented, and most plant genomes exhibit evidence of repeated whole genome duplication in their evolutionary history. However, less is known about the way such recurring duplication events affect well established gene families which often have strong selective constraints on their copy number and functional localization. In this study, we focus on the omega-3 fatty acid desaturase gene family and its evolution within the Rosid clade. This gene family is involved in the production of polyunsaturated fatty acids, a type of fatty acid that has been linked to cold temperature adaptation in plants. In addition to the existing gene function data available for Arabidopsis thaliana, we performed de-novo localization and stress response analysis in cotton and used the published genome sequences of arabidopsis, papaya, cotton, cacao, and grape to elucidate the evolutionary trajectory of the genomic regions containing these genes. Using a combination of phylogenetic, synteny, and functional analyses, we identified signals of copy number reduction post-polyploidy in the genomes of arabidopsis and paleo-polyploid cotton and likely sub-functionalization into organs under selection in cultivated neo-polyploid cotton. Moreover, we show that similar (and likely anciently established) stress response functions are performed by different members of the gene family in arabidopsis and cotton due to gene copy loss following polyploidy duplication in the arabidopsis lineage.

Drought tolerance of locally adapted Arabidopsis thaliana

Julius Mojica, Jack Mullen, John Lovell, Christopher Oakley, John McKay

1B_302A-Adaptation in Stressful Environments
Saturday, June 21, 2014 10:15 AM-10:30 AM

One of the major foci of evolutionary biology is to identify the key traits involved in adaptation. Drought tolerance is one such trait that can explain local adaptation between Sweden and Italy Arabidopsis ecotypes, which show contrasting levels of water content and water availability in their local environments. To identify quantitative trait loci (QTL) controlling drought tolerance traits and "adaptive trait" QTL (genomic regions where trait QTL and fitness QTL co-localize), we performed QTL mapping on 374 F9 Recombinant Inbred Lines (Sweden x Italy) in well watered and terminal drought conditions. We found a total of 72 QTL across five drought tolerance traits: δ13C, rosette area, dry rosette weight, leaf water content and % leaf nitrogen. Some of these genomic regions co-localize with fitness QTL and with each other in defined hotspots. In addition, we found signatures of conditional neutrality (increase/decrease in drought tolerance trait in one environment and no effect in another environment) and potential tradeoffs (opposite effect on drought tolerance traits from one environment to another). Finally, we identified highly divergent candidate genes, in silico. Our results suggest that adaptation through drought tolerance may be influenced by many genes with minor effects and that pleiotropic drought tolerance QTL may have fitness consequences.

Do effects of nutritional stress on reproductive traits translate from lab to field?

Carol Boggs, Kristjan Niitepõld

1B_302A-Adaptation in Stressful Environments
Saturday, June 21, 2014 10:30 AM-10:45 AM

Life history responses to nutritional stress have been intensely studied in recent years, particularly in the contexts of global change and ageing. Most studies have been done under laboratory conditions, yielding only limited understanding of how stress affects nutrient allocation and life history in the wild. We used a lepidopteran study system, Speyeria mormonia, to test whether effects of stress on egg traits were similar in the lab and field. We first review the effects of adult nutritional stress on egg traits in the lab, yielding predictions for effects in the field. Several of these predictions are upheld under natural nectar stress in the wild. This synthesis demonstrates that laboratory studies can indeed provide useful insight into life history dynamics in the field.

Investigation of salt tolerance in an association mapping population of cultivated sunflower (Helianthus annuus L.)

Caitlin Ishibashi, John Burke

1B_302A-Adaptation in Stressful Environments
Saturday, June 21, 2014 10:45 AM-11:00 AM

Domestication of wild plants by human selection has played a significant role in artificially changing plant traits for large scale cultivation. Because crop species have undergone tremendous selective pressures to refine plant architecture and maximize yield, it is theorized that cultivated varieties often show a loss of tolerance to withstand biotic and abiotic environmental stresses as a necessary trade-off to achieve increased growth. In this study, we used an association mapping population of cultivated sunflower, Helianthus annuus L., to assess variation in growth, resource allocation, and yield while grown under salt-stressed conditions. Salinity is a pervasive concern in agricultural fields, particularly in areas dependent on irrigation. Cultivated sunflower is an important worldwide seed-oil crop, and its ability to tolerate saline conditions is not yet well characterized. We addressed the following questions: (1) How much variation exists in salt tolerance among different genetic lines of Helianthus annuus? (2) Does an increased tolerance to salt stress necessarily correlate with reduced growth? (3)

To answer these questions, we grew H. annuus in a common garden greenhouse under constant salt stress and measured whole plant growth and biomass allocation. Plants exhibited a wide range of values in regards to biomass allocation and growth under salt stress, and did not show consistent signs of reduced growth with increased salt tolerance. These results are consistent with the theory that salt tolerance is a highly quantitative trait, with multiple QTL potentially interacting to generate a whole-plant "tolerant" phenotype. In addition, this study presents a unique opportunity to screen a large amount of genetic diversity across the sunflower germplasm and characterize cultivated sunflower's ability to tolerate salt stress. This knowledge may help inform growers to select and focus on growing putatively salt-tolerant sunflower lines in fields where high salinity levels may be present.

The genetics of adaptation to a granite outcrop environment in the Mimulus guttatus species complex

Kathleen Ferris, Laryssa Baldridge, John Willis

1B_302A-Adaptation in Stressful Environments
Saturday, June 21, 2014 11:00 AM-11:15 AM

A primary goal in evolutionary biology is to understand what traits and genes underlie adaptation to different environments. This is difficult since many traits diverge simultaneously between populations and species. However, genetic manipulation in combination with fitness measurements in the field provides a powerful means to investigate a trait's individual adaptive significance. Despite their recent divergence, members of the Mimulus guttatus species complex have adapted to a wide range of ecological conditions. One species the complex, M. laciniatus, occurs in dry, exposed granite outcrops from mid to high elevation in the Sierra Nevada, CA. The ancestral M. guttatus grows alongside these rocky outcrops in moist streams and grassy seeps. M. laciniatus flowers earlier than sympatric M. guttatus, has a highly self-fertilizing mating system, and a distinctive lobed leaf shape. These traits should be adaptive in dry environments. To investigate the genetic architecture and adaptive significance of flowering time, mating system, and leaf shape in M. laciniatus' granite outcrop habitat we mapped quantitative trait loci (QTL's) in the greenhouse, measured selection on F4 hybrids in a reciprocal transplant in the field, and tested whether our greenhouse QTL's contributed to F4 fitness in the field. We find that divergence in flowering time, mating system traits, and leaf shape between M. laciniatus and M. guttatus is due to few pleiotropic QTL's of large effect, that earlier flowering time is adaptive in M. laciniatus' granite outcrops, and that our major effect pleiotropic greenhouse QTL does not contribute to fitness in the field because the genetic architecture of our focal traits differs between greenhouse and field environments.

ADAPTIVE POTENTIAL AND TRAIT VARIATION OF A WIDESPREAD GRASS Andropogon gerardii ACROSS A GREAT PLAINS CLIMATE GRADIENT: IMPLICATIONS FOR CLIMATE CHAN

Loretta Johnson

1B_302A-Adaptation in Stressful Environments
Saturday, June 21, 2014 11:15 AM-11:30 AM

Midwest grasslands are dominated by big bluestem, Andropogon gerardii that grows across a strong precipitation gradient (500 to 1200 mm/yr from western KS to IL). Grassland response to drought is critical for informing restoration plantings and predicting response to climate. We used reciprocal gardens to investigate ecotype differences in vegetative and reproductive traits. Three ecotypes (from central KS (CKS), eastern KS (EKS), and southern Illinois (SIL)) were reciprocally planted in Colby, Hays, and Manhattan, KS, and Carbondale, IL. We evaluated ecotypic differences in vegetative (canopy area, height, blade width, and emergence) and reproductive features (seed production and flowering time) across planting sites. We predicted ecotypes would perform best in their home environment. Canopy area and height increased from west to east, with no evidence for any ecotype differences in Colby and Hays. However, in Carbondale, the SIL ecotype showed disproportionate increase indicating local adaptation. Ecotypes varied in blade width (SIL>CKS>EKS), and blade widths of all ecotypes increased eastward. For all ecotypes, leaves emerged earlier in eastern Illinois site. In Carbondale and Manhattan planting sites, the CKS ecotype flowered 20 days earlier than other ecotypes and showed a greater probability of seed production in the western sites relative to other ecotypes, while the SIL ecotype had greatest seed productivity in its home site. The CKS ecotype shows a suite of traits consistent with drought tolerance—reduced canopy, short stature, and early flowering in its home environment. Our results provide insight into plasticity of trait variation and ecotypic adaptability in drier climates.

Evolution of a mating preference for a trait used in intrasexual competition in genetically monogamous populations

Caitlin Stern, Maria Servedio

1B_302B-Sexual Selection
Saturday, June 21, 2014 10:15 AM-10:30 AM

The selection pressures by which mating preferences for ornamental traits can evolve in genetically monogamous mating systems remain understudied. Empirical evidence from several taxa supports the prevalence of dual utility traits, defined as traits used both as armaments in intrasexual selection and ornaments in intrasexual selection. Here, we study whether the evolution of mating preferences can occur according to the armament-ornament process under strict monogamy. We find that a mating preference for a trait used in intrasexual resource competition can evolve and affect the evolution of the trait. Trait and preference are more likely to persist when the fecundity benefit for mates of successful competitors is large, the viability cost of the trait is low, and the aversion to unornamented potential mates is strong. The preference can facilitate trait fixation even when costly. Our model applies equally to female preferences for male traits and male preferences for female traits.

The effect of sampling bias on the heritability of preference and the strength of sexual selection

Derek Roff, Daphne Fairbairn

1B_302B-Sexual Selection
Saturday, June 21, 2014 10:30 AM-10:45 AM

The evolution of mate choice is a function of the heritability of preference. Estimation in the laboratory is typically made by presenting a female with a limited number of males. We use an individual-based simulation model to demonstrate that such an approach produces a downwardly biased estimate of preference, which we term the heritability of choice. The threshold transformation method is shown to produce a less biased estimate particularly for preferences based on the relative value of the preferred trait. Because females in the wild typically survey less than 5 males before mating, we argue that the heritability of choice may be more meaningful than the heritability of preference. The effect of the restricted sampling of males on the strength of sexual selection depends upon both the number sampled and preference function. These results are discussed with reference to the Lek paradox and the common occurrence of multiple matings and extra-pair copulations.

The contribution of genes and the environment on traits important for pre and post copulatory reproductive success in the cactus bug, Narnia femorata

Daniel Sasson, Christine Miller

1B_302B-Sexual Selection
Saturday, June 21, 2014 10:45 AM-11:00 AM

Sexual selection has resulted in some of the most elaborate traits in the animal kingdom. Within-population variation in the expression of these traits is likely governed by genes, the environment, and by gene-by-environment (GxE) interactions. The vast majority of studies partitioning out the influence of these factors have focused on sexually selected traits important for attracting and defending mates. However, sexual selection does not end at mate acquisition; post-copulatory sexual selection, such as what occurs during sperm competition, can have a profound impact on an animal's reproductive success. Despite this realization, the number of studies evaluating the genetic and environmental influence on traits important for post-copulatory reproductive success are few and even less common are studies examining these effects on pre and post copulatory traits concurrently. This research is essential, however, since pre and post copulatory traits may not develop in isolation; resource allocation decisions may result in the increase of one trait at the expense of growth in another trait. In this study, we examined the contributions of genes, the environment, and GxE interactions on femur and testes size in Narnia femorata using a half-sib split brood design across three realistic developmental environments. Male

Narnia femorata display and grapple with each other over using their enlarged hind femurs and males with larger femurs are more likely to become dominant, gaining access to high quality territories that attract females. However, females mate multiply, making sperm competition common; thus testes size is likely an important factor in male post-copulatory reproductive success. Our results indicate that heritability for both traits is low and that the environment plays a significant role in determining adult trait expression. Additionally, we found that the environment affects the scaling relationship between femurs and testes, potentially suggesting that the allocation decision rule for these two traits may shift across developmental environments. However, we did not find any GxE interactions for either trait likely due to the low and non-significant heritability of these traits.

A novel application of proteomics to quantify adaptive responses to sperm competition

Dominic Edward, Paula Stockley, Jane Hurst, Rob Beynon, Amy Claydon

1B_302B-Sexual Selection
Saturday, June 21, 2014 11:00 AM-11:15 AM

Sperm competition, whereby the sperm of multiple males compete to fertilise a given set of ova, is a key selective force shaping the evolution of reproductive traits. Theory predicts that males should strategically allocate both sperm and non-sperm components of the ejaculate to maximise chances of success in sperm competition. However, testing these predictions is complicated by the difficulty of distinguishing contributions from different males when females mate multiply. In this study we employ a novel application of quantitative proteomics techniques in conjunction with differential stable isotope labelling to quantify strategic ejaculate allocation of competing male bank voles (Myodes glareolus) under sperm competition. This allows us to determine not only the number of sperm transferred by each male, but also to quantify differences in the non-sperm portion of ejaculate and the efficacy of the copulatory plug deposited by the first male to mate.

Trait-specific levels of sexual dimorphism vary across environments

Christine Miller, Allen Moore

1B_302B-Sexual Selection
Saturday, June 21, 2014 11:15 AM-11:30 AM

Conspicuous differences between the sexes are common in many species. Sexual dimorphism is likely the result of many counteracting sources of selection that result in different optima for males and females. Levels of sexual dimorphism are often assumed to be consistent within a species, yet variation can be found across populations and even over time for the same population. Recent evidence suggests that phenotypic plasticity, not evolved differences, is responsible for much of the variation in sexual dimorphism seen within species. However, little is known about how different types of traits respond to natural environmental variation and how these responses change the size and shape differences between males and females. The evolutionary history of different traits within organisms, specifically whether they have been under directional versus stabilizing selection, should result in predictable changes in the degree of dimorphism across environments. Using the leaf-footed cactus bug, Narnia femorata, we found that sexually-selected traits are highly condition-dependent in males and that sexual dimorphism vanished when individuals developed in poor environments. In contrast, sexual dimorphism in body size traits was maintained across developmental environments. In conclusion, the degree of sexual dimorphism is highly dependent upon the environments encountered during development, and traits can respond very differently to natural environmental variation.

Looking for evolutionary history of nematodes on the beach to better manage their populations in the fields

Cécile Gracianne, Michael Hickerson, Jaanus Remm, Sylvain Fournet, Catherine Porte, Sylvie Valette

1B_302C-Coevolution of Mutualists/Hosts/Parasties
Saturday, June 21, 2014 10:15 AM-10:30 AM

Heterodera schachtii and Heterodera betae are two cysts nematodes causing severe damages in sugar beet (Beta vulgaris subsp. vulgaris) crop every year. Several control methods exist but resistant varieties are often the most cost-effective alternative to pesticides. New varieties are currently developed with genes associated with resistance coming from the wild relative species of cultivated beet, Beta vulgaris subsp. maritima, which is a suitable host plant for both nematodes species. Beta maritima recolonized the Atlantic coastline after the Last Glacial Maximum and wild nematode populations are thus supposed to have historically evolved on this wild host and to have recently being transferred to cultivated fields. This hypothesis has hitherto not been tested though it may have non-negligible consequences on the management of nematode populations in crop fields.

In this context, we developed a phylogeographical approach to (i) evaluate similarities between evolutionary histories of both nematodes and the wild beet at the European scale and (ii) to develop hypotheses on coevolution in the Heterodera schachtii/Heterodera betae/Beta vulgaris subsp. maritima complex. We carried out a hierarchical sampling scheme from southern Spain to northern Europe in order to investigate the occurrence, the ecological preferences, and the spatial structuring of nuclear and cytoplasmic genetic diversity of the three species. Interestingly, results suggest that those species have different ecological niches with different pattern of genetic structure even though they are co-distributed.

Thymol mediates three-way interactions between Thymus (Lamiaceae), legumes, and rhizobia

Mary McKenna, Veronica Rodriguez-Rosas, Dawn Ruiz-Diaz

1B_302C-Coevolution of Mutualists/Hosts/Parasties
Saturday, June 21, 2014 10:30 AM-10:45 AM

Researchers have long known that species in the mint family (Lamiaceae) exude essential oils containing biologically active compounds. We are interested in exploring the potential ecological effects of these secondary compounds in natural plant communities and agroecosystems. Thymol (a principal component of the essential oil of Thymus spp.) is an anti-microbial compound used commercially for its broad-spectrum activity. This study examined the effect of thymol (in biologically realistic concentrations) on nodule formation in Medicago sativa (alfalfa) and Vigna unguiculata (cowpea). Experiments were initiated in a greenhouse at the University of Virginia's Blandy research station in Boyce, VA in summer 2012 and 2013. For alfalfa, we used three treatments: (1) control, (2) addition of 0.3 ng pure thymol (3) addition of thyme essential oil containing 0.3 ng thymol. For cowpea, we examined three extra-early maturing varieties of cowpea developed by the IITA in Nigeria with treatments (1) and (2) above as well as (3) growth with thyme seedlings. Inoculated seeds were sown in a high-drainage soil mixture in 50-cell deep plug trays. Trays were placed in randomized blocks with supplemental lighting (16:8 light L:D cycle), with watering as needed, and with weekly fertilization using 1/5 Hoagland solution without nitrogen. After three weeks, the thymol treatment significantly increased the number of nodules and seedling root weight in alfalfa. In older alfalfa seedlings (five weeks), the thymol treatment also significantly increased shoot weight. In all three varieties of cowpea, significantly more nodules per seedling were observed in treatments with thyme or thymol after five weeks. Two of the three varieties of cowpea also showed significantly larger roots in treatments with thyme and thymol. This study reinforces the importance of a wider community-level view in evaluating the interactions between legumes and their symbionts, particularly since mints (Lamiaceae) co-occur worldwide with legumes (Fabaceae) in natural communities. These results also have implications for improving plant nutrition and soil fertility in agroecosystems. Drought-tolerant legumes like cowpea are critical to food security in rainfed systems such as the Sahel that are threatened by increasing aridity due to global climate change. Further research is underway with carvacrol and other exudates from Lamiaceae to examine impacts on plant-microbial mutualisms. Much is still to learn about the role of bioactive root exudates in mediating multi-species interactions contributing to defense or mutualisms in the rhizosphere. A community-level perspective is essential since these interactions are likely to be diffuse and context-dependent.

The facultative symbiont Rickettsia protects whiteflies against cryptic Pseudomonas syringae pathogens

Tory Hendry, Martha Hunter, David Baltrus

1B_302C-Coevolution of Mutualists/Hosts/Parasties
Saturday, June 21, 2014 10:45 AM-11:00 AM

Facultative endosymbionts can benefit insect hosts in specific contexts, such as by protecting hosts against pathogens. It may be difficult to know how facultative symbionts are benefiting hosts in some populations, especially in the case of protection from cryptic pathogens. The sweet potato whitefly (Bemisia tabaci), an invasive agricultural pest, can possess facultative endosymbionts of the genus Rickettsia. Rickettsia is common in some whitefly populations where it improves host fitness in ways that are not entirely known. We investigated the interaction of a recently discovered cryptic pathogen of hemipteran insects, the common epiphytic bacterium Pseudomonas syringae, with whiteflies and Rickettsia. To determine if Rickettsia can protect whiteflies against cryptic pathogens, we tested whitefly lines with identical nuclear genetic backgrounds, but differing in Rickettsia infection status, for mortality after oral exposure to the pathogen. Sweet potato whiteflies became infected with P. syringae in either in vitro feeding assays or by feeding on plants painted with the bacteria. The bacteria multiplied in the insects and caused very high mortality (80-90%) within four days. The presence of Rickettsia provided whiteflies some protection against the pathogen, slowing the rate of death. The impact of Rickettsia was most pronounced at low infection levels from on plant exposure, suggesting that the interaction could be significant under natural conditions. Little is known about how insects and most environmental bacteria, including P. syringae, interact. Pseudomonas syringae is a common plant pathogen and is widely found on plant surfaces so it could have significant impacts on whitefly populations. These results also suggest that Rickettsia may benefit hosts by protecting against cryptic pathogens, which could contribute to the prevalence of Rickettsia in some populations.

Reduced specialization and modularity in an intimate mutualism diversifying on young oceanic islands

David Hembry, Rafael Raimundo, Erica Newman, Lesje Atkinson, Chang Guo, Paulo Guimarães

1B_302C-Coevolution of Mutualists/Hosts/Parasties
Saturday, June 21, 2014 11:00 AM-11:15 AM

Recent work in ecological network structure has shown that disparate interactions can show patterns of specialization. This raises two important problems in understanding what factors promote the evolution and maintenance of specialization. First, to what extent does interaction intimacy, the degree of biological integration between species, predict specialization? Second, how does network structure vary spatiotemporally in taxonomically related interactions? Prior work has suggested that high-intimacy mutualisms have high modularity and high reciprocal specialization compared to low-intimacy mutualisms. However, such high-intimacy assemblages often are characterized by low species richnesses (Nplants, Nanimals Glochidion) and leafflower moths (Lepidoptera: Epicephala) in continental (Japan) and oceanic island (Society Islands) assemblages. We sampled moths from 10 leafflower species on three of the Society Islands, determined species diversity and network structure using molecular and morphological approaches, and compared these to equivalent data from four sites in Japan from a previous study. We measured modularity using MODULAR, measured indirect effects using pathway proliferation, and measured reciprocal specialization using information entropy and multiplication of dependences of plant and animal taxa in the interaction matrix. We find more asymmetric regional assemblage richness in the Societies (10 leafflower spp. and 3 moth spp.) than in Japan (5 leafflower spp. and 5 moth spp.). One Societies Epicephala taxon appears to be a “super-generalist” which interacts with 9 out of 10 available hosts. All Japanese assemblages show high modularity and reciprocal specialization. Two Societies assemblages (Huahine and Tahiti) lack modularity while the third (Moorea) is modular. Pathway proliferation results show that structurally similar networks may have important differences in their potential for indirect effect propagation. For example, Tahiti and Huahine have a one-order-of-magnitude difference in the number of higher pathway lengths connecting pairs of species. These indicate that a) in continental regions, brood-pollination assemblages show similarly high modularity and reciprocal specialization as do ant-myrmecophyte assemblages, supporting the hypothesis that biological intimacy promotes these network properties; b) network properties and specialization can vary spatiotemporally within the same mutualism; c) "super-generalist" taxa may also exist in high-intimacy mutualisms; d) highly connected, non-modular small networks vary in their potential for the propagation of indirect effects, with potentially important consequences for convergent trait evolution. Finally, the novel methods presented here can be profitably applied to the topological analysis of other small networks.

Phylogenomics shows multiple human infectious lineages of Trypanosoma brucei

Mark Sistrom, Benjamin Evans, Serap Aksoy, Adalgisa Caccone, Paul Turner

1B_302C-Coevolution of Mutualists/Hosts/Parasties
Saturday, June 21, 2014 11:15 AM-11:30 AM

Using whole genome sequencing from 39 T. brucei strains, we construct the first comprehensive phylogenetic tree for the group based on over 750 sequence loci, totalling over 37kb in data. This analysis shows that multiple lineages of T. brucei are human infective, conclusively demonstrtating that the current taxonomy of the group does not reflect its evolutionary history. It also confirms the critical role that horizontal transfer of the Serum Resistance Associated (SRA) plays in the generation of human infective T. brucei strains, and that all circulating strains of T. brucei have the potential to become infective to humans.

Life-history evolution of serotinous trees: the role of inter-fire recruitment and dispersal

Alexander Kubisch, Ophélie Ronce, Jeanne Tonnabel, Frank Schurr

1B_303-Life History
Saturday, June 21, 2014 10:15 AM-10:30 AM

Many plant species have evolved serotiny, i.e. the retention of mature seeds in closed cones within the plant's canopy, as a means to deal with recurring fire events. We build on a recent model of serotiny evolution in fire-prone environments and extend it to explore the role of metapopulation dynamics and recruitment between fires. In this respect we are to our knowledge the first to investigate the interplay between dispersal and serotiny. We have therefore developed an individual-based metapopulation model of a serotinous tree species with several life-history traits evolving (age of first reproduction, reproductive effort, degree of serotiny).

When investigating the fire regime, we find that the age of first reproduction increases with increasing fire return interval, while reproductive effort decreases. Yet, our results show a unimodal response of the degree of serotiny to decreasing fire frequency, which can be explained by lowered benefits of being serotinous for very high or very low fire frequencies. We also find a positive relationship between the amount of seed dispersal and the optimal degree of serotiny. The reason for this can be found in the recruitment dynamics between fires, as more dispersal leads to a faster colonization of empty sites, thus increasing the benefit of producing seeds as early after a fire as possible. Inter-fire dynamics of serotiny additionally reveal that, even though the average serotiny level has reached an equilibrium at the metapopulation level, within populations genotypes with strong serotiny are advantaged just after fire occurrence but there is selection for lower serotiny between fires.

Genome wide association analysis reveals age-specific genetic effects on life history traits

Jeff Leips, Mary Durham, Tashauna Felix, Adrienne Starks

1B_303-Life History
Saturday, June 21, 2014 10:30 AM-10:45 AM

We used the Drosophila Genetic Reference Panel to identify polymorphisms influencing age-specific fecundity and immune response as well as life span. We find that the genetic basis of variation for fecundity and immunity changes dramatically with age. We discuss the implications of this result for life history evolution.

Strong interspecific interactions help drive the evolution of life histories in the Trinidadian guppy

Ronald Bassar, Brad Lamphere, Andres Lopez-Sepulcre, Joseph Travis, David Reznick

1B_303-Life History
Saturday, June 21, 2014 10:45 AM-11:00 AM

Populations of Trinidadian guppies (Poecilia reticulata) exhibit extensive, genetically based differences in life histories associated with the types of predators with which they co-occur. Prior research has focused on the contrast between low-predation environments, where guppies co-occur with just the killifish Rivulus hartii, and high-predation environments, where guppies co-occur with Rivulus plus other species of predatory fishes. These differences in predation pressure are associated with other ecological factors, including physical characteristics of streams, primary productivity, and other aspects of the biotic communities. The life history differences between guppies from high- and low-predation communities have long been attributed to the different risks of predation. However, while lowered predation risk at higher elevations is necessary for the low-predation life history to evolve, it is not sufficient. There are three additional hypotheses for this evolution, all of which postulate some form of feedback from the ecological effects of guppies on their ecosystems to the selection gradients favoring the low-predation life history. Here we present evidence for one of them, that strong pairwise interactions of guppies with Rivulus create selection pressures that facilitate the evolution of the low-predation life history. We show from a field introduction experiment that guppies decrease Rivulus population density and alter the size structure of Rivulus populations. The magnitude of these effects is associated with changes in guppy population density and phenotype. We show from mesocosm experiments that in the presence of Rivulus drawn from locations in which guppies do not occur, guppies with the low-predation phenotype have higher population growth rates than do guppies with the high-predation phenotype. We also show that low-predation guppies have higher population growth rates when paired with Rivulus drawn from locations in which the two species coexist than when they are paired with Rivulus drawn from locations where guppies do not occur. Taken together, these results indicate that strong ecological interactions between guppies and Rivulus create selection pressures that drive a coevolutionary feedback loop that contributes to the successful evolution of the low-predation phenotype.

Natural variation in seed germination speed of Arabidopsis thaliana: complex genetic architecture and response to strong selection

Wei Yuan

1B_303-Life History
Saturday, June 21, 2014 11:00 AM-11:15 AM
Natural variation in seed germination speed of Arabidopsis thaliana: complex genetic architecture and response to strong selection

The natural variation of the timing of developmental transitions associated with life history traits provides sources for, and reflects the outcome of adaptation. Germination timing of seeds is a key turning point during the plant life history with consequences in fitness and adaptation. Germination speed (i.e. the time lapse from reception of favorable germination cues to emergence of the earliest seedling cohort), is an integral component of germination timing, and exhibits strong correlation with plant’s fitness under competition and fluctuating environment. We characterized quantitative natural variation in germination speed among a worldwide collection of 17 Arabidopsis.thaliana natural accessions, under both regular and saline conditions, and found that germination speed is environmentally sensitive and density dependent. To dissect the genetic architecture of germination speed, we implemented the novel yeast eXtreme-QTL (X-QTL) mapping technique (Ehrenreich et al, 2010) in A. thaliana. Using population-based phenotyping and high-throughput bulk segregant genotyping, we overcame the lack of detection power of traditional QTL mapping methods whose resolution is limited by the number of recombination events. Rapid germinant pools sampled from replicates of 100,000 segregating seeds revealed 4 X-QTLs for rapid germination under normal conditions and 18 X-QTLs under extreme saline conditions. Based on low-coverage next-generation resequencing of individual fast germinating segregants, we annotated a 150-kb flanking genomic sequences on both sides of the X-QTL peak positions. Genomic polymorphism and germination transcriptomic data were collected from both parental accessions, which enabled the identification of several strong candidate genes. Our project uncovers the complex genetic architecture of germination speed natural variation, its gene-by-environment interaction, and establishes the X-QTL mapping in a multicellular eukaryotic organism.

Plasticity of seed dormancy compensates for differences in dispersal timing

Liana Burghardt, Brianne Edwards, Kathleen Donohue

1B_303-Life History
Saturday, June 21, 2014 11:15 AM-11:30 AM
Environmental variation can alter the expression of allelic variation: some environmental contexts can magnify the phenotypic differences between allelic variants and others can reduce, or canalize, that variation. Selection among genotypes occurs only under conditions in which phenotypic differences among genotypes are expressed. Environmental conditions can influence germination phenotypes 1) prior to seed dispersal by influencing seed dormancy and 2) post seed dispersal by changing the conditions seeds experience after dispersal. Here we consider how specific environmental factors influence the translation of genetic variation into phenotypic variation. We conducted germination experiments with four genotypes of A. thaliana known to differ in germination phenotypes. We tested how differences in seed-maturation temperature and the loss of dormancy with seed aging influence the range of temperatures over which germination can occur. The temperature over which germination occurred differed among genotypes, seed-maturation conditions, and after-ripening duration. Germination for all genotypes increased with seed maturation environment and seed aging, but genotypes differed in the degree of plasticity to seed maturation environment. We used these results to project germination timing in a seasonal environment and were able formulate predictions about how environmentally induced phenotypic expression may be manifest in an ecologically relevant scenario. We found three genotypes behaved quite similarly despite differences in measured dormancy, but one genotype deviated strongly. Our results also suggested that maternal effects can offset differences in dispersal time in seasonal environments. Consideration of how germination phenology is influenced by both seed-maturation temperature and post-dispersal conditions will be important for predicting phenology in response to climate change and introduction to novel environments.

The evolution of host perception in parasitic plants of the Orobanchaceae

Caitlin Conn, Drexel Neumann, Kelly Dyer, David Nelson

1B_304-Host-Parasite/Pathogen Interactions
Saturday, June 21, 2014 10:15 AM-10:30 AM
Parasitic plants of the Orobanchaceae attack crop species including grasses, grains, and legumes throughout the world. In sub-Saharan Africa alone, they cause billions of dollars of annual economic losses. Parasitic plants germinate in response to strigolactones, which are hormones exuded from host roots. Karrikins are structurally similar compounds found in smoke that stimulate post-fire germination in other plant species. Karrikins stimulate germination and strigolactones regulate plant architecture in the model species Arabidopsis thaliana. In A. thaliana the KAI2 and D14 proteins are putative receptors for karrikins and strigolactones, respectively. kai2 mutants have increased seed dormancy, no germination response to karrikin, and decreased light sensitivity.

d14 mutants germinate normally but have increased axillary branching, consistent with strigolactone insensitivity.

It is not known how parasitic plants perceive strigolactones, but this knowledge could result in the development of new strategies to control parasitic weeds. We hypothesized that D14 or KAI2 is involved in the germination response of parasites to strigolactones. To address this hypothesis, we have combined molecular evolutionary and functional analyses. We found that KAI2 has undergone gene duplication in parasitic plants. We performed phylogeny-based selection tests and found that parasite KAI2 orthologs belong to three clades with three different rates of evolution. In members of the fastest-evolving clade, we found evidence of positive selection on three amino acid residues predicted to contribute to ligand specificity. We transformed A. thaliana kai2 mutants with KAI2 orthologs from parasitic plants. Slow-evolving parasite KAI2 orthologs rescue the Atkai2 seedling light sensitivity phenotype. A parasite KAI2 ortholog with an intermediate rate of evolution confers a karrikin-specific germination response. Fast-evolving parasite KAI2 orthologs confer a strigolactone-specific germination responses. These data suggest that slower-evolving parasite KAI2 orthologs may retain evolutionarily conserved roles in light sensitivity and perception of karrikin-like compounds, while faster-evolving orthologs may have adapted to sense host-derived germination cues.

RNAseq analysis elucidate early responses to infection in scleractinian corals

Jorge Pinzon, Ernesto Weil, Laura Mydlarz

1B_304-Host-Parasite/Pathogen Interactions
Saturday, June 21, 2014 10:30 AM-10:45 AM

Diseases have become one of the major causes of coral mortality and coral reef deterioration worldwide. The emergence of coral diseases has been associated with climate change, yet disease prevalence and mortality are highly variable and apparently species dependent. In the Caribbean for example, important species, like Acropora spp. have suffered geographic-wide population crashes by what seemed to be a single disease. Other important reef builders such as Orbicella spp. have suffered significant population declines but caused by a host of several different diseases. However, there are species that seem to be resistant and are thriving. Porites spp, for example, are becoming more abundant even in areas were corals have been replaced by other fast growing organism (i.e. algae). To analyze the molecular basis of this disparity, we exposed coral colonies from four species to lipopolysaccharides (LPS) and analyzed changes in gene expression a few hours after exposure. We used RNA seq analysis to understand early responses to infection of corals differentially affected by diseases. Preliminary data suggest that coral species display particular responses to the initial stages of infection, with no apparent relation to the number of diseases affecting each host. Orbicella faveolata (8 diseases) and Porites astreoides (5) showed significant changes between exposed and control fragments. In Porites porites (3) and Pseudodiploria strigosa (6) changes in expression were significant at the individual colony level but not across treatments. It appears as if the molecular machinery in corals responds differentially based on the genetic composition of each species and the genotype of each individual colony.

Evolution and host manipulation of Nasonia venom

Ellen Martinson, Mrinalini Mrinalini, Jack Werren

1B_304-Host-Parasite/Pathogen Interactions
Saturday, June 21, 2014 10:45 AM-11:00 AM

Parasitoid wasps are abundant and ecologically important predators that inject venom into and then lay their eggs on other insects. Parasitoids vary in the hosts they utilize (flies, beetles, butterflies, etc), the life stage they parasitize (eggs, larvae, pupae). With their diverse life histories, parasitoid venom has evolved mechanisms for manipulating host immunity, physiology, and behavior in ways that enhance the development of parasitoid young, yet virtually nothing is known about the diversity or function of individual parasitoid venom proteins. A model ectoparasitoid wasp Nasonia vitripennis has at least 79 different venom proteins, of which 24 have no sequence similarity to any known proteins. Given the incredible diversity of parasitoids, their venoms represent an immense and untapped potential resource for novel traits. Here we investigate the diversity and evolution of venom proteins in different parasitoid wasps using proteomes and transcriptomes to evaluate four Nasonia species in order to assess how venom proteins are recruited and lost among closely related species. We have found rapid turnover of venom proteins among the four species. Additionally, we used a transcriptomic approach to measure changes in gene expression in stung and unstung hosts (Sarcophaga bullata, Diptera) following envenomation by N. vitripennis. The results indicate that venoms target very specific aspects of host gene expression with

---

Evolution of immune response in Drosophila melanogaster populations selected against a gram-negative bacteria

Vanika Gupta, zeeshan syed, N.G PRASAD

1B_304-Host-Parasite/Pathogen Interactions
Saturday, June 21, 2014 11:00 AM-11:15 AM

Immunity is a costly trait and is often observed to trade-off with other costly traits. Not only this, ability to mount better immune response against a pathogen is often thought to trade-off with ability to resist other pathogens. Phenotypic manipulation experiments using Drosophila melanogaster showed that same populations subjected to various pathogens respond differentially. However, direct empirical evidence that validate whether evolved resistance against one pathogen would provide resistance against other unrelated pathogens or not is lacking. We subjected this idea to populations of Drosophila melanogaster evolved for better survivorship against a gram-negative pathogen Pseudomonas entomophila. In our study, replicate populations of Drosophila melanogater were subjected to three selection regimes – I (Infected with bacteria), S (Sham – infected, injured with needle dipped in MgSO4) and U (Unhandled controls). After 30 generations of selection, we obImmunity is a costly trait and is often observed to trade-off with other costly traits. Not only this, ability to mount better immune response against a pathogen is often thought to trade-off with ability to resist other pathogens. Phenotypic manipulation experiments using Drosophila melanogaster showed that same populations subjected to various pathogens respond differentially. However, direct empirical evidence that validate whether evolved resistance against one pathogen would provide resistance against other unrelated pathogens or not is lacking. We subjected this idea to populations of Drosophila melanogaster evolved for better survivorship against a gram-negative pathogen Pseudomonas entomophila. In our study, replicate populations of Drosophila melanogater were subjected to three selection regimes – I (Infected with bacteria), S (Sham – infected, injured with needle dipped in MgSO4) and U (Unhandled controls). After 30 generations of selection, we observed that males and females of I- regime had better survivorship against Pseudomonas entomophila compared to S and U populations. We then subjected these populations to two other pathogens – Providencia retgerii (gram-negative pathogen) and Staphylococcus succinus (gram-positive pathogen) to address whether evolved resistance is general or specific. Interestingly, we found that both males and females of selected I populations survived better than controls when challenged with these pathogens. Also, we observed that I females clear more bacteria compared to controls. However, even though I males showed increased survivorship against both pathogens, we observed a pathogen specific response in terms of their ability to clear bacteria. We conclude that evolved immune response against pathogen selected for, can result in better immune response against multiple pathogens.

Evidence of pathogen-induced recombination among low-fitness lineages of Drosophila melanogaster

Nicholas Priest, *Weihao Zhong*

1B_304-Host-Parasite/Pathogen Interactions
Saturday, June 21, 2014 11:15 AM-11:30 AM

Hosts mount a multitude of responses to mitigate fitness losses from infection. But, we do not know whether such responses depend on fitness or alter the evolutionary potential of infected hosts. Theory predicts that fitness associated maternal effects can accelerate the rate of adaptive evolution, particularly when low fitness mother produce daughters with high rates of meiotic recombination. Here we provide evidence for this phenomenon when the fruit fly, Drosophia melanogaster, is topically infected with the fungal pathogen, Metarhizium robertsii. We show that this response only occurs in chronically infected lineages, which suggests that fly lineages only re-shuffle their genome when they have low fitness for multiple generations. These findings indicate that pathogen-induced maternal effects on recombination could be an effective mechanism for accelerating the adaptation of low-fitness lineages to pathogen rich environments.

The genetic basis of adaptation to serpentine soils in Mimulus guttatus

Jessica Selby, *John Willis*

1B_305A-Local/ecotype Adaptation in Plants
Saturday, June 21, 2014 10:15 AM-10:30 AM

While local adaptation has been frequently demonstrated via reciprocal transplant experiments, our understanding of the genetic basis of it remains minimal. There is a notable lack of studies that identify naturally segregating variants, determine the traits controlled by these variants and characterize their fitness effects in the field. Such studies are critical for understanding how spatially varying selective pressures can drive population divergence and maintain genetic variation. The experiments presented here aim to characterize the genetic basis of local adaptation to serpentine soils in Mimulus guttatus. First, I show that serpentine and non-serpentine populations of M. guttatus are locally adapted to soil habitat wherein non-serpentine plants are unable to survive on serpentine soils. Serpentine tolerance appears to come at a cost as serpentine plants are smaller than non-serpentine plants when growing on non-serpentine soils which may limit their competitive ability. Next I identify environmental variables that are important selective agents in the serpentine habitat. Using hydroponic assays to isolate individual chemical variables of serpentine soils, I show that serpentine and non-serpentine populations of M. guttatus have significant differences in tolerance to low calcium to magnesium ratio (low Ca:Mg ratio) as well as high nickel. I then characterize the genetic basis of these ecotypic differences in survival and tolerance using QTL mapping. I identify a single, major QTL the controls both the ability to survive on serpentine soils and tolerance to low Ca:Mg ratio. This suggests that M. guttatus populations have adapted to serpentine soils through an ability to tolerate the low levels of Ca while simultaneously not suffering from Mg toxicity. Furthermore, I show that this same QTL controls ability to survive on serpentine soils in a second, geographically distant population; however, preliminary work suggests that the two populations are not equally tolerant to each other's soils indicating that either other loci are involved or that different serpentine tolerance alleles at this QTL are not functionally equivalent. This work addresses long-standing questions in evolutionary biology regarding the number and effect size of loci that underlie adaptive traits by identifying a large effect locus that contributes to adaptive differences between M. guttatus populations.

Repeated evolution of serpentine tolerance across Monkeyflower species (Mimulus)

Annie Jeong, *Jennifer Coughlin, John Willis*

1B_305A-Local/ecotype Adaptation in Plants
Saturday, June 21, 2014 10:30 AM-10:45 AM

For plants, harsh soil conditions such as serpentine soils present a particularly challenging living environment, as soils provide the primary source of nutrients for a plant. Serpentine soils have greatly reduced essential nutrients such as calcium, and contain near toxic levels of magnesium and heavy metals. Despite such inhospitable conditions, many species have adapted to survive on serpentine soils. Within the Mimulus genus alone, there have been at least 14 independent origins of serpentine tolerance. Recent research in the Willis lab has identified genetic loci in Mimulus guttatus that are required for survival on serpentine soil and in low Ca:Mg environments. Limited experimental research suggests that tolerance can be achieved in many ways. In order to understand whether similar physiological and genetic mechanisms are used in the repeated evolution of serpentine tolerance in Mimulus, we must examine many more serpentine tolerant species. Multiple species that occur on serpentine soil were studied to determine their mechanisms of tolerance and compared to M. guttatus. Tolerant and non-tolerant populations of each species were grown on native serpentine soils in the lab and scored for signs of stress and non-tolerance. Non-tolerant individuals showed severe necrosis, a possible effect of insufficient calcium, while tolerant individuals appeared healthy and succeeded to flowering. When grown hydroponically in extreme levels of either magnesium, calcium, and nickel, species showed different responses to treatments that suggest that some species may share the same mechanisms of tolerance while others may not. However, QTL mapping is required to determine whether the same genetic loci are responsible for serpentine tolerance. This expansive study will allow us to better understand mechanisms of serpentine tolerance, and also provide insight into the extent that parallel or convergent adaptation occurs between closely related species.

How does soil environment influence growth and reproduction in a serpentine plant: the past and the present

Steve Travers, Magdalene Ovbiebo

1B_305A-Local/ecotype Adaptation in Plants
Saturday, June 21, 2014 10:45 AM-11:00 AM

Environmental effects on pollen performance have the potential to influence both the reproductive success of individuals and the degree of interbreeding between populations because success during gametophytic competition is linked to pollen performance. Previous studies have found that assortative mating can be affected by edaphic characters through effects of soil nutrition on the pollen performance of plants from different populations and soil types. We studied the potential for serpentine soils to alter pollen performance and reproductive success of Mimulus guttatus growing on or off of serpentine soils. Using a hydroponic format in a greenhouse we manipulated the nutritional conditions of plants grown from seed collected from either serpentine or control soils in California. We measured the effects of seed source (serpentine, control) and growth environment (low versus high Ca/Mg ratio) on plant growth, stem number and pollen performance. Plant biomass was highest for control plants grown in high Ca soils and for serpentine plants grown in low Ca soils. Pollen tube growth rates were higher for both types of plants when the female plant was grown in a high Ca environment suggesting a strong influence of maternal growth environment on pollen performance. As in the case of biomass, control plants improved more dramatically in high Ca styles compared to serpentine plants which had faster pollen tubes in low Ca styles relative to control plants. These results suggest that the success of ecotypes at gametophytic competition will be influenced by the growth environment of the female plant and competition could reinforce assortative mating in plants from different environments.

Experimental evidence of soil-mediated local adaptation of aphids to plants

Eduardo de la Pena

1B_305A-Local/ecotype Adaptation in Plants
Saturday, June 21, 2014 11:00 AM-11:15 AM

Plants are intimately associated with soil microbes and foliar feeding insects. This gives rise to three-way interactions that have important consequences for the functioning and evolution of these organisms. Although during the last decade above- and belowground interactions have received considerable attention, the consequences of plant-soil interactions for insect evolution remain still largely unexplored. To shed light on this matter, I tested experimentally whether insect herbivores could be adapted to plant populations by mediation of the soil community. Using the dune grass Ammophila arenaria, the aphid Schizaphis rufula and arbuscular mycorrhizal fungi (AMF), I conducted a series of rearing experiments in which aphid performance was compared on different grass populations. To test whether soil AMF could be mediating the interaction with the aphid, insect multiplication was compared on plants growing in sterilized soil inoculated with local or non-local soil communities and AMF. The results of the experiments showed that not only the soil community was important for aphid performance, but also its origin (local vs. non local). In general, local combinations of plants and soil communities had a greater influence on aphid multiplication than non-local combinations. These results highlight the importance of the soil biota, and AMF in particular, to understand plant insect interactions from an evolutionary perspective.

The genetics of divergence and reproductive isolation between ecotypes of Panicum hallii

David Lowry, Thomas Juenger

1B_305A-Local/ecotype Adaptation in Plants
Saturday, June 21, 2014 11:15 AM-11:30 AM

The process of plant speciation often involves the evolution of divergent ecotypes in response to natural selection imposed by differences in soil water availability between habitats. However, the genetic mechanisms that contribute to divergence and reproductive isolation between such ecotypes are poorly understood. The self-fertilizing C4 grass species Panicum hallii includes two major ecotypes: one found most commonly in water-limited habitats (var. hallii) and the other (var. filipes) occurring in mesic (wet) habitats. We constructed the first linkage map for P. hallii by genotyping a reduced representation genomic library. We then evaluated the genetic architecture of divergence between these ecotypes through quantitative trait locus (QTL) mapping. Overall, we mapped QTLs for nine morphological traits that are involved in the divergence between the ecotypes. Physiological traits were less divergent, but we still mapped nine QTLs across 14 traits. There were co-localizing QTLs for multiple traits, which suggests that pleiotropy may be important for evolution of the ecotypes. We discovered a two-locus Dobzhansky-Muller incompatibility system that contributes to sterility in hybrids. In addition, we have begun studying the landscape evolutionary genomics of adaptation across a large-scale moisture gradient through the whole genome resequencing of P. hallii accessions. Our studies collectively provide new insights into the evolution of divergence and reproductive isolation between ecotypes that have formed in response to selection imposed by variation in soil water availability.

An altitudinal cline in an ultraviolet floral trait is associated with changes in selection and pollination context

Matthew Koski, Tia-Lynn Ashman

1B_305B-Pollination
Saturday, June 21, 2014 10:15 AM-10:30 AM

Spatially varying selection can drive phenotypic diversification and lead to speciation. Floral phenotype, in particular, can covary with pollinator-mediated selection, but not all floral traits relevant to pollinators are obvious to humans and thus have not been subjects of selection studies. Here, we identify an altitudinal cline of increasing size of the ultraviolet (UV) bullseye pattern (UV-reflecting petal tips, UV-absorbing bases) on flowers of Argentina anserina (Rosaceae), and test whether pollinator-mediated selection is responsible for maintenance of the cline by documenting the pollinator assemblage, flower-visitor preferences, and selection at four populations along the gradient. The size of the UV bullseye increased with the proportion of flower-visitors that were dipterans. Flowers manipulated to have larger bullseyes were visited more often by insects than those with smaller bullseyes at high, but not at low altitude sites. Phenotypic selection via pollen receipt was stronger on the UV bullseye than on floral size, display, or color. Selection favored smaller bullseyes at the lowest altitude, larger bullseyes at the highest altitude, and increased with both dipteran abundance and preference for a larger bullseye. Results indicate that pollinators may exert selection on floral patterns invisible to humans, and thus influence clinal variation in these traits.

Identification of major QTLs underlying floral pollination syndrome divergence in Penstemon

Carolyn Wessinger, Lena Hileman, Mark Rausher

1B_305B-Pollination
Saturday, June 21, 2014 10:30 AM-10:45 AM

Distinct floral pollination syndromes have emerged multiple times during the diversification of flowering plants. For example, in western North America, a hummingbird pollination syndrome has evolved more than one hundred times, generally from within insect pollinated lineages. The hummingbird syndrome is characterized by a suite of floral traits that attracts and facilitates pollen movement by hummingbirds, while at the same time discourages bee visitation. These floral traits include large nectar volume, red flower color, elongated and narrow corolla tubes and reproductive organs that are exerted from the corolla. A handful of studies have examined the genetic architecture of hummingbird pollination syndrome evolution. These studies find that mutations of relatively large effect often explain increased nectar volume and transition to red flower color. In addition, they suggest that adaptive suites of floral traits may often exhibit a high degree of genetic linkage, which could facilitate their fixation during pollination syndrome evolution. We explored these emerging generalities by investigating the genetic basis of floral pollination syndrome divergence between two related Penstemon species with different pollination syndromes – bee-pollinated P. neomexicanus and closely related hummingbird-pollinated P. barbatus. In an F2 mapping population derived from a cross between these two species, we characterized the effect size of genetic loci underlying floral trait divergence associated with the transition to bird pollination, as well as correlation structure of floral trait variation. We find the effect sizes of QTLs for adaptive floral traits are in line with patterns observed in previous studies, with large effect sizes observed, particularly for flower color and nectar volume. We find strong evidence that suites of floral traits are genetically linked. This linkage may be due to genetic proximity or pleiotropic effects of single causative loci. Interestingly, our data suggest that the evolution of floral traits critical for hummingbird pollination was not constrained by negative pleiotropy at loci that show co-localization for multiple traits.

Evolution of hawkmoth pollination in the gourd family (Cucurbitaceae)

Tom Mitchell, Hanno Schaefer

1B_305B-Pollination
Saturday, June 21, 2014 10:45 AM-11:00 AM

Hawkmoth pollination evolved multiple times in the gourd family (Cucurbitaceae), with five of these lineages, together totalling more than 100 species, possessing showy tubular flowers with long-fringed petals. GCMS analyses of scent samples collected from the floral headspace of two of these lineages (Ampelosicyos and Trichosanthes) have identified a number of compounds well known as floral scent constituents in other hawkmoth-pollinated species, and highlighted some potentially interesting similarities and differences in their respective scent profiles. Furthermore micromorphological analysis of floral tissue has indicated the presence of osmophores on the petal fringes suggesting their role may not solely be a visual one. A shift to hawkmoth pollination leads to a significant increase in diversification rate in one of the five lineages (the snake gourds) but not in the other four lineages. The role of fringed petals as a key innovation in cucurbit evolution is therefore discussed.

Making sense of floral scents: floral scent in the genus Mimulus and its role in pollinator shifts

Kelsey Byers

1B_305B-Pollination
Saturday, June 21, 2014 11:00 AM-11:15 AM

Floral diversity is immense, with more than 250,000 species of angiosperms known. The number of phylogenetically diverse floral species that share common characteristics implies a background pattern of selection acting on floral traits. Unique combinations of these floral traits, or pollination syndromes, are hypothesized to reflect selective pressure imposed by certain classes of pollinators. One flower character in particular, scent, has been hypothesized to operate as an unseen signal to attract certain pollinators, particularly when combined with other signals such as color and shape. However, the contribution of scent in pollinator-mediated selection between sister taxa has nearly always been inferred and rarely directly tested, and pollinator sensory mechanisms that drive attraction often remain unclear. The genus Mimulus (Phrymaceae) forms a developing model system for studying floral diversity and pollinator-driven speciation using a combination of genetic tools and field ecology.

Within Mimulus, section Erythranthe contains seven species with two independent transitions from ancestral bee pollination to derived hummingbird pollination, making it an ideal system to study pollination syndrome transitions. The role of scent in these transitions remains unclear in most cases, but floral scent is known to be important to a variety of pollinating animals and thus is likely to have played a role in the diversity seen in the section. Populations and species within section Erythranthe cluster by floral scent profile despite broad overlap in the volatiles produced. Some volatiles appear to be under positive selection, while others appear to be under relaxed selection, representing differences in selective pressure due to a variety of potential selective agents acting on floral scent. Floral scent may provide a mechanism for diversification and pollinator adaptation in angiosperm taxa.

Genomic scale phylogeographic analysis of the endangered eastern massasauga rattlesnake (Sistrurus catenatus)

Michael Sovic, Anthony Fries, H. Lisle Gibbs

1B_306A-Biodiversity
Saturday, June 21, 2014 10:15 AM-10:30 AM
Identifying phylogenetically distinct lineages within endangered species can aid in defining conservation units. Genomic scale datasets generated from next generation sequencing approaches provide an unprecedented amount of data for such studies but also present analytical challenges. We conduct a phylogeographic analysis of the endangered eastern massasauga rattlesnake (Sistrurus catenatus) based on SNP data generated using a double digest RADseq method. We first use discriminate analysis of principal components to identify genetic clusters within a range-wide set of samples, and then assess whether the clusters represent phylogenetically distinct lineages using a novel approach involving coalescent-based species tree analyses. Specifically, we use repeated subsampling of individuals to estimate both topologies and branch lengths for lineages suggested by the clustering results, and then test for significance of branch lengths through comparisons to null models. Our analyses fail to support phylogenetically significant lineages within this species with the notable and previously unrecognized exception of a population west of the Mississippi River. In summary, by applying a novel method for lineage identification using genomic scale data, we have identified a previously unrecognized and phylogenetically distinct lineage within these snakes of special conservation concern.

Description of a Novel Genetic Marker for Species Identification of Freshwater Mussel Larvae Recovered from Naturally Infested Fish Hosts

Katie Bockrath, John P. Wares, Nathan Johnson

1B_306A-Biodiversity
Saturday, June 21, 2014 10:30 AM-10:45 AM
Freshwater mussels in North America are species rich and vastly diverse in morphology and habitat use. Because of this diversity, the ecosystem functions mussels provide (e.g.: water filtration, nutrient cycling) are likely to occur across freshwater systems. Due to habitat destruction, many mussel populations are in decline. In order to maintain current populations, larvae must successfully recruit to replenish populations as well as establish new populations. Because mussels have an obligate parasitic larval stage, recruitment is dependent on host availability. Some mussel species have adapted methods of attracting fish hosts with lures and host use is best understood for these taxa. Conversely, there is little known about host use in mussel taxa that lack conspicuous lures. Recently, genetic data have provided insights into host use in mussel taxa that lack lures because genetic markers can be used to identify mussel larvae on fish hosts in nature. Unfortunately, the genetic markers used in these studies are found in both mussel and host and the risk of contamination from host tissue is high. An ideal genetic marker would be unique to mussel genomes yet capable of distinguishing between mussel species. Here, we show that Female-specific Open Reading Frame (FORF) is an ideal genetic marker for mussel species identification and host use determination. The FORF database presented here is specific to mussel taxa in the Apalachicola River Basin (ACF), but could easily be extended to include other river drainages. Representatives of all extant mussel taxa were collected from the ACF and, using tissue samples, a FORF genetic barcode database was generated. Using mussel larvae recovered from naturally infested host fish, FORF was able to identify the mussel species. Additionally, fish host use for these mussel species was determined. To our knowledge, this study is the first to document host use in two species of the genus Elliptio (E. fraterna and E. fumata). The implication for the use of this genetic marker is simple species identification of mussel larvae collected from host tissue without host contamination.

Assessment of the subspecies status of Calidris maritima littoralis (Aves: Charidriiformes: Scolopacidae)

Derek Barisas, Julien Amouret, Gunnar Þór Hallgrímsson, Ron Summers, Snæbjörn Pálsson

1B_306A-Biodiversity
Saturday, June 21, 2014 10:45 AM-11:00 AM
The Icelandic Purple Sandpiper Calidris maritima littoralis represents one member of a poorly understood subspecies complex. Currently, differences in morphology define two other subspecies, C. m. belcheri, which breeds in northeastern Canada along the Hudson Bay and James Bay, and C. m. maritima , which breeds along the Arctic coasts elsewhere in northern Canada, Greenland, Svalbard, and Scandinavia to northcentral Siberia. As a circumpolar breeding bird, the Purple Sandpiper could provide an interesting perspective on the evolutionary changes following an expansion of a species northward following the Last Glacial Maxima. Considering the extent of the icesheet in the northern hemisphere during the last Ice Age and the short period since the Last Glacial Maxima, correct attribution of subspecies status within the Purple Sandpiper may either reflect a rapid diversification or an ancestral split of distinct evolutionary lineages which survived in isolation at southern latitudes. Applying a morphometric subspecies criteria, diagnosability by Amadon's Rule, and genetic analysis of five nuclear introns and the mtDNA markers, CO1 and ND2, to geographically diverse breeding populations clarified the

subspecies attribution of the Icelandic population. Weak but present diagnosability coupled with low levels of significant genetic divergence indicate a recent morphological differentiation of the Icelandic population from a shared refugia. The genetic data calls into question the subspecies attribution due to a lack of evolutionary relevance in the classification.

Exploring reticulate evolution in Amaryllidaceae tribe Hippeastreae using target enrichment and NGS of low-copy nuclear markers

Nicolas Garcia, Alan Meerow, Matthew Gitzendanner, Srikar Chamala, Douglas Soltis, Pamela Soltis

1B_306A-Biodiversity
Saturday, June 21, 2014 11:00 AM-11:15 AM

Amaryllidaceae tribe Hippeastreae constitute a horticulturally valuable group of approximately 180 species of American petaloid monocots, characterized by disploidy and polyploidy (x = 6, 8, 9, 10, 11; 2n = 12-150). A recent hypothesis based on ITS and chloroplast sequence data states that Hippeastreae experienced ancient diploid hybridization(s) that preceded the radiation of the major subclade, Hippeastrinae. Additionally, the Hippeastrinae have likely gone through successive events of allopolyploidization, which further obscure the inference of phylogeny and form a complex network-like pattern of evolution. We used transcriptomic data to identify putative single-copy nuclear genes in Hippeastreae and developed biotinylated RNA baits (MYbaits) to capture 48 genes longer than 2 Kb. Illumina DNA libraries were built for ~68 taxa, and pooled libraries were used in capture experiments. Captured genes were sequenced using the Illumina MiSeq platform (2x150 or 2x250 paired-end reads). Great care was taken to address the assembly of in-paralogs, which are likely to be encountered in a group with such a complex and reticulate pattern of evolution as Hippeastreae. Given the complex data, and our previous knowledge and hypotheses about the phylogeny of Hippeastreae, multiple markers were thoroughly and individually analyzed to compare gene trees. Several tests of the deep reticulation hypothesis were performed, including recombination detection, Lento plots, and network analyses. The resulting phylogenetic framework will serve as a basis for understanding patterns of character evolution in Hippeastreae and for reclassification of the tribe at the genus level.

Fusarium graminearum species complex from highland areas in Malaysia

Latiffah Zakaria

1B_306A-Biodiversity
Saturday, June 21, 2014 11:15 AM-11:30 AM

Fusarium graminearum species complex was recovered during a survey on biodiversity of Fusarium species conducted in three highland areas in Malaysia, namely Cameron Highlands, Fraser's Hill and Kinabalu Park. Based on morphological characteristics, among the isolates of Fusarium isolated were 77 isolates of F. graminearum species complex which was mostly isolated from mountain barley (Elyhordeum montanense) plant parts. Species identity of the morphologically identified species was analyzed using translation elongation factor 1α gene (TEF-1α) sequences. Based on BLAST search of Fusarium-ID database, isolates of F. graminearum species complex showed sequence similarity with several lineages of the species complex, namely F. austroamericanum (lineage 1), F. meridionale (lineage 2), F. boothii (lineage 3), F. mesoamericanum (lineage 4), F. acaciae-mearnsii (lineage 5), F. asiaticum (lineage 6) and F. cortaderiae (lineage 8). The most common lineage was F. asiaticum comprising 16 isolates. Mycotoxin analysis showed that 33 isolates as representative of the F. graminearum species complex produced zearalenone ranging from 0.002 – 0.437μg/kg, and the isolates did not produce fumonisin B1, beauvericin and moniliformin. To our knowledge, the present study is the first recorded Fusarium graminearum species complex with different lineages in tropical highland areas in Malaysia.

A single gene affects both ecological divergence and mate choice in Drosophila

Henry Chung, David Loehlin, Heloise Dufour, Kathy Vaccaro, Jocelyn Millar, Sean Carroll

1B_306B-Divergence and Speciation
Saturday, June 21, 2014 10:15 AM-10:30 AM

Evolutionary changes in traits involved in both ecological divergence and mate choice may produce reproductive isolation and speciation. However, there are few examples of such dual traits, and the genetic and molecular bases of their evolution have not been identified. We show that methyl-branched cuticular hydrocarbons (mbCHCs) are a dual trait that affects both desiccation resistance and mate choice in Drosophila serrata. We identify a fatty acid synthase mFAS (CG3524) responsible for mbCHC production in Drosophila and find that expression of mFAS is undetectable in oenocytes (cells that produce CHCs) of a closely related, desiccation-sensitive species, D. birchii, due in part to multiple changes in cis-regulatory sequences of mFAS. We suggest that ecologically influenced changes in the production of mbCHCs have contributed to reproductive isolation between the two species

---

Identifying genes affecting both adaptive divergence and reproductive isolation in Howea palms from Lord Howe Island using RNA-Seq

Luke Dunning, Helen Hipperson, Alex Papadopulos, Xueping Quan, Javier Igea, Vincent Savolainen

1B_306B-Divergence and Speciation
Saturday, June 21, 2014 10:30 AM-10:45 AM

Howea belmoreana and Howea forsteriana are sister species of palm tree; both endemic to Lord Howe Island (LHI) located in the Tasman Sea between Australia and New Zealand. Originally composed of solely volcanic substrate, the deposition of calcareous soil on LHI is thought to have led to ecological speciation. Currently, H. belmoreana adults are restricted to volcanic soils, whilst H. forsteriana is also found on the younger calcarenite soil. There are several ecological differences between these habitats; the calcareous soils on LHI are dryer, have higher pH, increased salinity and show stark differences in metal composition compared to volcanic soil. The species are largely reproductively isolated with a five week difference in peak flowering time in the wild and when cultivated ex situ. Differences in the peak flowering times are also maintained regardless of the soil type that H. forsteriana occurs on. Genes that have a dual role in controlling ecological adaptation and flowering time may have played a direct role in Howea speciation. To characterise such pleiotropic genes we first used RNA-Seq to identify differentially expressed genes between the Howea species using three tissue types (floral, leaf and root) sampled from 36 trees distributed across LHI. As we know that current phenological differences between the species are not a result of environmental induced plasticity, we targeted genes that were significantly differentially expressed, and which were consistently expressed at a higher level in all individuals of one of the species. Using this criterion, 191 genes were identified of varied known function. Of these 15 had gene ontologies associated with the ecological differences between the species and/or flowering time divergence. Finally, the effect these 15 genes have on flowering time in Arabidopsis knockout mutants was observed. Three were shown to have the expected effect on flowering phenology, and one of these genes (SAL1) has previously been shown to alter drought and salt stress tolerance when inactivated. Overall, we have identified pleiotropic genes that represent a plausible mechanism to drive ecological speciation in Howea.

Speciation and chemical differentiation in the aposematic and mimetic butterflies, Melinaea

Melanie McClure, Mathieu Chouteau, Karine Venne, Alexandra Furtos, Karen C. Waldron, Igor Baroja

1B_306B-Divergence and Speciation
Saturday, June 21, 2014 10:45 AM-11:00 AM

The tropical butterflies in the genus Melinaea possess conspicuous aposematic warning colors and they are extensively involved in Müllerian mimicry rings, including with silvaniform Heliconius. Previous studies using mitochondrial markers have failed to separate the different species, and as such are postulated to have only recently diverged. Here we present the population structure and diversification of 7 Melinaea spp. from San Martin, Peru, using 12 microsatellites. Based on these results, we redefine species boundaries. We also collected and analyzed pheromones from males, which gather pyrrolizidine alkaloids (PAs) pharmacophagously from certain flowers and withering plants for protection against predators and as precursors for their pheromones. We compared the chemical analysis with the population genetic analysis to determine whether communities are chemically structured, and to elucidate whether male chemical signals evolve to convey premating isolation. We found that the composition of individual blends was significantly more similar within species than between them, even when samples were collected from different localities. We discuss what this implies for species-specific accumulation of volatiles in male Melinaea and in species diversification.

Phylogenomics reveals rapid and complex evolutionary divergence and speciation in wild Solanum

Leonie Moyle, James Pease, Matthew Hahn

1B_306B-Divergence and Speciation
Saturday, June 21, 2014 11:00 AM-11:15 AM

To identify the genetic and genomic changes that accompany speciation, studies have begun to examine divergence across whole genomes in groups of closely related species. These phylogenomic studies can reveal the progression of evolutionary change along a ‘speciation continuum’, as well as the specific loci that contribute to ecological and reproductive differentiation among lineages. We used RNA-Seq from normalized multi-tissue transcriptomes to examine evolutionary relationships and historical divergence among all species in the diverse plant group Solanum section Lycopersicon (wild tomatoes). This diploid, chromosomally co-linear clade of 13 species began diversifying ~2 MYA. Extant species are distinguished by substantial ecogeographic, morphological, and physiological trait differences, in addition to well-characterized pre- and postzygotic isolating barriers. Transcriptomes from 24 genotypes (1-3 accessions from each species, plus an outgroup) generated 157.7 Gb of sequence (av. 6.6 Gb per accession). De novo and reference-based assembly generated a set of >16,000 high quality orthologous transcripts across all lineages (>45% of known coding regions in the tomato genome). Average pairwise sequence divergence among accessions was

---

Genetic and phenotypic divergence in an island bird: isolation by distance, by colonization or by adaptation?

Lewis Spurgin

1B_306B-Divergence and Speciation
Saturday, June 21, 2014 11:15 AM-11:30 AM

Discerning the relative roles of adaptive and nonadaptive processes in generating differences among populations and species, as well as how these processes interact, is a fundamental aim in biology. Both genetic and phenotypic divergence across populations can be the product of limited dispersal and gradual genetic drift across populations (isolation by distance), of colonization history and founder effects (isolation by colonization) or of adaptation to different environments preventing migration between populations (isolation by adaptation). We have attempted to differentiate between these processes using island populations of Berthelot's pipit (Anthus berthelotii), a passerine bird endemic to three Atlantic archipelagos, where multiple, morphologically distinct subspecies exist. We first estimate the demographic history of Berthelot's pipit using microsatellite markers and approximate Bayesian computation, and quantify genetic and morphological structure. We then extend simple tests of isolation by distance and isolation by adaptation to cover isolation by colonization, allowing us to quantify the roles of migration, adaptation and founder effects at the genetic and phenotypic levels. Our approaches provide a useful framework for other studies aiming to understand the causes of population divergence

---

Candidate barrier genes between G. firmus and G. pennsylvanicus are concentrated on the X-chromosome

Luana Maroja, Erica Larson, Rick Harrison

1B_306C-Hybridization and Speciation
Saturday, June 21, 2014 10:15 AM-10:30 AM

Species boundaries are known to be semi-permeable; whereas advantageous and neutral alleles can spread through a hybrid zone, genes that contribute to reproductive barriers or local adaptation have restricted gene flow. In previous work we characterized patterns of differential introgression for 125 loci across a hybrid zone between the field crickets, Gryllus firmus and G. pennsylvanicus. Now we have constructed a linkage map using these 125 well characterized loci, together with anonymous ddRAD loci. We used multiplex PCR Illumina sequencing combined with ddRAD data to score 90 offspring from a backcross (F1 male x G. pennsylvanicus female). Of the 50 loci with restricted gene flow across a fine scale transect of the cricket hybrid zone, 39 are X-linked, 9 are tightly linked in LG13 and the remaining 2 are tightly linked in LG2. Of all the X-linked loci, only 7 out of 46 do not show an abrupt transition across the hybrid zone. Thus, the diagnostic SNPS that we have identified map to two main regions, a very small region in LG13 (9 loci mapping to same position) and the X-chromosome. At this point we cannot yet tell if the X-linked loci with steep clines are tightly linked. Our results are consistent with the idea that genes on sex chromosomes make a large contribution to reproductive isolation in the early stages of speciation.

The effects of interspecific hybrid incompatibilities on gene flow during complex speciation

Christina Muirhead, Daven Presgraves

1B_306C-Hybridization and Speciation
Saturday, June 21, 2014 10:30 AM-10:45 AM

Genomic scans for interspecific introgression— e.g., between house mouse subspecies, Drosophila species, Neanderthals and modern humans— have revealed apparent X versus autosome differences in the capacity for gene flow during complex speciation. We develop theory to evaluate the degree to which these chromosomal patterns can be attributed to hybrid incompatibilities. We model a neutral locus flanked by one or two genetically linked hybrid incompatibility loci and derive simple expressions for the probability of successful introgression of the neutral variant under a variety of genetic and selective scenarios. We find that dominance and the incompatibility strength are important determinants of the X-autosome difference in introgression probabilities. Weakly selected incompatibilities can limit gene flow at closely-linked sites but fail to yield pronounced X-autosome differences in introgression. On the other hand, strongly selected and highly recessive incompatibilities-- the kind typically studied in speciation genetic analyses-- can easily produce the X-autosome differences of the magnitude observed in genomic data.

Gene flow dynamics between two Indian fruit bats: what can whole genome scans reveal?

Balaji Chattopadhyay, Kritika Garg, Uma Ramakrishnan

1B_306C-Hybridization and Speciation
Saturday, June 21, 2014 10:45 AM-11:00 AM

Sympatry provides an opportunity to understand speciation dynamics and the biology of isolation between divergent lineages. The identification and study of hybrid zones remains a major challenge when interacting species overlap in morphology. The Cynopterine fruit bats present such an interesting case allowing the evaluation of the evolutionary consequences of sympatry. Using a set of nuclear microsatellite markers and mitochondrial cytochrome b sequences we had previously demonstrated the presence of ancient gene flow, obtained evidence of enhanced genetic isolation in and local adaptation in sympatry. In the present study, we have used reduced representation libraries (ddRAD) to obtain thousands of snps across the genome of 48 individuals from both species. We further addressed the question of gene flow and isolation in sympatry and present our findings.

Patterns of gene flow and reproductive isolation in closely related species of mushroom-feeding Drosophila

Devon Humphreys, Kelly Dyer

1B_306C-Hybridization and Speciation
Saturday, June 21, 2014 11:00 AM-11:15 AM

How much gene flow occurs during the early stages of divergence is important for understanding the evolution of reproductive barriers, and how strong they may be at various time points in the speciation process. Here, I investigate the potential for gene flow among three closely related species of Drosophila that vary in their extent of geographic overlap, including D. subquinaria, D. recens, and D. transversa. A pattern of reproductive character displacement has been shown for D. subquinaria and D. recens, but how much gene flow occurs between these species and how they are genetically and behaviorally isolated from D. transversa is unknown. First, I ask whether introgression is possible by characterizing patterns of both pre- and post-mating isolation between each pair of species. Second, I take a multilocus phylogenetic approach to investigate patterns of introgression among these species, and use modeling to differentiate between phylogenetic hypotheses of hybridization and incomplete lineage sorting.

Smells like fish species: massively parallel sequencing supports sympatric speciation of coral reef fishes (genus: Haemulon)

Moises Bernal, Michelle Gaither, Brian Simison, Anna Sellas, Luiz Rocha

1B_306C-Hybridization and Speciation
Saturday, June 21, 2014 11:15 AM-11:30 AM

Despite advances in evolutionary biology over the past century, speciation remains one of the most controversial topics in the field. This is especially true for marine systems, where there are few obvious physical barriers to gene flow and most marine organisms have a pelagic larval stage with tremendous potential for dispersal, greatly reducing opportunities for isolation. In spite of these apparent obstacles, coral reefs harbor levels of diversity only comparable to tropical rainforests. Recent studies have reinvigorated interest in sympatric speciation, by providing models of how speciation can occur in the presence of gene flow. In this study we focus on two species of the genus Haemulon, H. flaviguttatum and H. maculicauda, with completely overlapping distributions throughout shallow reefs of the Tropical Eastern Pacific. Estimates of time to most recent common ancestor in these species show discordance between mitochondrial and nuclear markers (0.2Mya mtDNA; 6.5Mya nDNA), a signal that is consistent with a scenario of recent introgressive hybridization. To explore this further, we sequenced more than 2000 loci with SNPs via double digested RADSeq. Analyses of these loci revealed introgression of a small fraction of the nuclear genome, reinforcing the case for recent hybridization. We detected signals of disruptive selection at several loci, indicating that selection may be driving divergence in this pair of sister species. Taken together our results suggest a case of ecological speciation in the presence of gene flow. Similar analyses for allopatric populations of H. steindachneri, separated by the Isthmus of Panama for 3Mya, revealed no evidence of introgression and no signals of selection. This study between closely related lineages of the genus Haemulon reveals contrasting patterns of divergence between lineages diverging due to geographic isolation and genetic drift (populations of H. stenidachneri), versus lineages diverging under the influence of selection in the face of gene flow (H. flaviguttatum and H. maculicauda).

Stationary Peaks: the alphas are not what they seem (in OU models of trait evolution)

Gavin Thomas, Natalie Cooper, Chris Venditti, Andrew Meade, Robert Freckleton

1B_402-SSB Symposium: The "dark side" of phylogenetic comparative methods
Saturday, June 21, 2014 10:15 AM-10:45 AM

Phylogenetic comparative methods have embraced a suite of models that extend the Brownian constant variance model to attempt to capture a range of evolutionary patterns and processes. The Ornstein-Uhlenbeck model has become perhaps the most widely used alternative model. I use simulations to confirm the long-held suspicion that the parameters of the OU model are biased and only asymptotically behave in a statistically predictable way as datasets become large. This does not seem to be widely appreciated. I will discuss the extent of bias in estimating the parameters of the OU model, the implications of these results for the OU and other extensions of the Brownian model, and make recommendations for best practice.

Difficulties of using trait evolution methods on large trees and power to discriminate between complex models

Cecile Ane

1B_402-SSB Symposium: The "dark side" of phylogenetic comparative methods
Saturday, June 21, 2014 10:45 AM-11:15 AM

Methods are available to model non-neutral trait evolution under selection, but how much can be discovered from data on contemporary taxa? I will show what can (or cannot) be inferred accurately from large comparative data sets, and will address the inherent difficulties of detecting changes in selection regimes.

Assessing the adequacy of phylogenetic trait models

Matthew Pennell, Richard FitzJohn, William Cornwell, Luke Harmon

1B_402-SSB Symposium: The "dark side" of phylogenetic comparative methods
Saturday, June 21, 2014 11:15 AM-11:45 AM

All models are wrong and sometimes even the best of a set of models is useless. Modern phylogenetic comparative methods (PCMs) are almost exclusively model--based and therefore making robust inferences from PCMs requires using a model of trait evolution that is a good explanation for the data. To date, researchers using PCMs have primarily evaluated the explanatory power of a model only in terms of relative, not absolute, fit. Here we develop a general statistical framework for assessing the absolute fit, or adequacy, of phylogenetic models for the evolution of quantitative traits. We use our approach to test whether commonly used models are adequate descriptors of the macroevolutionary dynamics of real comparative data. We fit models of trait evolution to 337 comparative datasets covering three key Angiosperm functional traits and evaluated the absolute fit of the models to each dataset. Overall, the models we used are very inadequate for the evolution of these traits; this was true for many different groups and at many different scales. Furthermore, the relative support for a model had very little to do with its absolute adequacy. We argue that assessing model adequacy should be a key step in comparative analyses.

Do additional functional demands promote or inhibit morphological diversification? A test on turtle shells

C. Tristan Stayton

1C_201-Morphology
Saturday, June 21, 2014 1:30 PM-1:45 PM

There is currently little consensus regarding the degree to which functional demands, in particular the number of different functions that a given structure performs, are expected to influence the morphological diversification of structures. Classically, the view has been that additional functions would carry with them additional functional constraints, and that the need to compromise among those constraints would lead to decreased phenotypic diversification. More recent work involving the evolution of simulated clades, suggests in contrast that additional functions expand Pareto fronts, permitting clades to diversify within an expanded region of morphospace, depending on the relative selective pressures for performance on different functions. Empirical support is available for both views, raising the possibility that the effect of additional functions may be affected by additional factors. Here, I test the possibility that the shape of the performance landscape can have a major influence on the effects of additional functional demands on subsequent morphological diversification. In particular, I focus on whether many-to-one mapping of form onto functional performance is common in one or more functions. The shells of aquatic turtles evolve in response to selective pressures to increase mechanical strength (to resist predator attacks) and hydrodynamic efficiency (to reduce drag during swimming), among other selective pressures; terrestrial turtles share all of these pressures except hydrodynamic efficiency. The shells of terrestrial turtles evolve more rapidly, and with less convergence, than those of aquatic turtles, producing more overall disparity; moreover, a greater variety of shell shapes for a given level of mechanical performance is seen in terrestrial species, relative to aquatic species. These observations are more consistent with a classical view of diversification under multiple selective pressures, but more importantly, they highlight the importance of considering broad many-to-one mapping when predicting the influence of functional performance on diversification (besides more particularly suggesting an important role for many-to-one mapping during the diversification in turtle shells). Given that many-to-one mapping is a common phenomenon in functional morphology, this pattern is likely generalizable to many other evolving clades. However, the data also indicate the importance of Pareto optimality concepts in explaining the distributions of evolving clades: aquatic taxa seem to lie on a Pareto front defined by mechanical and hydrodynamic performance.

Tinkering with the axial skeleton: vertebral number variation in ecologically divergent threespine stickleback populations

Windsor Aguirre, Kendal Walker, Shawn Gideon, Katie Carlson

1C_201-Morphology
Saturday, June 21, 2014 1:45 PM-2:00 PM

Understanding how the vertebral column is impacted as populations adapt to different habitats favoring distinct body forms can provide insight into the origin of evolutionary diversity in the axial skeleton. We examine variation of vertebral number and body shape in morphologically and ecologically divergent threespine stickleback populations from Alaska. Variation in vertebral number was substantial and was associated with body shape variation. Both vertebral homeosis and region-specific changes in vertebral number were present. Sexual dimorphism in vertebral number was significant and resulted from vertebral homeosis; females had more abdominal vertebrae and males more caudal vertebrae, but total vertebrae did not differ. Body elongation was associated with an increase in vertebral number, especially in the caudal region, although this varied among populations. Variation among individuals indicated that external similarity in body form masks significant vertebral variation in stickleback. Although more research on the underlying mechanisms and functional significance is needed, our findings highlight the potential of the threespine stickleback as a model for studying the evolution of the vertebrate axial skeleton.

Arms and Armor: ecomorphological diversification in the girdled lizards

Edward Stanley

1C_201-Morphology
Saturday, June 21, 2014 2:00 PM-2:15 PM

The Cordylidae is a species poor but ecologically and morphologically diverse family of lizards endemic to sub-Saharan Africa. Although the majority of the cordylid species are strictly rupicolous, the family also contains a diverse array of other specialist ecotypes. Due to this concentrated ecological and morphological variation, the family has been proposed as an excellent system for studying macroevolutionary processes. Previous studies have hypothesized that the majority of diversity in the family evolved rapidly at the base of the viviparous subfamily (Cordylinae), possibly representing an adaptive radiation, but this has not been investigated empirically.

A time calibrated phylogeny was produced, using an 11 gene, squamate-wide dataset with ten fossil calibrations. Morphological variation of the Cordylidae was quantified through a combination of standardized ecomorphological measurements and novel, volumetric measurements of osteoderm distributions recovered using High-Resolution CT scanning. Ecological data for known cordylid localities was extracted from multiple commonly used climate layers, and the dataset binned into a series of discrete microhabitat types.

The phylogenetic analysis reveals that viviparous cordylines underwent a period of rapid cladogenesis across the Oligocene-Miocene boundary, radiating into nine well- supported lineages, distributed around the edge of the great escarpment in South Africa. Morphological variation was shown to be correlated with microhabitat choice, but not with climatic variation. Finally, a series of existing and novel disparity-based analytical techniques reveal that the viviparous cordylids experienced an early burst of morphological diversification, while the oviparous subfamily, Platysaurinae, did not. These findings strongly support the hypothesis that the live-bearing Cordylinae underwent a period of adaptive radiation during the Oligocene, possibly as a result of shifts in the climate and geological uplift of South Africa's Great Escarpment.

Deterministic Evolution in Greater Antillean Boid Snakes: an Extension of the Caribbean Ecomorph Paradigm?

R. Graham Reynolds

1C_201-Morphology
Saturday, June 21, 2014 2:15 PM-2:30 PM

Some of the most important insights into the ecological and evolutionary processes of diversification, colonization, and speciation have come from studies of organisms on islands in the Caribbean. In particular, Anolis lizards are a textbook example of adaptive radiation and convergence, as the remarkable repeated evolution of convergent ecomorphs has occurred in situ on each of the Greater Antillean islands. Indeed, the ecomorph concept has been an important paradigm for examining adaptive radiation and convergent evolution of other squamates in the Caribbean. However, not all squamate groups (e.g., alsophiine snakes; scincid lizards) have undergone the same degree of ecomorphological diversification despite apparent ecological opportunity. West Indian boid snakes (Chilabothrus) might represent an interesting additional extension of the ecomorph concept, though this has never been explicited investigated. This monophyletic clade of 11 nocturnal species exhibits a wide variety of ecological and gross morphological difference- occupying habitats from xeric scrub to tropical rainforest, and maximum adult body sizes ranging from less than one meter to nearly four meters. Two main morphotypes have been recognized in this genus: large-bodied generalists (6 species) and small-bodied specialists (5 species). Both large and small species are distributed across the range of WI boas, sometimes occurring on the same island.It is clear that WI boas have radiated both ecologically and morphologically, hence we wish to examine whether this group might conform to the general ecomorph paradigm. Specifically, we test the ecomorph concept (adaptive radiation and convergent evolution) in this group by combining the first comprehensive multilocus molecular dataset for the clade with morphological measurements of an ecologically relevant structure (the head), to test: 1) whether small ecotypes have evolved repeatedly in-situ from large ancestors on different islands; and 2) whether these small ecotypes are morphologically convergent.

Transcriptomic and morphometric analyses of recently evolved sympatric Arctic charr morphs

Arnar Palsson, Kalina Kapralova, Johannes Gudbrandsson, Ehsan Pashay Ahi, Sigridur Franzdottir, Zophonias Jonsson

1C_201-Morphology
Saturday, June 21, 2014 2:30 PM-2:45 PM
After the end of the last glacial period, about 10.000 years ago, many northern freshwater fishes invaded new habitats. Recurrent evolution of benthic/pelagic resource specializations is seen in many species, including Arctic charr (Salvelinus alpinus). In Iceland, dwarf form with benthic morphotype has evolved repeatedly and is often found in sympatry with pelagic charr. Using Illumina sequencing and morphometrics we studied the developmental differences between three sympatric charr morphs from Lake Thingvallavatn, two benthic a large (LB) and a small (SB) as well as a small pelagic charr (PL). At expression level the most difference is between the LB charr and the smaller two forms (SB and PL). However at the genetic level, the two benthic forms cluster together. We have confirmed genetic and expression differences for dozens of genes that relate to several aspects of craniofacial development and resource polymorphism. In parallel we did morphometric analyses on developing embryos, with landmarks summarizing jaw morphology, the ethmoid plate, and gill arches. The data show significant differences between morphs in several craniofacial elements, even before hatching. We also analyzed the morphology in developing hybrids of small pelagic and small benthic charr. Those reveal curious patterns in shape divergence and growth, that will be discussed in the context of data that show relatively restricted gene flow between these sympatric morphs.

Genomic studies of red snapper (Lutjanus campechanus) in U.S. waters of the Gulf of Mexico and Atlantic Ocean

Jonathan Puritz, John Gold

1C_206-Population Structure and Genetics
Saturday, June 21, 2014 1:30 PM-1:45 PM
Red snapper (Lutjanus campechanus) historically has supported extremely important commercial and recreational fisheries in U.S. waters, but has been overfished for at least the last 25 years. Successful rebuilding efforts and future management of these fisheries depend on accurate knowledge of how genetic connectivity and localized selection are shaping the genomic structure among subpopulations. Using double-digest restriction-site associated DNA tags (ddRAD), we surveyed variation in >3,500 single nucleotide polymorphisms (SNPs) from red snapper sampled at eight geographic localities: five from the northern Gulf of Mexico and three from the U.S. southeast Atlantic coast. Here, we present estimates of genetic structure and population connectivity based on presumed, selectively neutral loci, and we examine the geographic partitioning of putative loci under selection (identified by FST outliers). Lastly, we will present evidence of post-recruitment, environmental selection by exploring frequencies of putatively adaptive loci among adult and young-of-the-year samples, and discuss the role of using both neutral and adaptive loci in delineating the population structure of an exploited marine fish.

Microgeographic genetic structure of a resident songbird in British Columbia, Canada

Rachael Adams, Theresa Burg

1C_206-Population Structure and Genetics
Saturday, June 21, 2014 1:45 PM-2:00 PM
Understanding how the landscape influences the genetic integrity of populations is crucial. Individual dispersal can be restricted by barriers which can affect microevolutionary processes such as gene flow and adaptation. A reduction in gene flow as a result of restricted dispersal can lead to isolated populations, and, over time divergence. Barriers occur at both macro- (mountains) and micro- (habitat fragmentation) geographic scales. Although birds have high dispersal potential, evidence suggests dispersal is restricted by barriers. Birds are also susceptible to changes in the environment so serve as ideal mobile indicators of habitat quality. In this study, microsatellite genetic markers were used to assess the spatial distribution of genetic variation of the black-capped chickadee (Poecile atricapillus) in British Columbia, Canada. Using a landscape genetics approach, we revealed significant population structuring at a micro-geographical scale. For example, two populations (Prince George and Fort St. James) in British Columbia were genetically distinct despite being separated by less than 120 km comprised of continuous habitat and lacking any obvious dispersal barriers. Genetic discontinuities identified at this scale suggest that even the smallest change within the landscape (i.e. suitable habitat, microclimate, hybridization) can play a major role in population dynamics and ultimately, the evolutionary potential of a species.

Genetic structure of parasitoids in a fragmented landscape

Abhilash Nair, Christelle Couchoux, Saskya van Nouhuys

1C_206-Population Structure and Genetics
Saturday, June 21, 2014 2:00 PM-2:15 PM
Species living in a fragmented landscape exhibit high spatial structure. Depending on their movement in the landscape, limited gene-flow between local populations, drift and founder effects play a significant role in shaping of the overall genetic population structure. The genetic structure exhibited by interacting species at multiple trophic level system can differ significantly depending on resource specialization and dispersal behaviour. The Glanville fritillary butterfly Melitaea cinxia, lives as a metapopulation in the Aland islands, a 50 x 70 km archipelago, where it hosts multiple parasitoid species at different trophic levels. The host butterfly is highly differentiated spatially and genetically in the fragmented landscape. We compared the genetic structure of the specialist parasitoid (Hyposoter horticola) and hyperparasitoid (Mesochorus stigmaticus) that depend on the butterfly, using microsatellite data developed for the respective species. We found the parasitoids to be hierarchically genetically structured but the level of differentiation and isolation by distance was weak in comparison to the host butterfly. While the parasitoid and hyperparasitoid are more dispersive than the butterfly, they are constrained by its dispersal ability and distribution in the landscape. Studying the

population differentiation of these strongly interacting species at different trophic levels helps us understand the influence of landscape fragmentation on demographic histories and evolution of spatial genetic structure.

Comparative seascape genetics of coral reef fishes: integrating genetic datasets and biophysical models across a common seascape

Libby Liggins, Eric A. Treml, Hugh P. Possingham, Cynthia Riginos

1C_206-Population Structure and Genetics
Saturday, June 21, 2014 2:15 PM-2:30 PM
Most landscape genetic studies aim to understand which land or seascape features shape patterns of genetic diversity and population structure across the range of a single species. Whether land or seascape features are consistent in their effects across species is less known. Comparative landscape genetic studies require the integration of multi-species genetic datasets and corresponding land or seascape data to look for consistent patterns among species, and consistent influences of land or seascape features across species. However, few studies evaluate landscape genetic patterns across multiple species in a quantitative manner. We use a matrix comparison approach to investigate the influences of seascape features on genetic diversity and population structure of coral reef fishes from around Australia, parts of the Coral Triangle, and the West Pacific. We focus on four co-distributed coral reef fishes that differ in early life history characteristics and habitat use (Pomacentrus coelestis, Dascyllus trimaculatus, Halichoeres hortulanus, Acanthurus triostegus). First, genetic data (mitochondrial DNA) for each species are individually analysed to reveal genetic patterns across the studied range as a consequence of known seascape history and a species-specific biophysical model of contemporary connectivity. Second, to reveal patterns of congruence and incongruence across species, the genetic datasets are combined in a series of matrix comparisons alongside seascape data. Both approaches identified variable genetic patterns across species, despite common seascape history and contemporary oceanography. Some were predictable according to the dispersal potential of species, whereas others were related to particular seascape features. Most notably, likely differences in colonisation timing of reefs within the Arafura Sea drove unexpected differences among biologically similar species. Our research highlights the complexity of combining multi-species datasets and offers some novel methods of analysis for such studies.

Higher-order epistasis between a mutation and four or more segregating variants generates a 'new' phenotype in a cross

Matthew Taylor, Ian Ehrenreich

1C_301A-Genetics of Traits
Saturday, June 21, 2014 1:30 PM-1:45 PM
Recent research suggests that genetic interactions involving more than two loci may influence a number of complex traits. How these ‘higher-order’ interactions arise at the genetic and molecular levels remains an open question. To provide insights into this problem, we dissected a colony morphology phenotype that segregates in a yeast cross and results from synthetic higher-order interactions. Using backcrossing and selective sequencing of progeny, we found five loci that collectively produce the trait. We fine-mapped these loci to 22 genes in total and identified a single gene at each locus that caused loss of the phenotype when deleted. Complementation tests or allele replacements provided support for functional variation in these genes, and revealed that pre-existing genetic variants and a spontaneous mutation interact to cause the trait. The causal genes have diverse functions in endocytosis (END3), oxidative stress response (TRR1), RAS-cAMP signalling (IRA2), and transcriptional regulation of multicellular growth (FLO8 and MSS11), and for the most part have not previously been shown to exhibit functional relationships. Further efforts uncovered two additional loci that together can complement the non-causal allele of END3, suggesting that multiple genotypes in the cross can specify the same phenotype. Our work sheds light on the complex genetic and molecular architecture of higher-order interactions, shows how such interactions can generate 'new' phenotypes, and raises questions about the broader contribution of such interactions to heritable trait variation.

The genetic basis of environmental adaptation in house mice

Megan Phifer-Rixey, Ke Bi, Rachel Thayer, Sara M. Keeble, Jeffrey Good, Michael Nachman

1C_301A-Genetics of Traits
Saturday, June 21, 2014 1:45 PM-2:00 PM
Understanding the genetic basis of adaptation is a fundamental goal of evolutionary biology. Nevertheless, there are surprisingly few adaptive traits for which the genetic details are known. One approach is to focus first on patterns of genetic variation across the genome that suggest the action of selection and then work back to the trait. This strategy has the significant advantage of being unbiased with respect to traits and broad in scope. The recent, rapid, and remarkably successful colonization of the Americas by house mice (Mus musculus) provides a unique opportunity to study the effects of selection on DNA sequence variation and to identify the genetic basis of environmental adaptation. Exposure to novel environments is expected to result in strong directional selection. In addition, the short generation time of house mice and published data documenting adaptive variation in phenotypes in these populations suggest that selection has had sufficient time to shape genetic variation. In this study, we characterize variation within and among five populations on the East Coast of North America using a combination of low coverage, whole genome sequencing and exome sequencing for 50 individuals. We use a variety of statistical approaches to identify specific genomic regions that may contribute to environmental adaptation.

Intraguild predation results in genome wide adaptation in the Threespine Stickleback

Sara Miller, Dolph Schluter

1C_301A-Genetics of Traits
Saturday, June 21, 2014 2:00 PM-2:15 PM
Natural selection has long been appreciated as a crucial component in the generation of phenotypic diversity. However, the genomic consequences of natural selection in natural populations remain largely unknown. Recent advancements in

next generation sequencing now provide us with the ability to study the genomic architecture of adaptation. Using the unique natural history of the threespine stickleback (Gasterosteus aculeatus), we examined genome wide selection in contrasting environments. Marine stickleback became isolated in the coastal freshwater lakes of British Columbia following the last ice age. We identified a subset of these lakes, which differed by the presence or absence of the prickly sculpin (Cottus asper): an intraguild predator of threespine stickleback. Intraguild predation (IGP) occurs when a predator kills and eats a species that is a potential competitor for shared resources. As a consequence, sculpin can have a dual impact on the stickleback either via direct predation or indirectly by removing resources and increasing competition. Stickleback populations sympatric with prickly sculpin show evidence of parallel phenotypic adaptations. The presence of sculpin is correlated with an increase in stickleback anti-predator defenses, a shift in diet, and a change in body shape. We report the results of a genome wide analysis examining the genetic basis of stickleback adaptation to IGP. Using whole genome re-sequencing of 17 freshwater populations and 3 marine populations we generated over 5 million SNPs. Genome scans reveal that IGP has resulted in widespread but unevenly distributed selection across the genome. Regions of high divergence occur on multiple chromosomes and can span many genes. Many of the genomic regions that diverge between freshwater populations with and without IGP overlap with regions that have been implicated in marine and freshwater stickleback divergence. As a result, stickleback populations sympatric with sculpin are more genetically similar to the marine stickleback than stickleback from populations without sculpin. Selection from prickly sculpin has resulted in parallel phenotypic and genotypic adaptation in the threespine stickleback.

The Genomic Architecture of Adaptive Quantitative Trait Variation in Darwin's Finches

Kenneth Petren, *Lucinda Lawson*

1C_301A-Genetics of Traits
Saturday, June 21, 2014 2:15 PM-2:30 PM

Revealing the genomic architecture of quantitative ecological traits has remained an elusive goal. We used a novel comparative landscape approach among species to reveal the genetic basis of adaptive differences in Darwin's finches (Geospiza) that differ primarily with regard to beak shape. The long history of hybridization, purifying selection, gene flow and recombination among dozens of island populations allows us to isolate the genetic genomic loci that distinguish these species. Genome wide contrasts among four species revealed 526 significant polymorphisms that cluster near the start of the mRNA transcripts of 392 genes. These genes are highly enriched for craniofacial and developmental processes and have a rich history of interaction with genes known to affect beak shape. The surprisingly large number of genes and their prevalance in regulation suggests evolutionary divergence primarily involves changes in tissue-specific gene expression through transcriptional modifiers and enhancers. Variation at these adaptive loci mirror patterns of morphological allometry. The cactus finch lies away from evolutionary lines of least resistance by maintaining higher heterozygosity with alleles that are rare in the other ground finches. These alleles are associated with longer, narrower beaks within populations, which establishes a common mechanism between natural selection and species divergence. Comparative landscape genomics offers considerable power to provide insight into longstanding questions of evolution where natural selection acts in parallel across the landscape.

Genetic basis of adaptive behavior: do proximate genetic mechanisms suggest evolutionary causes?

Corbin Jones, *Eric Earley*

1C_301A-Genetics of Traits
Saturday, June 21, 2014 2:30 PM-2:45 PM

Thanks to advances in genetics and genomics, dissecting the genetic basis of adaptive phenotypes is now possible in many evolutionarily interesting species. As a result our understanding of the genetics of adaptive traits is better than ever before. How informative these data are about the evolutionary mechanisms shaping these traits remains unclear. Using case studies of genetic and evolutionary analyses of chemosensory behavior in fruit flies, we show how incomplete information affects inference about evolutionary mechanisms. Underpowered tests of selection, the complications of population history, and the idiosyncrasies of specific genes can result in incomplete or biased results. Our data suggest that genome wide genetic analysis and direct functional tests of adaptive alleles are critical for understanding how observed genetic differences contributed to the evolution of an adaptive trait.

Evolution of imprinted genes in the Mimulus guttatus species complex

Elen Oneal, *Janet Zhang, Josh Puzey, John Willis*

1C_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 1:30 PM-1:45 PM

Genomic imprinting is the differential expression of alleles dependent upon parent-of-origin. In flowering plants, a subset of genes exhibit imprinted expression in the endosperm, the tissue that provides nutrition to the embryo during germination. Such imprinted expression may have evolved via parent-offspring-conflict (POC), where mothers and offspring (ie, fathers), conflict over the degree and length of maternal investment. POC may be particularly prominent in flowering plants, where mothers often mate promiscuously invest substantially in offspring, and where maternal investment is a dynamic process mediated by a placental connection that allows mothers to alter investment over the course of embryonic development. Moreover, endosperm has a 2:1 maternal:paternal genome ratio, unlike the 1:1 ratio of the embryo, introducing another source of conflict between mother and offspring. Dosage imbalances in imprinted gene expression is linked to premature seed death, and it has been suggested that allopatric divergence in protein sequences of regulatory elements and/or their targets may be a common cause of hybrid failure in flowering plants. If true, genes that exhibit imprinted expression in endosperm should evolve more rapidly in comparison with genes that do not. We test this prediction using genomic sequence data from several members of the Mimulus guttatus species complex.

Specifically, we compare rates of evolution in a species pair whose primary isolating barrier is known to be hybrid seed lethality: serpentine-adapted M. guttatus and M. nudatus. In addition, we test whether endosperm imprinted genes are evolving more rapidly in outcrossing taxa (e.g., M. nudatus) where POC should be potent, than in selfing taxa (e.g., M. nasutus) where POC should be muted. This work will shed light on whether intragenomic conflict, and particularly POC, expressed through genomic imprinting, may contribute to speciation in plants.

Evolutionary genetics of pigmentation variation in natural populations of Drosophila melanogaster

Rocio Ng

1C_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 1:45 PM-2:00 PM

Research on insect melanism has been informative in understanding how evolutionary mechanisms can produce phenotypic diversity. My work examines how genes participating in the pigment biosynthesis pathway may be contributing to natural variation of pigmentation traits in Drosophila melanogaster. I uncovered significant variation in abdominal and thoracic pigmentation both within and among populations of D. melanogaster in the eastern United States. I closely examined how polymorphisms within the pigmentation genes, ebony, Pale, Ddc, and tan are associated with pigmentation traits. I also looked for patterns of nucleotide diversity in each gene as well as evidence for selection. Each of the genes had loci that were significantly associated with pigmentation, with some being in regions that may be experiencing possible balancing or purifying selection. Adult expression of ebony and pale were also significantly correlated with pigmentation levels. These results suggest that various components in the pigmentation pathway are evolving together in order to produce phenotypic variation in these populations. Additionally, there was evidence for independent regulation of pigmentation expression in the thorax and the abdomen. Analysis of pigmentation phenotypes has revealed significant geographic patterns with a possible cline in thoracic traits. We also sequenced a group of alleles of the ebony and pale genes in these populations to examine clinal patterns and confirm associations with pigmentation traits. My work has the potential to increase the understanding of how polymorphisms at the nucleotide sequence level contribute to population level differences and possibly adaptation in D. melanogaster and other insect species.

The genetic architecture of natural variation in abdominal pigmentation of Drosophila melanogaster females

Lauren Dembeck

1C_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 2:00 PM-2:15 PM

Pigmentation varies within and between species and is often an adaptive trait crucial for fitness. It is also a relatively simple morphological trait which serves as a model for mapping the genetic basis of complex traits. We measured natural variation in female abdominal pigmentation in 175 sequenced inbred lines of the Drosophila Genetic Reference Panel, derived from the Raleigh, NC population. Females were scored for the proportion of melanization on two abdominal segments, tergite 5 and tergite 6. There is significant genetic variation in the proportion of melanization and high broad-sense heritability for each tergite. Our genome-wide association studies identified 84 genetic variants and 34 SNPs associated with the proportion of melanization on tergite 5 and tergite 6, respectively. There were SNPs associated with the genes tan, ebony, and bric-a-brac1, all of which are known to affect variation in D. melanogaster abdominal pigmentation; these results provide a proof of principle for genome-wide association analyses using the DGRP. Mutant and RNAi-knockdown studies demonstrated that 19 of the 30 candidate genes tested (63%) have significant effects on the pigmentation of tergite 5, tergite 6, or both. Several of these genes are involved in chitin production, cuticle structure, and vesicle formation and transport. These findings show that genes directly involved with the biosynthesis of the cuticle and melanin and other tyrosine derivatives, as well as genes with pleiotropic effects contribute to natural variation in abdominal pigmentation in D. melanogaster females.

Evolutionary genetics of the selfish Segregation Distorter complex

Cara Brand, Amanda Larracuente, Daven Presgraves

1C_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 2:15 PM-2:30 PM

The selfish gene complex Segregation Distorter (SD) on chromosome 2 of Drosophila melanogaster is one of the best studied meiotic drive systems. Heterozygous SD/SD+ males sire almost exclusively SD-bearing offspring rather than the expected 1:1 Mendelian ratio. Since the first discovery of SD chromosomes over 50 years ago, the genetics and molecular basis of the system has been intensely studied, however, there are few studies that consider the evolutionary history and dynamics of the SD complex in natural populations. To investigate the age, biogeographic origins, and population genetic history of SD, we studied DNA sequence variation at the major driving locus, Sd-RanGAP, from 55 SD chromosomes recovered from European and African populations. The results suggest parallel evolutionary arms races on the two continents that entail the rapid spread of new and different SD chromosome types in geographically separated populations.

Population genetics of Lialis burtonis: Expanding radiation during Australia's aridification

James Titus-McQuillan, Matthew Fujita

1C_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 2:30 PM-2:45 PM

Much of the endemic biodiversity of Australia arose during the aridification of the continent at the end of the Tertiary period. This caused contractions of mesic biota to refugia. However, new adaptive zones opened up spurring range expansion and diversification in arid-adapted lineages. Using Burton’s legless lizard (Lialis burtonis) as a model, we illustrate the dynamics these climatic events had on gene flow, biogeography, and speciation on L. burtonis. These geckos cover a wide expanse throughout Australia and portions of Papua New Guinea among many habitats, covering both tropical and arid biomes. L. burtonis is an effective model to understand how extrinsic environmental and intrinsic genealogical factors affect the biogeography and gene flow across a large area. L. burtonis may shed light on the origin for colonization during this aridification. Sequencing of ND2 yields 4 distinct clades: a large arid clade sister to the Pilbara clade and two wet region clades, sister to one another – one to the northern monsoon region and one to the Eastern portion of the continent. The use of restriction site associated DNA sequencing (RADseq) show distinct populations that corroborate phylogenetic analysis. Relative genetic mixing is low between populations. This study demonstrates the varied responses to aridification in Australia including localized persistence of lineages in the tropical monsoonal biome.

A genomic selection component experiment in Mimulus guttatus

John Kelly, Patrick Monnahan

1C_302A-Genetics of Adaptation
Saturday, June 21, 2014 1:30 PM-1:45 PM

We combine a field selection experiment with multiplexed shotgun genotyping. Genotype and fitness measurements on plants over two successive field seasons yields estimates for natural/sexual selection on thousands of SNP markers dispersed across the Mimulus genome.

Functional genomics of adaptation to hypoxic cold stress in high-altitude deer mice (Peromyscus maniculatus)

Zachary Cheviron

1C_302A-Genetics of Adaptation
Saturday, June 21, 2014 1:45 PM-2:00 PM

In species that are distributed across steep elevational gradients, adaptive variation in physiological performance may be attributable to transcriptional plasticity in underlying regulatory networks. Because hypoxia imposes constraints on the capacity for aerobic thermogenesis, high-elevation endotherms face a dual challenge because their thermogenic capacity is compromised under conditions where thermoregulatory demands are especially severe. We performed a series of common-garden experiments that were designed to elucidate the role of regulatory plasticity in evolutionary adaptation to hypoxic cold-stress in deer mice (Peromyscus maniculatus), a widely distributed North American rodent. Using a system-biology approach, we integrated genomic transcriptional profiles with assays of metabolic enzyme activities, tissue-level phenotypes, and measures of whole-animal thermogenic performance under hypoxia in highland (4350m) and lowland (430m) mice from three experimental groups: (1) wild-caught mice that were sampled at their native elevations; (2) wild-caught/lab-reared mice that were deacclimated to low-elevation conditions in a common-garden lab environment; and (3) the F1 progeny of deacclimated mice that were maintained under the same low-elevation common-garden conditions. In each experimental group, highland mice exhibited greater thermogenic capacities than lowland mice, and this enhanced performance was associated with upregulation of transcriptional modules that influence several hierarchical steps in the O2 cascade, including tissue O2 diffusion (angiogenesis) and tissue O2 utilization (muscle fiber composition, metabolic fuel use, and cellular oxidative capacity). Most of these performance-related transcriptomic changes occurred over physiological and developmental timescales, suggesting that regulatory plasticity makes important contributions to fitness-related physiological performance in highland deer mice.

Simultaneous optimization of growth rate and thermal stability in bacteriophages under pleiotropic constraints

Andrew Sackman, Darin Rokyta

1C_302A-Genetics of Adaptation
Saturday, June 21, 2014 2:00 PM-2:15 PM

It has been hypothesized that tradeoffs exist between the improvement the assembly rate of proteins and their overall stability. In order to determine whether tradeoffs resulting from pleiotropic constraints prevent the simultaneous optimization of these two traits in viral capsids, we performed long-term adaptive walks of replicate bacteriophage populations initiated from single plaque isolates under a two-stage protocol of alternating selection for increased growth rate under standard lab culture conditions and for increased thermal stability in a high-temperature heat shock environment. One set of replicate adaptations was performed using a genotype that had been previously adapted for optimal growth rate (ID8a80), and a second set of lines used the wild-type ancestor of the first genotype (ID8). Our preliminary results indicate that in all lines, sequential fixation of the first few mutations proceeded with beneficial effects mostly improving one phenotype at a time, sometimes with deleterious consequences for the alternative phenotype. At the end of adaptation, all lines showed great improvements in thermal stability, measured as death rate during a heat shock period. The pre-adapted lines showed no decrease in growth rate at the end of adaptation, and the lines begun from the wild-type ancestor achieved a similar growth rate to that of the line that was originally adapted strictly for increased growth rate. These results indicate that while individual mutations may be constrained by antagonistic pleiotropy, it may have little effect on long-term evolution.

Quantitative circadian phenotypes vary over the growing season and determine fitness

Matthew Rubin, Cynthia Weinig, Marcus Brock

1C_302A-Genetics of Adaptation
Saturday, June 21, 2014 2:15 PM-2:30 PM

Circadian clocks are common in all three domains of life, suggesting that internal mechanisms of time-keeping are adaptive. Consistent with adaptive hypotheses, the circadian clock exhibits pervasive transcriptomic and phenotypic effects in controlled settings. Functional allelic variation at clock loci likewise suggests the potential for ongoing adaptive evolution of the circadian clock in response to selection. However, the fitness consequences of either a functional vs. non-functional clock or quantitative clock variation remain largely unresolved in nature, and quantitative genetic parameters that determine the potential for evolutionary responses of the clock remain likewise uncharacterized in ecologically relevant settings. In field studies, we show that disruption of clock function via mutation reduces both survival and fecundity, while subtler adjustments via genomic introgression of naturally occurring alleles indicate that clock cycles 24 hrs in diverse species. The results also translate functional analyses of clock behavior performed in controlled settings to natural ones, demonstrating that in segregating populations circadian phase is both highly responsive to diverse seasonally variable abiotic inputs and showing that the circadian clock may undergo adaptive evolution.

Testosterone and sexually transmitted bacterial communities in a wild bird

Camilo Escallon, Matthew H. Becker, Jenifer B. Walke, Lisa K. Belden, Ignacio T. Moore

1C_302B-Sexual Selection
Saturday, June 21, 2014 1:30 PM-1:45 PM

Sexually transmitted infections have been suggested as major costs of sexual reproduction and important players in the evolution of mating systems, but the mechanisms underlying transmission have been largely overlooked. Testosterone is a hormone that mediates several aspects of reproduction, including the number of sexual contacts. Therefore, testosterone has the potential to affect sexually transmitted infections, either indirectly by behaviors that increase contact rates with parasites, or directly by decreasing immune function. Our hypothesis is that males with high levels of testosterone would exhibit more promiscuous behaviors that increase their chances of being infected with a wider diversity of cloacal bacteria. To test this hypothesis, we sampled breeding Zonotrichia capensis males for circulating testosterone levels and performed cloacal swabs to collect bacteria. The bacterial DNA from the swabs was sequenced on an Illumina MiSeq. Sequence data were analyzed for cloacal bacteria diversity and community composition. There was a positive correlation between testosterone levels and bacterial phylogenetic diversity, even though there was high intra-individual variability in the abundance of bacterial taxa. Contrary to our expectations, in a multivariate analysis, high and medium testosterone individuals had communities that were more similar to each other than to low testosterone individuals. Proteobacteria was dominant in low testosterone individuals. Finally, looking at several avian pathogenic bacteria, the abundance of Chlamydiae was positively correlated with testosterone levels. Two nonexclusive explanations for these results are that testosterone is mediating sexual contact rates and thus the acquisition of more bacterial strains, and that testosterone is directly weakening the immune system and bacteria infect more easily. Alternatively, infections at pathological levels might be preventing some individuals from raising their testosterone to normal breeding levels. Overall, increased exposure to sexually transmitted pathogens in the form of cloacal bacteria can constitute a strong selective pressure for the modulation of testosterone levels.

Phylogeny suggests non-directional and isometric evolution of sexual size dimorphism in argiopine spiders

Ren-Chung Cheng, Matjaz Kuntner

1C_302B-Sexual Selection
Saturday, June 21, 2014 1:45 PM-2:00 PM

Sexual dimorphism describes substantial differences between male and female phenotypes. In spiders, sexual dimorphism research almost exclusively focuses on size, and recent studies have recovered steady evolutionary size increases in females, and independent evolutionary size changes in males. Their discordance is due to negative allometric size patterns caused by different selection pressures on male and female size (converse Rensch's rule). Here, we investigated macroevolutionary patterns of sexual size dimorphism (SSD) in Argiopinae, a global lineage of orb weaving spiders with varying degrees of SSD. We devised a Bayesian and maximum likelihood molecular species level phylogeny, then used it to reconstruct sex specific size evolution, to examine general hypotheses and different models of size evolution, to test for sexual size coevolution, and to examine allometric patterns of SSD. Our results, revealing ancestral moderate sizes and SSD, failed to reject the Brownian motion model, which suggests a non-directional size evolution. Contrary to predictions, male and female sizes were phylogenetically correlated, and SSD evolution was isometric. We interpret these results to question the classical explanations of female-biased SSD via fecundity, gravity, and differential mortality. In argiopines, SSD evolution may be driven by these or other selection mechanisms, but perhaps at different phylogenetic scales.

Coexistence of sexual and asexual reproduction in the wild mustard Boechera retrofracta

Catherine Rushworth, Michael D. Windham, Tom Mitchell-Olds

1C_302B-Sexual Selection
Saturday, June 21, 2014 2:00 PM-2:15 PM

Evolutionary theory predicts that sexual and asexual reproduction should not coexist. Yet apomixis (asexual reproduction via seed) is widespread, co-occurring with sexual reproduction in hundreds of flowering plant genera from numerous families. In nearly all of these groups, apomixis is strictly associated with hybridization and polyploidy. However, in the perennial mustard species Boechera retrofracta, diploid and polyploid apomixis co-occurs with sexual reproduction within multiple populations. What evolutionary and ecological factors permit asexual and sexual reproduction to coexist in these populations? We used a four-garden reciprocal transplant to explore the hypothesis that selection may favor one reproductive mode over another, or vary spatially or temporally to maintain this polymorphism. We found no significant difference in fecundity between sexuals and asexuals. However, asexuals experience significantly higher levels of herbivory than sexually reproducing individuals. No evidence for spatially variable selection was found. We also examined the hypothesis that asexuality, tightly associated with hybridization in this largely self-fertilizing genus, may be maintained by heterosis. Results from a greenhouse experiment comparing fitness of interspecific F2 hybrids and their self-fertilized parents show that selfed individuals enjoy higher fitness in early life stages, but surviving hybrids have higher fecundity. Although all hybrids display fecundity higher than the mean of their progenitors, cumulative fitness deviates from this pattern in some hybrid lineages. These results suggest that asexual reproduction may be maintained by heterosis in this group, but that the effect strongly depends on the identity of hybrid parents.

Patterns of malaria transmission may affect sex ratio evolution

Allison Neal

1C_302B-Sexual Selection
Saturday, June 21, 2014 2:15 PM-2:30 PM

Malaria parasites have distinct male and female forms, and their sex ratios tend to be female-biased and show considerable variation among species, among infections within a species and within infections over time. An explanation for this variation should emerge from sex ratio theory, a focus in evolutionary biology that explores how selection shapes the ratios of males to females. Specifically, Hamilton's Local Mate Competition (LMC) model has been emphasized because its assumptions match well the distribution of malaria parasites among hosts and it predicts female-biased sex ratios that vary based on the number of genetic lineages present in a host. However, this model assumes a linear relationship between the number of females produced in a host and the number of offspring in the next generation, which may not be accurate for malaria parasites due to their transmission biology. Instead, producing an increasingly greater number of females may have diminishing returns. I developed a mathematical model that incorporates this modified relationship and I explore the implications for sex ratio evolution. In particular, I highlight trends that are predicted by the new model that are not expected under LMC. I then present new data and review existing data relating to these divergent trends. While much of the data on malaria parasite sex ratios is qualitative and consistent with either model, some data, especially those comparing among species, show trends consistent with the new model that are not predicted by LMC.

Female color preferences, ecological selection, and the evolution of male nuptial coloration in darters (Percidae: Etheostomatinae)

Patrick Ciccotto, Tamra Mendelson

1C_302B-Sexual Selection
Saturday, June 21, 2014 2:30 PM-2:45 PM

The interplay of natural (ecological) and sexual selection in shaping biological diversity is increasingly recognized as a central question in evolutionary biology, and male sexual ornamentation is a primary focus. Theory predicts sexual selection will lead to the elaboration of an ornament if there is an associated increase in mating success. However, ecological factors should inhibit ornamentation when there is a reduction in survival. We examined sexual and ecological selection on male ornamentation in darters (family Percidae), a diverse group of freshwater fishes that vary in the presence of male nuptial coloration from achromatic (black) to elaborate chromatic signals. Our objectives were to determine 1) if female color preferences (one component of sexual selection) are predictably associated with male nuptial color and 2) whether differences in ecological selection pressures predict the presence of male nuptial coloration. Female darters were presented with a series of motorized models to simulate courting males colored red, blue, black, or grey, and association preferences with these different stimuli were measured. Across several species, females exhibited significant preferences for particular colors, and preferred colors varied across species. Phylogenetic comparative analyses also indicate that the presence of male nuptial coloration, specifically red and orange, is significantly associated with environments that would support fewer predators. A laboratory study of color preferences in a common darter predator, largemouth bass (Micropterus salmoides), indicates a strong preference for red prey items, providing additional evidence that predation may contribute to variation in darter coloration. Results from behavioral and comparative analyses are discussed in light of sexual and ecological selection on male ornamentation to elucidate factors that shape color variation in darters.

Life-history evolution and the role of a chromosomal inversion for ecotype divergence in Mimulus guttatus

Alex Twyford, Jannice Friedman

1C_302C-Local Adaptation, Ecotypes and Diversity
Saturday, June 21, 2014 1:30 PM-1:45 PM

Organisms demonstrate a diverse range of life-history strategies as an adaptive response to environmental variation. One of the most dramatic life-history shifts is from perenniality, where organisms persist and reproduce over multiple years, to annuality, where the life-cycle is completed within a single growing season. The yellow monkey flower Mimulus guttatus provides an unparalleled example of life-history variation within a species, with the early flowering annual and late flowering perennial ecotype broadly coexisting across Western North America. Here, we test the evolutionary relationship between ecotypes by applying genotyping-by-sequencing to populations from across the species' native range. Our use of 40,000 SNPs allows us to generate the first well-resolved intraspecific phylogeny for this recently diverging species. Our results show strong geographic structuring of genetic variation, both at the local scale, and a broad latitudinal gradient in variation. Annuals and perennials do not appear as monophyletic clades, instead the two ecotypic forms are scattered across the phylogeny. In contrast to the genome wide pattern of genetic variation, SNPs within a chromosomal inversion separate out populations by life-history. Overall, our results indicate that key-life history characters may be extremely variable among closely related populations, with inversions playing a critical role in divergence between populations on a potential trajectory towards speciation.

Diverging genomes of an emerging ecogenomic model using Restriction-site Associated DNA (RAD)-sequencing

Benjamin Clifford, Jacqueline Lopez, Michaël C. Fontaine, Michael Pfrender

1C_302C-Local Adaptation, Ecotypes and Diversity
Saturday, June 21, 2014 1:45 PM-2:00 PM

Divergence landscapes provide a crucial benchmark from which to ascribe functional diversification to environmentally-divergent genomes. Using ecotypes from the ecological model microcrustacean Daphnia pulex species complex, we probe the landscape of divergence and test nascent speciation hypotheses using a Restriction-Site Associated DNA (RAD)-Sequencing approach. Upon mapping 2.5 x 108 barcoded Illumina reads to our reference genome and calling variants via local de-novo haplotype assembly, we show strong habitat-based clustering between D. pulex, the vernal pond dweller; and D. pulicaria, which inhabit lakes. Moreover, D. pulex and pulicaria ecotype clustering occurs quite strongly along a single component axis when analyzed via PCA, with the variant PC loadings bearing a striking relationship to traditional variant population genetic parameters. By connecting reference sequence scaffolds to linkage groups (LGs) revealed in earlier mapping efforts, we render habitat-associated divergence at the chromosomal level. Variants with known linear LG placement reveal clustered segments showing differentiation that deviates significantly from neutral expectation, and Bayesian selection-detection algorithms identify variants as candidates for positive selection. Several variant loci occur within genes having associated gene ontologies, or in genes with known environmentally-triggered differential expression from earlier transcriptomic inquiry. Identifying patterns of genome-wide divergence is of central interest to evolutionary biologists seeking to interrogate recently-sequenced genomes for signs of real-world functional differentiation.

Water availability influences reproductive output between sexes in two divergent Silene latifolia populations

Laura Weingartner, Lynda Delph

1C_302C-Local Adaptation, Ecotypes and Diversity
Saturday, June 21, 2014 2:00 PM-2:15 PM

Local adaptation is a widespread phenomenon and is thought to be important in maintaining genetic variation within species. Silene latifolia is an herbaceous flowering plant that shows extreme phenotypic variation across its native European range. This species is also dioecious (separate male and female individuals), and many traits are sexually dimorphic. As such, S. latifolia provides a novel approach to local-adaptation studies because the sexes may be under differing selection across varying habitats. We completed a common-garden experiment between two divergent populations of S. latifolia from Spain and Croatia that differ considerably in life history, floral morphology, and functional-leaf traits. These common-garden studies suggest that the phenotypic differences seen in the field likely have a genetic basis. The two habitats of origin also vary markedly in rainfall and temperature. To address the importance of precipitation differences as a possible selective agent in the native habitats, we completed a water-manipulation experiment that tracked plant performance over multiple flowering seasons. While both sexes exhibited reduced reproductive output under limited-water regimens, the reduction was more severe for males. Individuals originating from the wetter habitat (Croatia) also showed a more severe decrease in reproductive output in restricted water conditions than individuals originating from the dry habitat (Spain). These results suggest that water availability likely acts as an important selective agent in the natural habitat, and these findings will allow us to make predictions about traits that are important in local adaptation and the selective forces that drive divergence.

Inbreeding depression and the potential for genetic rescue in a rare cutthroat trout

Sierra Love Stowell, Andrew Martin, Kevin Rogers

1C_302C-Local Adaptation, Ecotypes and Diversity
Saturday, June 21, 2014 2:15 PM-2:30 PM

The cold, swift waters of Colorado were once home to a diverse clade of cutthroat trouts, but at least three of those lineages have gone extinct. A fourth lineage is on the brink: the greenback cutthroat trout, Oncorhynchus clarkii stomias, persists as single population of fewer than 800 individuals in a small stream in the Arkansas drainage, outside of its native range in the South Platte drainage. This population, known as “Weird Bear Creek” (WBC), is morphologically and genetically distinct from other cutthroat trout lineages. WBC trout are being propagated in a state fish hatchery with the intent of re-establishing wild populations within the South Platte drainage. The hatchery population has passed through at least two recent population bottlenecks: first during the founding of the wild population and subsequently during the establishment of the hatchery population. Genetic analysis of shows depleted genetic diversity, and reduced fitness is common in the hatchery population, both suggestive of inbreeding depression. To determine the extent of inbreeding and ID in WBC and to assess the potential for genetic rescue, we used a combination of reciprocal crosses and a genotyping-by-sequencing approach to generate lineage-specific SNPs. We performed three crosses: between two WBC parents, between two parents from another cutthroat trout subspecies native to west of the Continental Divide (CAR), and between WBC and CAR parents. We measured survival and growth of all offspring in a common environment and collected all individuals that died during development. We extracted and barcoded DNA from all parents and a subset of the offspring, including individuals that died as eggs and fry and those that survived to fingerlings. Using a reduced representation library from the pooled samples sequenced with a 1x300 Illumina MiSeq run, we found several thousand SNPs between the two lineages, and several hundred SNPs that allowed assignment of parentage to the offspring. We found that outbred offspring show significantly higher fitness than inbred offspring, suggesting recovery from inbreeding depression by genetic rescue. Future work on subsequent generations will demonstrate whether such hybrid vigor and the effects of genetic rescue persist after sexual reproduction disrupts interacting gene complexes. In general, the quantification of inbreeding depression and, potentially the identification of genomic regions and individual genes involved in inbreeding, can be used to plan genetic rescue efforts in a diversity of taxa threatened by small population size.

Selection, drift and plasticity contribute to sensory trait variation in echolocating bats

Lizelle Odendaal, David Jacobs, Jacqueline Bishop

1C_302C-Local Adaptation, Ecotypes and Diversity
Saturday, June 21, 2014 2:30 PM-2:45 PM

Across heterogeneous environments adaptive trait differentiation in the absence of gene flow is commonly reported. But this relationship is clearly more nuanced because ample evidence also supports trait differentiation in the presence of gene flow, highlighting the role of local selection gradients across different environments. If the selection gradient is steep enough to reduce immigrant fitness the effects of gene flow on trait variation may be minimised; while if selection is weak and there are minimal costs to immigration, even nominal gene flow will limit local adaptation.

But variation in adaptive traits is also influenced by genetic drift and disentangling the relative affects of these processes in natural populations remains a challenge. Here we explore the evolution of sensory trait variation in two closely related bats, the Cape and Dent's horseshoe bats of southern Africa. Both species occur along substantial environmental gradients of increasing aridity and use echolocation frequencies (as measured by resting frequency, RF) that appear attuned to local environmental conditions for enhanced hunting success. To test the general hypothesis of 'adaptive differentiation with minimal gene flow' we measured resting frequencies across both species' distributions and estimated long-term patterns of gene flow using mitochondrial DNA sequence data. Our analyses revealed geographically structured patterns of increasing RF in both species; however drift does not contribute equally to our two study systems. While extensive trait differentiation is best explained by habitat discontinuities across the distribution of Cape horseshoe bats, this has evolved in the presence of extensive gene flow. Here, local selection for both increased detection distance in relatively less cluttered habitats together with adaptive phenotypic plasticity may have influenced the evolution of matched echolocation frequencies and habitats in this species, despite gene flow. In contrast, echolocation variation in Dent's horseshoe bat is best explained by drift, where minimal gene flow characterises the system and trait variation is not well explained by habitat structure and environmental variables. Our results emphasise the importance of population level analyses to better understand adaptive trait evolution, particularly across highly variable environments, and draws attention to the rather neglected (and possibly important) role of plasticity in the echolocation behaviour of bats.

The evolution of bet-hedging and phenotypic plasticity

Jeremy Van Cleve

1C_303-Plasticity
Saturday, June 21, 2014 1:30 PM-1:45 PM

In light of an uncertain future, organisms face a difficult trade-off. They can either specialize on a single phenotype across a range of environments, hedge their bets by randomly choosing among a set of phenotypes, or invest in physiological machinery to adjust their phenotype plastically to the environment. Understanding the evolutionary relationship between these strategies remains a puzzle. Here, we present a simple model for the evolution of specialization, bet-hedging, and plasticity that reveals how these strategies are fundamentally sensitive to how the fitness cost of sensing varies with plasticity. When costs accelerate as a function of plasticity, the level of plasticity depends on how fast costs change. In contrast, decelerating costs can lead to full adaptive plasticity, but only when initial conditions are right. The shape of the cost curve is almost certainly due to the genetic and metabolic network machinery underlying plastic traits, which means that certain networks are more likely than others to evolve adaptive plasticity.

Mechanistic overlap between plastic and evolved responses to heat stress, revealed through RNA-seq

Morgan Kelly, David Plachetzki, Sabrina Pankey

1C_303-Plasticity
Saturday, June 21, 2014 1:45 PM-2:00 PM

There is currently substantial debate over the role of phenotypic plasticity in adaptation to new environments. The genetic assimilation hypothesis holds that environmentally induced phenotypes are often the first step in adaptation to environmental change, and later become genetically "assimilated," such that the original environmental stimulus is no longer required to produce the phenotype. An important test of this hypothesis lies in the identification of genes involved in both the plastic and evolved responses to an environmental stress. If genetic adaptation occurs through the assimilation of plastic phenotypes, then the assimilation hypothesis predicts that the genes that are up- or down-regulated during the plastic stress response will become permanently up- or down-regulated in populations that have evolved increased stress tolerance. We combined artificial selection and heat shock experiments with next-generation sequencing to identify the genetic basis of adaptation to heat stress, and to elucidate the genetic linkage between phenotypic plasticity and genetic adaptation in the crustacean Tigriopus californicus. Our results show important functional linkages between the adaptive and plastic response to heat stress, and have implications for understanding the mechanistic basis of adaptation to new and changing environments.

Genetic basis of life history plasticity in D. melanogaster

Katherine O'Brien, Paul Schmidt

1C_303-Plasticity
Saturday, June 21, 2014 2:00 PM-2:15 PM

Identifying genes and gene networks that are involved in the ability to respond plastically to environmental stimulus is an emerging field in ecological genetics. We have demonstrated that natural populations of D. melanogaster are plastic for development time and that there is variation in the strength of the response between different populations. However, the genes that underlie these responses are unknown. Using the Drosophila Genetic Reference Panel (DGRP) we were able to get biologically replicated data for the response of four phenotypes (development time, mass, lipid content and pupation height) to two environmental parameters, day length and food type. Plasticity was measured using Hedge's g to calculate the magnitude and direction of change resulting from the different environments. The modularity of the plastic response was addressed by using phenotypic correlation to test the independence of the strength of response across all four traits. To identify the genetic basis of plasticity we used two approaches a GWAS and GSEA. For one gene, couch potato, we present data that confirms the gene has pleotropic effects on the ability to produce a plastic response across multiple phenotypes.

Breaking G: Variable pleiotropy and environmentally induced changes in the correlated response to selection

Kristin Sikkink, Rose Reynolds, William Cresko, Patrick Phillips

1C_303-Plasticity
Saturday, June 21, 2014 2:15 PM-2:30 PM

Selection in novel environments can lead to a coordinated evolutionary response across a suite of characters. However, environmental conditions can also affect the genetic architecture of complex traits, which in principle can alter the pattern of the multivariate response to selection. We describe a factorial selection experiment in the nematode Caenorhabditis remanei in which two different stress-related phenotypes were selected under three different environmental conditions.. In each case, the pattern of covariation in the evolutionary response among traits differed depending on the environment in which selection occurred, including asymmetrical responses to selection in some cases. This suggests variation in pleiotropy across the stress response network that is highly sensitive to the external environment. These results highlight the complexity of the interaction between genes and environment that influences the ability of organisms to acclimate to novel environments, as well as the need to identify the underlying genetic basis of genetic correlations in order understand how patterns of pleiotropy are distributed across complex genetic networks.

The molecular basis of gene by environment interaction in Arabidopsis thaliana

David Des Marais, Jesse Lasky, David Lowry, Thomas Juenger

1C_303-Plasticity
Saturday, June 21, 2014 2:30 PM-2:45 PM

Individuals in natural populations vary considerably in their response to the environment. Although widely observed at the phenotypic level, until recently these variable responses, or Genotype-by-Environment Interactions (GEI), have been challenging to dissect at the molecular level. Detailed molecular work in a small number of reference genotypes has begun to assemble the cellular toolkit of organismal response to environmental perturbations. It remains unclear, however, which of these components vary in natural populations, and how selection acts on different stages of regulatory network hierarchies. We present evidence from two experiments which show that both cis- and trans-acting natural variants drive regulatory variation in a plant hormone signaling network. First, we use transgenic analysis to demonstrate that two intermediate-frequency natural alleles in a core signaling protein drive different sets of downstream transcriptional targets in response to environmental cues. These data suggest a role for trans-acting variation in GEIs. We next use a population genomic approach to demonstrate that natural variation in a particular transcription factor binding motif is associated with natural variation in expression response to environmental cues. These data suggest a role for cis-acting variation in GEIs. Collectively, these data reveal the complex genetic architecture of plant-environment interaction, and suggest that natural populations contain abundant functional genetic variation in environmentally-responsive molecular machinery.

Characterization of Amphibian Species-Specific Cutaneous Bacterial Communities and Metabolites

Patrick McLaughlin, Piotr Lukasik, Gail Hearn

1C_304-Microbiomes and Microbial Symbionts
Saturday, June 21, 2014 1:30 PM-1:45 PM

Amphibians have become the most threatened class of animals in the world, with over 30% of all known species at risk of extinction. Most species suffer from the effects of multiple major threats, including climate change, habitat destruction, pollution, and disease. Among the most destructive of these forces is chytridiomycosis, a fungal disease that has spread globally in the past few decades, now implicated in the recent rapid disappearance and likely extinction of many species across North and South America. Recent research suggests some species may have evolved resistance to such fungal skin pathogens via anti-fungal metabolites produced by skin bacteria. Future conservation efforts may rely heavily upon knowledge of this relationship, with possible transmission of beneficial microbial resistance to threatened populations. We sought to characterize the metabolite profiles and bacterial communities of amphibian species from Bioko Island, Equatorial Guinea. Species in this region of Africa appear to carry chytridiomycosis infection, but do not succumb to the disease, suggesting possible resistance. Results indicate the presence of anti-fungal bacteria and metabolites, and principal coordinate analysis shows strong clustering of bacteria/metabolite (Bac-Met) profiles by species. These results may help advise ongoing conservation efforts, and may also provide insights into the role of bacteria in amphibian evolution and speciation. Future research will focus on the specific mechanisms of this apparent symbiosis, and the extent of this observed Bac-Met profile relationship with species across greater geographic distances and additional taxa.

Microbiome Diversity and Dynamics under Neutral and Selective Models

Qinglong Zeng, Jeet Sukumaran, Allen Rodrigo

1C_304-Microbiomes and Microbial Symbionts
Saturday, June 21, 2014 1:45 PM-2:00 PM

Many current studies of host-associated microbial communities (or microbiomes) focus on descriptions of microbial dynamics within hosts over short periods, or on the composition and diversity of these communities between hosts. To understand how microbiomes vary over time within and between hosts, it will be essential to develop a unified ecological and evolutionary framework that takes account of mechanisms of microbial acquisition, and determinants of microbe and host evolutionary history. For this we developed an explicit framework for modelling the evolutionary and ecological dynamics of microbial communities within a population of hosts. By taking account of basic microbial species acquisition mechanisms, we built our neutral models under different scenarios and explored different effects on the composition and diversity of host-associated microbial communities using simulations. We found that host inheritance plays an important role in restricting the diversification of microbial communities while immigration from the environment, as an opposing force, tends to increase the local and overall diversity of the microbial communities. Acquisition from hosts and environment also affects the frequency distribution of species abundances within this host population, and even with our simple models, we are able to recover the typical log-normal species distributions so often seen in nature. On the other hand, selective pressures on microbiome evolution were implemented in our selective models at host level and bacterial level, and under both of these two selection effects, microbial diversities are significantly reduced and the log-normality of species abundance distribution is more evident.

Genetics of host regulation of maternal microbial transmission

Lisa Funkhouser-Jones, Seth Bordenstein

1C_304-Microbiomes and Microbial Symbionts
Saturday, June 21, 2014 2:00 PM-2:15 PM

Many animals maternally transmit microbial symbionts in the face of profound fitness consequences should symbiont titers go awry, making host regulation of inherited microbes crucial. However, little is known about the evolution of host genes involved in symbiont titer control or the molecular mechanisms by which this regulation is achieved. In Nasonia parasitoid wasps, interspecific transfer of the Wolbachia bacterial symbiont wVitA from its resident host, N. vitripennis, to a closely-related but naïve host, N. giraulti, results in a nearly 100-fold increase in infection titers. We have determined that a maternal effect acts dominantly in N. vitripennis to massively suppress Wolbachia titers and establish the native infection level in resulting offspring. Thus, we sought to identify the host genetic factors that underlie this symbiont regulation using genetic tools available to Nasonia, including introgression, genotyping microarrays, quantitative trait loci analyses and RNA-seq. We report four key findings: (i) Two genomic regions, one each on chromosomes 2 and 3 (out of the five Nasonia chromosomes), have a major effect on the maternal suppression trait. (ii) These two regions act additively to reduce titers by more than 80% compared to N. giraulti controls. (iii) RNA-seq of Nasonia ovaries identified several genes located within our candidate regions that are differentially expressed between N. vitripennis and N. giraulti. (iv) One of these candidate genes, a lysosome-associated membrane glycoprotein, appears to be under positive selection. Together, these results suggest that tight control of maternal microbial transmission may have a relatively simple genetic basis in Nasonia that has evolved since the divergence of the two Nasonia species approximately 1 MYA.

The diversity and evolution of the primate skin microbiome: how different are humans from our closest relatives?

Sarah Council, Amy Savage, Julie Urban, Megan Ehlers, Rob Dunn, Julie Horvath

1C_304-Microbiomes and Microbial Symbionts
Saturday, June 21, 2014 2:15 PM-2:30 PM

It is becoming increasingly evident that the skin microbiome plays a key role not only in body odor but also human health and disease. However, little is known about the diversity of microbial inhabitants of the skin, nor of how these assemblages may persevere or turnover throughout evolutionary time. By taking a comparative approach and studying the microbial associates of non-human primates, we seek to broaden our understanding of host dependent effects on microbial composition and provide insights into the extent to which the modern condition of our skin microbiome is similar to that of our closest relatives or is uniquely human (whether as a function of our hygiene or other aspects of our biology). To answer these questions, we characterized the microbes living on the skin of humans, chimpanzees, gorillas, rhesus macaques and baboons. We evaluated the bacterial and archaeal residents associated with the axilla of these primate species through high throughput sequencing of the 16S rRNA gene. These axillary samples provide a glimpse into the evolution of the primate skin microbiome and are the first study of the skin microbiome of non-human primates using non-culture dependent methods. In our study, we found that human skin microbial communities were unique relative to other primates, both in terms of which lineages were present and which were absent. In part these differences may reflect the broad story of primate evolution. Alternatively, some of the unique attributes of the human skin microbiome (the absence of lineages present in all other primates) may reflect modern shifts in the skin microbiome as a function of human hygiene.

Distribution, specificity and horizontal transmission of microbial symbionts in army ant colonies

Piotr Lukasik, Justin Newton, Yi Hu, Jon Sanders, Ryuichi Koga, Daniel Kronauer

1C_304-Microbiomes and Microbial Symbionts
Saturday, June 21, 2014 2:30 PM-2:45 PM

Symbiotic microorganisms play a variety of important roles in the biology of their arthropod hosts. Despite this, symbiont diversity, distributions and functions are poorly understood outside of a few model systems. Even less is known about the horizontal transmission of microbes between species under natural conditions. Neotropical army ants (Formicidae: Ecitoninae), predatory social insects known to host specialized microbes and whose colonies are inhabited by dozens of species of unrelated arthropods, offer an excellent opportunity to investigate these processes. We use a collection of over 30 Ecitoninae species from across the Americas to characterize the symbiont diversity at species, regional, colony and individual levels, as well as to understand host-specificity of the dominant microbial associates of army ants. Furthermore, we investigate the microbial communities of 15 species of myrmecophile beetles collected from colonies of one of the army ant species.

Our data indicate that despite large variation between individual ants and consistent differences between species, the microbial communities of Ecitoninae workers are dominated by the two previously reported symbionts, Unclassified Firmicutes and Unclassified Entomoplasmatales. These bacteria form host species-specific clades, with evidence for geographic differentiation within these clades – but multiple and often divergent strains are present within each colony. Weissella (Firmicutes) and Arsenophonus are the dominant microbes in ant larvae. Strikingly, Weissella and Entomoplasmatales are among the most common microbes in most species of myrmecophile beetles. Sequencing of protein-coding genes revealed that in many cases the same bacterial genotypes are hosted by ants and beetles. Thus, colonies of social insects, where different organisms constantly interact, may serve as arenas facilitating transmission of microbes across unrelated hosts. We discuss the possible ecological and evolutionary consequences of these processes, including the evolution of vertebrate pathogenicity in a close relative of the army ant Weissella.

Evolutionary history and traits, not invasive status, influences community assembly

Nathan Lemoine, Jessica Shue, Brittany Verrico, David Erickson, W. John Kress, John Parker

1C_305A-Invasion and Evolution
Saturday, June 21, 2014 1:30 PM-1:45 PM
Determining community assembly mechanisms is a primary goal of ecologists, particularly in modern communities that have both native and introduced species and variable disturbance histories. Phylogenetic and trait-based quantitative tools can unravel these patterns but have been used mostly at continental and regional scales, not at the local scale where limiting similarity might be more apparent. We compiled a phylogenetic, trait, and abundance database for 71 understory species, including 53 native and 18 introduced species, in 25 deciduous forest stands with known disturbance history. Environmental filtering of traits and phylogeny strongly dictated the occurrence and abundance of species. Importantly, these relationships were similar for both native and introduced species in the majority of forest stands. Thus, most differences between native and introduced species could be quantified in terms of phylogenetic and functional distance, and native/introduced status per se was of relatively minor importance to predicting plant success.

Post-invasive evolution of Hawaii's feral chickens

Eben Gering, Pamela Willis, Tom Getty, Dominic Wright

1C_305A-Invasion and Evolution
Saturday, June 21, 2014 1:45 PM-2:00 PM
Feral animals provide unique opportunities to learn how lineages with diverse selection histories adapt to the complex selection regimes found in nature. Here, we combine molecular, behavioral and morphological analyses to identify the origin(s) of Kauai's feral chickens (Gallus gallus), and to characterize their evolution.

The potential sources of Kauai's feral chickens include several farmed breeds, which are products of divergent artificial selection for male-male competition (cockfighting roosters), rapid reproduction (egg-layers), and efficient metabolism (meat producers). Polynesians also introduced red junglefowl to Kauai ca. 1000 years ago, which are conspecific (and can interbreed) with chickens. It is not known if these animals persisted.

We conducted phylogenetic studies of Kauai's chickens, and recovered two divergent mitochondrial clades. The low-frequency mitotype was identical to one recovered from ancient bones that predate European contact. The high-frequency clade clusters with contemporary samples from throughout the Pacific, thought to descend from European breeds that only recently became feral.

We also analyzed behavioral (vocalization) and morphological data, which we sampled in the field and mined from social media (Youtube). Kauai chickens' behavior and morphology were intermediate between those of red junglefowl and domesticated individuals, perhaps indicating genetic introgression.

Together, our results indicate Kauai's chickens are genetically and phenotypically diverse, and may result from admixture between lineages with divergent selection histories. We are now examining the evolutionary role of sexual selection within the feral environment.

Darwin's conundrum revisited: does phylogenetic distance predict invasibility?

Emily Jones, Scott Nuismer, Richard Gomulkiewicz

1C_305A-Invasion and Evolution
Saturday, June 21, 2014 2:00 PM-2:15 PM
A key goal of invasion biology is to identify the factors that favor species invasions. One potential indicator of invasiveness is the phylogenetic distance between a non-native species and species in the recipient community. However, predicting invasiveness using phylogenetic information relies on an untested assumption: that both biotic resistance and facilitation weaken with increasing phylogenetic distance. We test the validity of this key assumption using a mathematical model in which a novel species is introduced into communities with varying ecological and phylogenetic relationships. Contrary to what is generally assumed, we find that biotic resistance and facilitation can either weaken or intensify with phylogenetic distance, depending on the mode of interspecific interactions (phenotype matching or phenotype differences) and the resulting evolutionary trajectory of the recipient community. Thus, we demonstrate that considering the mechanisms that drive phenotypic divergence between native and non-native species can provide critical insight into the relationship between phylogenetic distance and invasibility.

Fishery-induced selection: what can be learned from introduced salmonids in Sierra Nevada Lakes?

Sebastien Nussle, Mike Bogan, Roland Knapp, Mitch Lockhart, Stephanie Carlson

1C_305A-Invasion and Evolution
Saturday, June 21, 2014 2:15 PM-2:30 PM
Size-selective fishing is expected to trigger evolutionary responses but the potential for fishery-induced selection to significantly modify population characteristics is controversial and not yet well understood. More research is needed to understand how and when size-selective fishing alters traits and dynamics in harvested populations. In this study, we analyzed data from over 30 populations of non-native brook trout (Salvelinus fontinalis) and rainbow trout (Oncorhynchus mykiss) that were completely removed from lakes in California's Sierra Nevada during the course of a habitat restoration program. In total, over 45,000 fish were harvested via gill nets and electro-fishing, and length-at-capture and time-at-capture were recorded for nearly every fish. We used these data to estimate fishery selection on body length in replicate populations, and to relate the strength of fishery selection to population- and habitat-specific characteristics. Even though "non-selective fishing gear" (e.g. variable mesh size gill nets) was used in removal efforts, we found that fishing was more likely to remove larger individuals. Due to this size selectivity, we observed a dramatic decline in the mean and variability of fish length within a few months across populations. The magnitude of this decrease

may be linked to population-specific parameters, such as initial size distribution, which could be in turn be driven by local environmental factors (e.g. lake size, elevation). Our study demonstrates that size-selective fishing not only affects population structure by removing the largest individuals, but also that the environment can mediate the impact of fishing. These findings highlight how fishery-induced selection may influence harvested populations and may help inform population-specific management or conservation plans.

Is genetic rescue a valid option for arid zone Acacia?

David Ayre, Andrew Denham, David Roberts, Cairo Forrest, Amy-Marie Gilpin

1C_305A-Invasion and Evolution
Saturday, June 21, 2014 2:30 PM-2:45 PM

Throughout Australia’s arid and semi arid southeast canopy forming Acacia species have been severely impacted by European agricultural practices. Several widespread species now exist only as relatively small and highly fragmented stands with little or no seed set or recruitment for decades prior to 2010. In contrast, however, one species, Acacia ligulata is apparently thriving. We have used a comparative approach to evaluate the causes of reproductive failure and the potential value of genetic augmentation of populations using a combination of widespread demographic and population genetic surveys and investigation of pollination biology and mating systems. Our key findings include striking variation in pollinator services for threatened vs thriving taxa, a major episode of seed production for several threatened species following a historic rain event, evidence of pollen transfer and outcrossing between stands separated by several km and evidence of historic population subdivision and variation in reproductive mode between populations separated by the Darling River and its floodplain - a major biogeographic barrier. Critically our data suggest that sexual reproduction in some species has been limited by drought or over-emphasised by patchy demographic data. Across huge areas populations of these species remain genetically diverse and have been maintained by sexual recruitment, although one species Acacia loderi is largely clonal to the west of the Darling River barrier. Recruitment in these species could be boosted by habitat management alone. In contrast, however, our data show that Acacia carneorum, currently listed as vulnerable, is with few exceptions restricted to isolated mono-clonal stands (all occurring to the west of the Darling River) and showed no response to recent rains. While it could be hypothesised that two centuries of increased grazing has favoured clonal genotypes, clonality instead appears to be an ancient response to aridity. Here we discuss the potential for ‘genetic rescue' of Acacia carneorum but question its likely effectiveness. Genetic augmentation may be needed to allow adaptation in the face of climate change, but the persistence of extant clones, the great age of mature stems (> 200 years) and the absence of fruit set suggest that long term selection has favoured clones with high general fitness and limited capacity for sexual reproduction. Only three populations, all with neighbouring stands within 5km, show evidence of fruit set but many comparable stands remained barren throughout our study.

Rapid evolution of reproductive isolation between outcrossing and selfing subspecies of Clarkia xantiana

Ryan Briscoe Runquist, David Moeller

1C_305B-Reproductive Isolation
Saturday, June 21, 2014 1:30 PM-1:45 PM

Speciation requires the evolution of reproductive isolating (RI) barriers that prevent hybridization between diverging lineages. Mating system transitions, specifically from outcrossing to selfing, are common in plant speciation but the contribution of shifts in mating system to reproductive isolation of diverging taxa has not been well studied. In this study, we documented the sequential components of pre-mating and post-mating RI between two recently diverged (ca. 65,000 years bp) Clarkia subspecies that have diverged in mating system and have come into secondary contact, C. xantiana xantiana and C. xantiana parviflora. We found that the two taxa are nearly completely isolated and that pre-mating barriers, specifically flowering phenology and pollinator preference (for the outcrosser over the selfer), contribute most to RI between the taxa. We also discovered a substantial and asymmetric crossing barrier despite the fact that the lineages have very recently diverged. There was no evidence that pollen-pistil interactions contribute to RI. Instead, hybrid inviability occurs during seed development and is not observed in later stages of hybrid development.

Divergence and reproductive isolation along elevation gradients in the Hawaiian landscape-dominant tree, Metrosideros

Elizabeth Stacy, Jennifer Johansen, Jill Ekar

1C_305B-Reproductive Isolation
Saturday, June 21, 2014 1:45 PM-2:00 PM

At least 60,000 tree species are recognized, yet the conditions that drive their origin remain poorly understood. Hawaii’s Metrosideros species complex comprises five species and numerous varieties of woody taxa that have arisen within the islands’ heterogeneous landscapes since the group’s common ancestor arrived on Kaua`i roughly 4 mya. Currently, O`ahu (2.6 – 3.0 myo) supports the greatest taxonomic richness of any island with ~12 varieties and species of Metrosideros, most of which occur in a predictable sequence from low to high elevation. To examine the strengths of ecological divergence and reproductive isolation among these incipient taxa we contrasted the seedling responses of eight taxa to contrasting light and phosphorus levels in a greenhouse experiment and conducted controlled crosses within and among five taxa in the field. All taxa examined were cross-compatible, and pure and F1 hybrid seedlings from the controlled crosses were outplanted in parental environments. Preliminarily, both the greenhouse and reciprocal outplanting experiments reveal significant differences among the regeneration niches of taxa that span elevation gradients, and the crossing study reveals a postzygotic barrier in the form of reduced survivorship of F1s in parental environments as well as possible life history character divergence among taxa. Final results of these year-long experiments will be presented and implications for the role of elevation gradients in tree speciation will be discussed.

Morphological and genetic analyses of interspecific introgression in a natural damselfly population

Alexandra Barnard, Mark McPeek, Ola Fincke, J.P. Masly

1C_305B-Reproductive Isolation
Saturday, June 21, 2014 2:00 PM-2:15 PM

Species that hybridize in nature can deepen our understanding of how reproductive isolation evolves to give rise to new species. In particular, species in the earliest stages of divergence provide an opportunity to identify reproductive isolating mechanisms that evolve early during speciation. Enallagma damselflies (Odonata: Coenagrionidae) show striking interspecific differences in male and female reproductive structure morphology, and these structural differences contribute to premating reproductive isolation (RI) between species. Enallagma anna and E. carunculatum are sympatric North American damselflies that appear to hybridize in nature, based on males and females with with morphologies intermediate to those of the parental pure species. We collected 40 male and 32 female putative hybrids from a sympatric population in Whitefish, MT. We use 3D morphometric techniques to quantify the shapes of male and female reproductive structures in putative hybrids and compare their morphologies to the parental species. We also assay gene flow between E. anna and E. carunculatum in the Whitefish population using AFLP markers, and examine the relationship between morphology and introgression of certain markers. These results will verify introgression in the natural population and help facilitate a finer-scale mapping study on the genetics of male-female morphological coevolution using laboratory-reared individuals.

Evolving isolation mechanisms between two incipient species of an endoparasitic wasp

Justin Bredlau, Karen Kester

1C_305B-Reproductive Isolation
Saturday, June 21, 2014 2:15 PM-2:30 PM

Rapid speciation of parasitic wasps results in many cryptic species; however, the mechanisms underlying this process are largely unknown. Further, most studies on speciation in parasitic wasps have focused on phylogenetic patterns based on molecular differentiation. We evaluated potential pre- and post-mating barriers to reproduction between two genetically distinct sources of the gregarious parasitic wasp, Cotesia congregata (Hymenoptera: Braconidae), originating from sphingid hosts, Manduca sexta on tobacco (MsT) or Ceratomia catalpae on catalpa (CcC). We compared male responses to female pheromones, elements of male acoustic courtship signals, and mating and reproductive success of F1 hybrid and F2 sibling crosses. Males displayed a ~30% decreased response to female pheromone from the reciprocal source and male courtship songs differed significantly in duration, frequency, and amplitude. Wasps from both sources mated and produced F1 hybrid offspring in the laboratory; however, 90% of hybrid females resulting from one of the reciprocal crosses failed to produce offspring due to encapsulation and melanization of wasp eggs. Results demonstrate that MsT and CcC wasps are incipient species in the process of evolving both pre- and post-zygotic reproductive barriers.

Selfing, Local Mate Competition, and Reinforcement

Mark Rausher

1C_305B-Reproductive Isolation
Saturday, June 21, 2014 2:30 PM-2:45 PM

Due to local mate competition, highly selfing plant species often evolve to produce less pollen, and thus lower pollen/ovule ratios, than related outcrossing species. If the two species share floral visitors, there is the potential for gene flow between the two species. Under these conditions, intuition suggests that gene flow from the selfer to the outcrosser may favor the evolution of increased pre-zygotic isolation in the outcrosser, i.e. the evolution of reinforcement. This expectation arises because the offspring of a cross between an outcrosser and a selfer will produce less pollen, and thus have reduced male fitness, compared to the offspring of a cross between two outcrossers. I present the results from analyzing a four-locus diploid model of this process in which prior selfing prevents gene flow from the outcrosser to the selfer. The model indicates that reinforcement can evolve, but only under a restricted set of conditions that include: (1) discrimination against selfer pollen must be caused by mutations of large effect and substantial dominance; and (2) alleles causing reduced pollen production must exhibit some degree of dominance. In addition, for a given level of gene flow, there is a threshold value of pollen production by selfers above which reinforcing selection will not occur.

Using sequence capture to reconstruct North American mammoth phylogeny and phylogeography

Jacob Enk, Alison Devault, Chris Widga, Jeff Saunders, Paul Szpak, John Southon, Jean-Marie Rouillard, Grant Zazula, Duane Froese, Ross MacPhee, Dan Fisher, Hendrik Poinar

1C_306A-Characterizing Biodiversity
Saturday, June 21, 2014 1:30 PM-1:45 PM

Using a rapid, highly scalable and cost-effective targeted enrichment technique, we reconstructed the complete mitochondrial genomes of dozens of extinct North American woolly and Columbian mammoths from previously-uncharacterized areas of their range. Though we uncovered strong phylogeographic patterns in their matrilineal diversity during the Late Pleistocene, their overall "interspecific" mitophylogeny is not consistent with conventional paleontological models of North American mammoth evolution. Rather than having evolved entirely separately for over a million years, we found evidence that woolly and Columbian mammoths were likely biologically conspecific, the two paleontological species having interbred at different times and places during the Pleistocene. We also characterized the sensitivity, specificity, and predictability of the capture experiments, and thereby outline various design considerations for sequence capture experiments whatever the target organism or state of DNA preservation.

Determining asexual versus sexual propagation in the octocoral Paramuricea using RAD sequencing

Rachel Clostio

1C_306A-Characterizing Biodiversity
Saturday, June 21, 2014 1:45 PM-2:00 PM

Deep-sea habitats are highly diverse communities, with underwater canyons often acting as biodiversity hotspots. However, because corals are slow growing and long-lived traditional markers are not very useful for delineating populations or examining parentage. Paramuricea is a common deep-sea coral found at depths >200 meters. Corals, including Paramuricea, are often found in groups located close together because suitable substrates are limited in the deep-sea. It is unknown if these groups are the result of asexual or sexual recruitment. We employed restriction-site associated DNA sequencing (RAD-seq) to identify SNPs in natural populations of the octocoral Paramuricea. Our goals were then to examine genetic diversity in populations of the North Atlantic and along the Florida shelf. As well as identify clonal individuals and examine their distribution.

Inferring the phylogenetic relationships of early dipteran lineages based on more than 1,000 orthologous genes from transcriptome data.

Karen Meusemann, Michelle Trautwein, Brian Wiegmann, David Yeates

1C_306A-Characterizing Biodiversity
Saturday, June 21, 2014 2:00 PM-2:15 PM

Phylogenetic relationships between the earliest evolving lineages of Brachycera are not resolved while there is no doubt that this is a monophyletic group. We present the first results of our phylogenomic analysis using more than 1,000 orthologous single copy genes derived from transcriptome data from the 1KITE project: using 40 terminal taxa spanning the phylogenetic region of interest, we aim to conduct partitioned analyses based on protein domains and optimized partitioning schemes to improve modeling during phylogenetic inference. We reduce the amount of missing data by selecting only partitions for phylogenetic inference that have the necessary taxon coverage for the question at hand.

Who Are the Fathers? Characterizing Hybrid Origins of Parthenogenetic Aspidoscelis Lizards

Alex Hall

1C_306A-Characterizing Biodiversity
Saturday, June 21, 2014 2:15 PM-2:30 PM

Recent advances in genomic subsampling techniques and associated data analysis pipelines now permit interrogating difficult problems in phylogenetics at the population level. Over the last fifty years, conclusive population assignments for North American whiptail lizards (Aspidoscelis; formerly Cnemidophorus) eluded investigators utilizing morphology, skin histocompatibility, karyotypes, and mitochondrial gene trees. Hybridization between several whiptail species complicates phylogenies because female F1 hybrids reproduce independently from males via true parthenogenesis. Typically these hybrids are diploid with one complete set of chromosomes from each 'parent' species. Interestingly, primarily clonal parthenogenetic lizards exhibit some phenotypic variation in scalation, size, and color. In one example, six pattern classes A-F exist for the parthenogenetic hybrid lizard A. tesselata which was subsequently divided into three species: A. neotesselata (triploid and secondarily hybridized), A. dixoni (diploid with two pattern classes in two small, disjunct populations), and three remaining diploid pattern classes still considered A. tesselata.

In this study, I sought to infer lineages within the Aspidoscelis tesselata/dixoni complex. I hypothesized multiple hybridization events between the parent species A. marmorata and A. scalaris (cf. A. gularis). To capture the maximal genetic information across multiple (~50) individuals per species and across species, I implemented double digest restriction associated DNA sequencing (ddRADseq). ddRADseq captures thousands of homologous unlinked loci between many individuals without reference genomes. Multiplexing and sequencing these loci on the Illumina HiSeq platform allows for inferring single nucleotide polymorphisms to use in many population genetic analyses. I will present preliminary parental population assignments to A. tesselata/dixoni inferred using structure in the context of each population's geographic range. Multiple origins of a vertebrate parthenogen would constitute diversity not otherwise expected of a completely clonal lineage from one origin.

Disentangling phylogenetic relationships complicated by polyploidy in the genus Phlox (Polemoniaceae)

Katherine Waselkov, Bethany Wright, Shannon D. Fehlberg, Mark H. Mayfield, Carolyn J. Ferguson

1C_306A-Characterizing Biodiversity
Saturday, June 21, 2014 2:30 PM-2:45 PM

Phlox, the largest genus among Polemoniaceae, exhibits intriguing diversity among its ca. 60 mostly North American species. The genus shows evidence of complicated evolutionary processes at low (intra- and interspecific) taxonomic levels, which has made reconstructing relationships among species quite difficult. Of particular interest are patterns of variation in ploidy level among and within species. Here we discuss general patterns of congruence and incongruence between ITS and cpDNA phylogenies based on comprehensive sampling of Phlox taxa. Incorporating ploidy level information for samples, we demonstrate that phylogenies that exclude polyploid samples show better agreement. These diploid sample phylogenies are discussed in light of current taxonomy, highlighting placement of taxonomic groups of interest, including the upright eastern taxa, western edaphic endemics, upright southwestern taxa, eastern mat-forming taxa, annuals, and diploid members of the P. hoodii and P. longifolia complexes. We further present available phylogenetic data for several low copy regions, which improve resolution of relationships for the genus. Several examples of diploid and polyploid taxa are highlighted and considered in the context of all data sets. We discuss challenges to reconstructing relationships for groups with extensive polyploidy, as well as some strategies for obtaining sufficient sequence data in light of potential allelic variation. This study provides an improved phylogenetic framework for Phlox, advancing it as an excellent system for investigating aspects of diversity relative to polyploidy.

A genome wide exploration of the pleiotropic theory of senescence. Are human disease and senescence the result of natural selection?

Arcadi Navarro, Juan Rodriguez

1C_306B-Diversity and Diversification
Saturday, June 21, 2014 1:30 PM-1:45 PM

Changing demographic patterns and the ageing of the World's population, have spurred the interest on the causes and mechanisms of senescence. Senescence has long been a mystery, with no single universally accepted theory accounting for its ultimate evolutionary causes (if indeed these causes exist). Perhaps the most popular of the evolutionary explanations proposed so far is the pleiotropic theory of senescence, suggested by G. Williams in 1957[1]. This theory states that mutations conferring risk for traits that are damaging for the organism late in life (e.g. after the fertile stage) might be maintained in a population if they are advantageous early in life, when they can result in an increased reproductive success.

In humans, this theory is consistent with evidence coming from certain genes, from specific conditions or from the life-long reproductive patterns of a few animal models. However, an exhaustive assessment of the impact of all these pleiotropic effects in the senescence of our species has not yet been carried out.

Using public metadata from Genome-Wide Association Studies (GWAS)2 we quantified the global extent and evolutionary implications for our species of the kind of early-late age antagonistic pleiotropy predicted by the theory. Diseases were split in early or late onset conditions and pleiotropies were computed among the SNPs reported to be associated with the diseases.

Our preliminary results are two-fold. First, they reveal some non-trivial antagonistic pleiotropies, that may be relevant to diagnosis and treatment of age-related pathologies. Second, and more interestingly in evolutionary terms, we observe a significant excess of early-late antagonistic pleiotropy in our genomes, some of which present the signature of natural selection.

At the time of submission, we are examining the consistency of the signatures of natural selection around pleiotropies with their putative role in the evolution of senescence.

References:

1. Williams, G. (1957). Pleiotropy, natural selection, and the evolution of senescence.

2. Hindorff, LA et al., (2009) – NHGRI GWAS Catalog: https://www.genome.gov/26525384

A Comprehensive Multilocus Phylogeny of the Neotropical Cotingas with Comparative Analysis of Breeding System and Plumage Dimorphism

Jacob Berv, Richard Prum

1C_306B-Diversity and Diversification
Saturday, June 21, 2014 1:45 PM-2:00 PM

The Neotropical cotingas (Cotingidae: Aves) are among the most phenotypically and behaviorally diverse groups of passerine birds. This diversity has obfuscated cotinga taxonomy, and the resolution of previous phylogenetic hypotheses have been limited by taxon and character sampling. Here, we present a comprehensive phylogeny of the Neotropical cotingas based on molecular data for up to 7500 base pairs across six nuclear and mitochondrial loci for a sample of 61 cotinga species in all 25 genera, and 22 species of suboscine outgroups. We analyze these phylogenetic data using a Bayesian species tree method, and concatenated Bayesian and maximum likelihood methods, and present a highly supported phylogenetic hypothesis. We confirm the monophyly of the cotingas, and present the first comprehensive hypothesis of intrageneric relationships. Key findings include the first placement of Phibalura flavirostris as sister group to Ampelion and Doliornis, the paraphyly of Lipaugus with respect to Tijuca, and the first resolution of the diverse radiations of Cotinga, Lipaugus, Pipreola, and Procnias genera. Finally, we use our phylogeny to test the hypothesis that the increase in sexual selection associated with polygynous breeding systems fosters the evolution of sexual dimorphism in plumage coloration.

Dynamic gradients of river systems mediating dispersal and vicariance of fishes

Benjamin Keck, Phillip Hollingsworth, Thomas Near

1C_306B-Diversity and Diversification
Saturday, June 21, 2014 2:00 PM-2:15 PM

Hypothesized mechanisms of diversification for many lotic, freshwater fishes focus on dramatic geologic events such as glaciations and river re-arrangement. However, these vicariant events do not explain all of the standing diversity and often ignore the requirement of dispersal. For instance, within North America there are groups of endemic species within the Cumberland and Tennessee rivers, in the Eastern Highland region, that diversified within these drainages without the influence of dramatic geologic events. Hypotheses of the mechanism/s of speciation within such drainages are vague at best and are usually limited to references about long-term geologic stability. We discuss likely mechanisms of within drainage diversification based on time-calibrated phylogenies of percids and North American cyprinids. Specifically, we outline expectations of phylogeographic patterns resulting from the erosional differences of underlying geology and epeirogeny acting within these drainages. We propose that stochastic rates of erosion and epeirogeny have resulted in on-going cycles of dispersal and isolation of fishes within these otherwise geologically stable rivers.

On the origin of snakes: inferring the ecology, behavior, and evolutionary history of ancestral snakes

Allison Hsiang, Daniel Field, Adam Behlke, Matthew Davis, Rachel Racicot, Timothy Webster

1C_306B-Diversity and Diversification
Saturday, June 21, 2014 2:15 PM-2:30 PM

The astounding diversity and disparity of snakes has long inspired debate regarding their evolutionary origin. Here, we present the first comprehensive analytical reconstruction of the ancestor of snakes, incorporating new data from species of less modified basal snakes ranging in age from 105-40 Ma, new information on the anatomy of the stem snake Dinilysia patagonica, and a deeper understanding of the distribution of phenotypic apomorphies among the major clades of fossil and Recent snakes. We further infer a time-calibrated divergence tree, which provides novel insight into when, where, and how snakes originated. The major crown-group subclade Henophidia first radiated in the Cenozoic around the K/Pg Mass Extinction (66 Ma). Although error margins preclude certainty as to whether crown Henophidia initially diverged before or after the K/Pg boundary, the widespread distribution and astonishing diversification of henophidian snakes (> 3,000 extant spp.) clearly occurred after the mass extinction event. The snake total group diverged much earlier, sometime around 100 Ma, during a burst of radiation that coincides with the so-called ‘Cretaceous Terrestrial Revolution’. Although the ancestral crown snake is inferred to have originated in Gondwana, the ancestor of the snake total group may have originated on Laurasia, based on the biogeographic distribution of the basalmost stem-group snake Coniophis precedens and a succession of other anguimorph outgroups. Both the total-group and crown-group snake ancestors unambiguously reconstruct as having lived on land, rather than in a marine setting, thus supporting the ‘terrestrial origin’ hypothesis for the origin of snakes, and rejecting the controversial ‘marine origin’ hypothesis. For much of their early evolutionary history, snakes are inferred to have preferred warm, equable, well-watered, broad-leafed, tropical to subtropical forests, which may account for their surprising absence among the otherwise diverse lizard faunas of the Upper Cretaceous of Mongolia. The ancestral snake emerged at night to forage widely for relatively large, soft-bodied prey (likely small vertebrates). Constriction, which is often associated with all snakes, did not evolve early in snake history, and the re-acquisition of diurnal habits appears to have occurred within crown-group Colubroidea, specifically in the clade stemming from the last common ancestor of Elapidae + Colubridae. This reconstruction may explain the clade’s success at invading the cooler and drier habitats that emerged at higher latitudes during the latter half of the Miocene, when colder night-time temperatures no longer favored the nocturnal snakes of the jungle forest floor.

Differentially expressed genes unite phenotypes amidst undifferentiated anonymous loci in the phenotypically diverse redpoll finches (Acanthis)

Nicholas Mason, Scott Taylor

1C_306B-Diversity and Diversification
Saturday, June 21, 2014 2:30 PM-2:45 PM
Understanding what constitutes a species is a vital enterprise of evolutionary biology. Recently, reduced-representation genome-wide datasets have provided unprecedented resolution of species boundaries. Moreover, transcriptomic studies have linked patterns of differential gene expression to phenotypic variation in a variety of systems. However, few studies have considered large panels of anonymous loci in combination with gene expression data to examine species limits within recent radiations of non-model organisms. Here, we combine SNPs across many thousands of loci with gene expression data to study the evolutionary history of redpolls (Acanthis). The redpoll complex is a widespread, phenotypically diverse lineage of finches whose taxonomic status remains unresolved. Redpolls breed throughout much of the Holarctic; however, previous studies have found little to no genetic differentiation between geographically disparate populations or morphologically distinct races. Here, we evaluate species limits in the redpoll complex using high-throughput sequencing and ecological niche modeling. We evaluate genomic differentiation at 3631 loci across 86 individuals using ddRAD-Seq (including all three of the currently recognized species: Acanthis flammea, A. hornemanni, and A. cabaret) and compare gene expression profiles of ten individuals (including both A. flammea and A. hornemanni) using RNA-Seq. We construct ecological niche models (ENMs) for A. flammea and A. hornemanni in North America to evaluate whether favored abiotic breeding conditions differ between these taxa. Our analyses suggest that all currently recognized species of redpolls are part of a single panmictic metapopulation. However, our RNA-Seq analyses indicate that there are over 200 differentially expressed transcripts between A. flammea and A. hornemanni, and overall gene expression profiles cluster by phenotype. Our ENMs indicate that A. flammea and A. hornemanni do not share identical niches, but they are more similar than expected given the range of abiotic conditions available to redpolls throughout North America. Taken together, our findings suggest that gene expression and phenotypic plasticity may play an important role in the generation locally adapted populations of redpolls, which are best treated as a single, phenotypically diverse species.

Latitudinal clines in genome-wide variation predict host race differences in Rhagoletis pomonella

Meredith Doellman, Scott Egan, Gregory Ragland, Glen Hood, Jeffrey Feder

1C_306C-Hybridization and Speciation
Saturday, June 21, 2014 1:30 PM-1:45 PM
Rhagoletis pomonella (Diptera: Tephritidae), the apple maggot fly, is a classic example of speciation with gene flow. Following the introduction of the apple tree (Malus domestica), a host shift from the native hawthorn (Crataegus spp.) occurred, resulting in the formation of R. pomonella apple and haw host races. Previous research has shown that, despite low levels of gene flow, these races differ significantly in allele frequencies, host odor preference, and eclosion/diapause timing, mirroring the fruiting phenology of their respective host plants. In addition to differences between host species, fruiting phenology also varies substantially across latitude, within host species. Thus, we predict that genetic variation, specifically that associated with eclosion timing in the R. pomonella host races, should vary across latitude, as well. Here we use SNPs generated from RAD-seq data to examine geographic patterns of genetic variation within and between host races. We show that allele frequencies for both apple and haw races of R. pomonella are highly correlated with latitude. In addition, the north-south cline in allele frequencies within the haw race strongly predicts allele frequency differences between apple and haw races, suggesting that the host shift from haw to apple produced a shift toward “southern” allele frequencies. Within-race clines are also

correlated with results of a previous experiment, indicating that selection for surviving a longer pre-winter period during diapause (i.e. "apple-like" conditions) may result in more "southern" allele frequencies. These results could have important implications for understanding genetic variation underlying key traits in the differentiation of R. pomonella apple and haw host races.

Gene flow and local adaptation at the lower elevation range limit of the montane salamander, Plethodon ouachitae

Marta Lyons, Donald Shepard, Kenneth Kozak

1C_306C-Hybridization and Speciation
Saturday, June 21, 2014 1:45 PM-2:00 PM

Many species range limits appear to be stable, even when occurring along gradual environmental gradients. A widely discussed but under-tested hypothesis is that asymmetric migration from the densely populated range center to the sparsely populated periphery limits potential for local adaption at the range edge as alleles with the highest average reproductive success across the range get fixed even though these genotypes are poorly adapted to conditions on the periphery. We are testing predictions of this hypothesis in the terrestrial salamander, Plethodon ouachitae, which occurs at higher elevations on six mountains in the Ouachita Mountains. To quantify gene flow, we sampled 100 individuals across four elevation transects that descend the north slope of Winding Stair Mountain, analyzed one mitochondrial, three anonymous nuclear, and eight microsatellite loci. We measured local adaptation to abiotic conditions through closed system respirometry, which resulted in multiple measures of standard metabolic rate at temperatures spanning 5–30ºC for individuals collected at the highest and lowest elevation populations along two transects. Preliminary results using Migrate-N shows little difference in effective population size within transects and high levels of gene flow in both directions. Additionally populations within all but one transect showed little to no genetic differentiation. However, we found significant differences in thermal sensitivity of standard metabolic rate between salamanders from high and low elevations on one of two transects based on a mixed model regression analysis. Salamanders collected from the highest elevation displayed thermal depression at high temperatures with metabolic rate plateauing, while those collected from the lower elevation point followed a linear increase in metabolic rate with increased temperature. Future work will examine additional transects increase sampling resolution at mid elevations and expand the metabolic rate sampling to more transects and test temperatures.

Genome-wide analysis of hybrid incompatibilities using an allele-frequency method in Tigriopus californicus

Christopher Willett, Thiago Lima

1C_306C-Hybridization and Speciation
Saturday, June 21, 2014 2:00 PM-2:15 PM

In the early stages of speciation, the formation of maladaptive hybrids can usually be explained by deleterious interactions between the incipient species' genomes. These incompatibilities, known as Dobzhansky-Muller incompatibilities (DMI), arise as a consequence of the populations diverging in allopatry, and can be due to selection or drift. In many animal hybrids sex chromosomes have been show to play an important role in this form of reproductive isolation. However, much less is known about how DMIs accumulate in animal taxa that do not have sex chromosomes. Here we used the intertidal copepod Tigriopus californicus, a species that lacks sex chromosomes, to determine how DMIs that lead to inviability accumulate between divergent populations. We sequenced pools of F2 hybrids from crosses between 3 populations of T. californicus and performed genome scans to determine regions of the genome that are affected by DMIs causing hybrid inviability. Allelic ratios in hybrids were compared to an expected 1:1 Mendelian ratio. In one cross, between two southern California populations two chromosomes are entirely skewed towards one of the parental allele types and two others have large regions that are skewed as well. In another cross, between a southern and northern California population, none of the chromosomes show the same pattern as in the previous cross, where the entire chromosome is skewed with only three chromosomes showing broad regions with skewed allelic ratios. Theory predicts the number of incompatibilities will increase faster than linearly with time (the snowball effect), however, the present results suggests this may not be the case for inviability DMIs in this species. While we cannot at this point determine the actual number of incompatibilities affecting these hybrids, the portion of the genome affected by DMIs in the first cross is much higher than in the second, even though the second cross involves populations that are more distantly related to one another.

Evolution of a genetic incompatibility in the genus Xiphophorus

Samuel Scarpino, Patrick Hunt, Francisco Garcia-De-Leon, Thomas Juenger, Manfred Schartl, Mark Kirkpatrick

1C_306C-Hybridization and Speciation
Saturday, June 21, 2014 2:15 PM-2:30 PM

Genetic incompatibilities are commonly observed between hybridizing species. Although the importance of this type of isolating mechanism has received considerable attention, we have few examples describing how genetic incompatibilities evolve. We investigated the evolution of two loci involved in a classic example of a Bateson-Dobzhansky-Muller (BDM) incompatibility in Xiphophorus, a genus of freshwater fishes from northern Central America. Hybrids develop a lethal melanoma due to the interaction of two loci, an oncogene and its repressor. We cloned and sequenced the putative repressor locus in 25 Xiphophorus species and an outgroup species, and determined the status of the oncogene in those species from the literature. Using phylogenetic analyses, we find that the promoter region of the repressor is coevolving with the oncogene. The results suggest a variation on the BDM hypothesis for the evolution of incompatibilities where incompatible genotypes have been produced at several times during the evolutionary history of the genus Xiphophorus, and have further implications for sexually antagonistic selection and the evolution of cancer.

Combining living and fossil taxa into phylogenies: the missing data issue

Thomas Guillerme, *Natalie Cooper*

1C_402-Ernst Mayr Symposium
Saturday, June 21, 2014 1:15 PM-1:30 PM

Living species represent less than 1% of all species that have ever lived. Ignoring fossil taxa may lead to misinterpretation of macroevolutionary patterns and processes such as trends in species richness, biogeographical history or paleoecology. This fact has led to an increasing consensus among scientists that both fossil and living taxa must be included in macroevolutionary studies. One approach, the Total Evidence Method, uses molecular data from living taxa and morphological data from both living and fossil taxa to infer phylogenies with both fossil and living taxa at the tips. Although the Total Evidence Method seems very promising, it requires a lot of data and is therefore likely to suffer from missing data issues which may affect its ability to infer correct phylogenies.

In this study we assess the effect of missing data on tree topologies inferred from total evidence supermatrices. Using simulations we investigate three major factors that directly affect the completeness of the morphological part of the supermatrix: (1) the proportion of living taxa with no morphological data, (2) the amount of missing data in the fossil record and (3) the overall number of morphological characters in the supermatrix. We find that, in a Bayesian framework, difficulties in recovering a stable topology are mainly driven by the missing data in the molecular part of the matrix (for which fossil taxa have no data). In a Maximum Likelihood framework, however, topology is not directly affected by missing data per se, but by the number of morphological characters shared among the taxa. Therefore, the two main drivers of incorrect topologies are the overall number of morphological characters and the number of living species with no morphological data.

Our results suggest that, in order to use total evidence methods, one should reduce the missing data in the morphological part of the supermatrix for living species and use a Maximum Likelihood framework to fix the topology prior to the overall Bayesian phylogenetic inference process. We apply our method to a comprehensive data set of both living and fossil primates. We find that using this integrative method modifies previous estimates of rates of body mass evolution within primates.

Species versus subspecies designations in Hercules beetles: quantitative delimitation using multiple data types and an integrative Bayesian approach

Jen-Pan Huang, *L. Lacey Knowles*

1C_402-Ernst Mayr Symposium
Saturday, June 21, 2014 1:30 PM-1:45 PM

With the recent attention and focus on quantitative methods for species delimitation, an overlooked, and equally important issue regards what has actually been delimited. This study highlights the arbitrariness in how taxonomic distinctions, and in particular species and subspecies, are assigned, and the downstream consequences of these decisions for biodiversity and conservation studies. Specifically, we use a model-based delimitation approach to show that in the Hercules beetles (genus Dynastes) there is no statistical difference in the probability that putative taxa represent different species, irrespective of whether they were given species or subspecies designations. Moreover, by considering multiple data types, as opposed to relying exclusively on genetic data alone, we show that the putatively delimited species do not represent similar points along the dynamic lineage splitting spectrum. For example, the taxa differ in the degree to which they are statistically distinguishable based an evolutionary model for phenotypic divergence, as well as the extent to which genetic data indicates that they belong to independent lineages, as modeled under the coalescent. Because both phenotypic and genetic data are analyzed in a common Bayesian framework for delimiting species, our study provides a framework for investigating whether disagreements in species boundaries among data types reflect (i) actual discordance with the actual history of lineage splitting, or instead (ii) differences among data types in the amount of time required for differentiation to become apparent among the delimited taxa. We discuss how the answers to these questions have ramifications not only for how and what characters are used to delimit species, but can also provide insights into the diverse processes involved in the origin and maintenance of species boundaries.

Toward a mechanistic understanding of trait-dependent diversification: The role of niche breadth in the diversification of foregut-fermenting mammals

Lucy Tran, *L. Lacey Knowles*

1C_402-Ernst Mayr Symposium
Saturday, June 21, 2014 1:45 PM-2:00 PM

The degree of ecological specialization is an important determinant of the richness and diversification of species. Specialist species with narrow niche breadths have traits (e.g., low dispersal ability, small effective population size) that promote speciation through population isolation. On the other hand, the features of generalists are thought to constrain speciation. In fact, broad niche breadth has been linked to reduced opportunities for allopatric speciation. Herbivorous mammals have evolved two suites of digestive physioanatomical adaptations for the microbial fermentation of ingested plants: an enlarged cecum or colon (i.e., hindgut fermentation), or a sacculated stomach (i.e., foregut fermentation). By making a larger proportion of vegetation nutritionally accessible to herbivores (i.e., extending dietary niche breadth), foregut fermentation may be the optimal strategy when food is limited and of poor quality. We test the hypothesis that the suite of traits producing foregut fermentation depresses rates of net diversification through the expansion of niche breadth. Therefore, foregut lineages are predicted to have larger niche breadths and lower rates of net diversification than hindgut lineages.

This study finds that lineages of foregut-fermenting herbivorous mammals occupy broader niches (quantified with 20 bioclimatic variables and GIS occurrence data) than hindgut-fermenting lineages. However, evidence from maximum likelihood, trait-dependent diversification analyses indicates that foregut-fermenting lineages generally have higher rather than lower net diversification rates relative to hindgut fermenters. Furthermore, niche differences between species with the two strategies are not significant in comparisons that explicitly consider phylogenetic structure. Therefore, together our results at the lineage but not species level indicate that enlarged niche breadth is associated with elevated diversification rates in foregut-fermenting herbivorous mammals. It is extremely difficult to robustly link pattern and process in macroevolutionary studies of trait-based speciation and extinction, but this study offers one approach of testing a factor (i.e., niche breadth) that is commonly invoked to explain differences in diversification outcomes among mammals but that is tied to the ecological function of a proposed adaptive trait.

Geographic history of long-distance seasonal migration in the largest New World radiation of migratory birds

Benjamin Winger, F. Keith Barker, Richard Ree

1C_402-Ernst Mayr Symposium
Saturday, June 21, 2014 2:00 PM-2:15 PM

Determining where species arose and how they spread across the globe is paramount to understanding geographic patterns of biodiversity. For migratory organisms, this task has been difficult due to the complex geography of seasonal migration: migratory species exhibit seasonal variation in their geographic ranges, often inhabiting geographically and ecologically distinct breeding and nonbreeding areas. The complicated geography of seasonal migration has long posed a challenge for inferring the geographic origins of migratory species as well as evolutionary sequences of change in migratory behavior. For example, one longstanding hypothesis is that migratory animals originated in the tropics and migration evolved through shifts of breeding ranges to temperate regions. To test this hypothesis, we developed the first phylogenetic model of the joint evolution of breeding and non-breeding (winter) ranges of migratory species. Our model — which we term the Domino Model — is inspired by the dispersal-extinction-cladogenesis model of geographic range evolution, in which geographic range evolves via dispersal and local extinction along phylogenetic branches and via inheritance and subdivision at speciation events. The Domino Model follows similar logic, but is novel in jointly considering the evolution of both the breeding and winter range. To analyze the model's results, we implemented a novel application of graph theory for phylogenetic character analysis. We applied our model to the inference of biogeographic history in the largest New World radiation of migratory birds, the emberizoid passerine birds. We found that seasonal migration between breeding ranges in North America and winter ranges in the Neotropics evolved primarily via shifts of winter ranges towards the tropics from ancestral ranges in North America. This result contrasts with an entrenched paradigm that hypothesized migration evolving out of the tropics via shifts of the breeding ranges. We also show that major lineages of tropical, sedentary emberizoids are derived from northern, migratory ancestors and that seasonal migration promoted colonization of the tropics from North America.

Author contributions (for student award consideration):

Ben Winger (student) is the first author; he conceived of and developed the project, analyzed the data, and wrote the manuscript. Keith Barker (second author) contributed a phylogenetic tree of the emberizoids used for analysis. Richard Ree (third author) assisted with implementation and development of the model, study design, and data analysis.

Pervasive introgression masks the true phylogeny in the Anopheles gambiae species complex

James Pease, Matthew Hahn

1C_402-Ernst Mayr Symposium
Saturday, June 21, 2014 2:15 PM-2:30 PM

Determining the phylogenetic relationships among closely related species is often difficult due to the conflicting signals from incomplete lineage sorting (ILS) and introgression. In the Anopheles gambiae species complex, a majority of trees inferred from autosomal loci support one tree topology, while X-linked loci nearly all support a different topology. To resolve this conflict, we analyzed the divergence times of trees from across the genomes of five species. This analysis revealed older divergence times for trees with an "X-like" topology on both the autosomes and the X. We conclude that the X-like tree represents the true species relationship, and the autosome-like topology is the result of pervasive introgression between A. arabiensis and A. gambiae sensu stricto. We confirmed the presence of introgression by developing a five-taxon extension of the "ABBA/BABA" test (D-statistic), which indicated introgression was common throughout the autosomes. These results demonstrate a situation where introgression almost completely masked the true phylogeny, and indicates a lack of introgression on the X-chromosome likely due to the presence of many genes involved in reproductive isolation.

Diversification of East African Soda Lake Cichlids

Antonia Ford, Kanchon Dasmahapatra, Lukas Rüber, Julia Day

1C_402-Ernst Mayr Symposium
Saturday, June 21, 2014 2:30 PM-2:45 PM

Cichlid fishes have radiated in many freshwater lakes; however, uniquely they have also colonised the East African soda lakes (Lakes Natron and Magadi). The Alcolapia species flock includes three sympatric species in Lake Natron (A. alcalicus, A. latilabris, A. ndalalani) and a further species (A. grahami) restricted to Lake Magadi. Here, we aim to characterise this radiation using an integrated approach combining genomic, ecological and morphological datasets. Stable isotope analysis indicates trophic niche segregation between A. alcalicus and the two other sympatric species in Lake Natron (A. latilabris, A. ndalalani), and geometric morphometric analysis demonstrates significant morphological differences between all described species. However, analysis of genome-wide variation using RAD-Seq data reveals shallow divergences between species, with on-going gene flow. Phylogenetic analysis includes maximum likelihood and Bayesian methods, while population genetic approaches are used to test for introgression and admixture including clustering algorithms, FST, and the f4 (four-population) test. Taken together, these results suggest a recent radiation with extensive ecological and morphological diversification.

From dogs to apes: does survival of the friendliest lead to smarts?

Brian Hare

1D_201-Behavior/Cognition
Saturday, June 21, 2014 3:15 PM-3:30 PM
Cognition presents evolution one of its greatest challenges. How do we measure the private mental lives of animals in such a way that we can test how cognition evolves? I will present work examining the evolution of dog and bonobo psychology that suggests that social cognitive evolution can result from selection for friendliness. I will also present data from citizen scientist collecting data via dognition.com to illustrate how hypotheses of cognitive evolution might be tested in the future.

Sympatric species of stickleback differ in cognition and brain structure in ways consistent with adaptation to divergent environments

Jason Keagy, Janette Boughman

1D_201-Behavior/Cognition
Saturday, June 21, 2014 3:30 PM-3:45 PM
Fundamental questions remain about how the brain generates behavior and how brain structure and cognition evolve in response to selection. An ideal system to study cognitive evolution is one with recent and strong divergent selection, providing clear predictions about the differences in cognitive abilities or brain structures between the recently diverged groups. Marine threespine sticklebacks (Gasterosteus aculeatus) colonized multiple lakes in British Columbia, and subsequently adapted to two distinct ecological niches, the “limnetic” and “benthic”, over the course of ~12K years, in the process becoming reproductively isolated. We use two different, but complementary approaches to study cognitive evolution in this system. First, we conduct behavioral experiments to assess specific cognitive abilities in each species. Second, we collect neuroanatomical data on specific brain structures, for example, by using magnetic resonance imaging (MRI). As an example of the first approach, we tested individuals on social information use, specifically the ability to use the feeding behavior of others to locate a food patch. In two lakes we found evidence for parallel evolution of species differences in social information use; benthic fish use social information to locate a food patch whereas limnetic fish do not. These differences are reversed in Enos lake, where the two former species have been hybridizing after human disturbance. Given a previous finding of parallel evolution of faster spatial learning in benthic fish compared to limnetic fish, it is possible that benthic fish are better at learning in general. Neuroanatomical evidence for this would be larger telencephalons (forebrains) in benthic fish than limnetic fish. We found that telencephalon size is indeed larger in benthic fish, even after controlling for body size. Other brain regions, for example, olfactory bulbs, also differ in size in the direction predicted by behavioral and ecological differences between the species. Sticklebacks are a model system for evolutionary biology, and further study of their cognition will provide an opportunity to address long-standing questions regarding the evolution of cognition and the brain.

Absolute brain volume and dietary breadth predict species differences in self-control

Evan MacLean, Brian Hare, Charles Nunn

1D_201-Behavior/Cognition
Saturday, June 21, 2014 3:45 PM-4:00 PM
A broad comparative approach has yielded advances in diverse areas of evolutionary biology, yet studies of animal cognition have typically focused on describing the cognitive skills of one or a few species. This approach has yielded progress toward identifying the proximate mechanisms of cognition in model species, but at the cost of having low power to test hypotheses about how and why cognition evolves. I will present data from a large-scale collaboration investigating cognitive skills for self-control in 36 species of mammals and birds. Using this dataset we explored the leading hypotheses for how and why cognition evolves. Phylogenetic analyses revealed that absolute brain volume was a robust predictor of species differences in self-control, and explained considerably more variance than brain volume controlling for body mass. This result complements recent advances in evolutionary neurobiology and illustrates the cognitive consequences of cortical reorganization through increases in brain volume. Within primates, dietary breadth was a significant predictor of skills for self-control, whereas social group size was not. Collectively, our results implicate robust evolutionary relationships between dietary breadth, absolute brain volume, and cognitive skills for self-control.

Sex-specific effects of brain size on survival under semi-natural conditions in the guppy (Poecilia reticulata)

Alexander Kotrschal, Séverine D. Büchel, Sarah M. Zala, Alberto Corral, Dustin Penn, Niclas Kolm

1D_201-Behavior/Cognition
Saturday, June 21, 2014 4:00 PM-4:15 PM
Large brains are costly to produce and maintain but are believed to confer fitness benefits in challenging environments by facilitating the construction of adequate behavioural responses. While results from comparative analyses suggest positive relationships between relative brain size and facets of fitness, experimental evidence is lacking. Here we test how relative brain size affects survival, one critical aspect of fitness. We mixed selection lines of marked large- and small-brained guppies (Poecilia reticulata, 400 large-brained and 400 small-brained fish with 50/50 sex ratio per replicate) in six large semi-natural ponds together with their natural predator, the pike cichlid (Crenicichla alta). We then monitored survival in weekly censuses until 50 % of the original population size remained. We found that large-brained females survived better under predation pressure compared to small-brained females. In males, brain size did not affect survival. We explain our survival results by a cognitive advantage in large-brained animals, which allows them to better evade predation, and we suggest that the greater colourfulness, which exists in large-brained males, may have counteracted this effect in males. We thereby provide the first experimental evidence that a large brain can confer survival benefits in naturalistic conditions and propose that such survival benefits constitute a major selective force on brain size in natural populations.

The effect of herbicide resistance on mating system in the common morning glory, Ipomoea purpurea

Adam Kuester, Shu-Mei Chang, Regina Baucom

1D_206-Modes of Reproduction
Saturday, June 21, 2014 3:15 PM-3:30 PM

Plant mating systems are labile and affected by various biotic and abiotic environmental conditions. Although modeling efforts suggest that the mating system can directly influence the evolution of herbicide resistance in nature, empirical examination of the relationship between resistance and variation in the mating system is absent in the literature. Here, we investigated populations of the common morning glory, Ipomoea purpurea, across the species' weedy range in the Midwest and Southeast of the United States to assess the relationship between mating system and resistance to glyphosate, which is the active ingredient in the widely used herbicide RoundUp. We examined resistance by performing population dose-response screens and measured the neutral genetic diversity of progeny arrays across 23 field-collected populations to determine if the mating system (outcrossing versus inbreeding) has been influenced by resistance evolution (or vice versa) across the species' range. We found a positive correlation between resistance and inbreeding (F), suggesting either demographic shifts from glyphosate use leading to greater self-fertilization and sib-mating in resistant populations than in susceptible populations, or evolutionary changes in the mating system as a result of resistance evolution. Additional temporal examination of mating system estimates, in particular of populations that increased in resistance level between 2003 and 2012, will aid to our understanding of how variation in the mating system is influenced by the process of resistance evolution.

A phylogenetic analysis of gynodioecy and its correlates in the flowering plants

Katherine Eisen, Andrea Case, Christina Caruso

1D_206-Modes of Reproduction
Saturday, June 21, 2014 3:30 PM-3:45 PM

Gynodioecy, a breeding system where plants are female or hermaphroditic, has been hypothesized to facilitate the evolution of dioecy, a breeding system where plants are male or female. Despite the importance of gynodioecy, a database of gynodioecious species has not yet been assembled. This has limited our ability to test whether the evolution of gynodioecy and dioecy are correlated and to identify traits associated with gynodioecy. We assembled a database of gynodioecious species, and used it determine the frequency and distribution of gynodioecy across the angiosperms. We also tested whether gynodioecy is associated with dioecy, or with traits previously associated with gynodioecy: an herbaceous growth form, and a temperate zone distribution. We found that fewer than 1% of species were gynodioecious, but gynodioecious species occur in 81 of 428 families. Compared to previous studies that surveyed breeding systems within local floras, we found fewer gynodioecious species, but more families that contained gynodioecious species. These 81 families were more likely to also contain dioecious species, herbaceous species, and species with a temperate zone distribution. Although our results supported the hypothesis that dioecy evolves via gynodioecy, we also found that gynodioecy was associated with different morphological and ecological traits than dioecy. This suggests that different conditions select for the evolution of gynodioecy versus dioecy.

Gynodioecy and sex ratio variation within a large network of natural populations

Mathilde Dufay

1D_206-Modes of Reproduction
Saturday, June 21, 2014 3:45 PM-4:00 PM

Gynodioecy is the co-occurrence of females and hermaphrodites within the same plant species. It is often due to conflicting interactions between cytoplasmic genes of male sterility (CMS) which effect can be counteracted by nuclear genes that restore pollen production. The maintenance of such polymorphism has been shown to depend on patterns of frequency dependent selection within populations, but also on metapopulation dynamics. In this study, we have documented the variation of sex ratio, CMS and nuclear restorers frequency within 85 natural populations of gynodioecious, wind-pollinated plant Beta vulgaris ssp. maritima. By analyzing the effects of population isolation, population size, level of disturbance and neutral genetic diversity on sex ratio variation, and by comparing our results to theoretical predictions, we investigate how selective vs. non selective processes affect the maintenance of females in populations.

Genetic diversity of two crustaceans with presumed different reproductive modes in ponds of the Chihuahuan Desert, North America

Rebekah Horn

1D_206-Modes of Reproduction
Saturday, June 21, 2014 4:00 PM-4:15 PM

Inbreeding modes of reproduction are known to decrease a species genetic diversity, making it vulnerable to changing environmental conditions. However, there are various forms of reproduction that can alleviate potentially strong effects of pure clonal reproduction, such as self fertilization (hermaphroditism), hermaphrodites that can outcross with other hermaphrodites, and a rare mix of hermaphrodites that can outcross with males called androdioecy. The tadpole shrimp (Notostraca: Triops), a temporary pond crustacean occurring in the arid regions of western North America, is presumed to use four different modes of reproduction. The method of reproduction used by a Triops species has been determined by prior researchers based on the proportion of males (no ovisacs) to ovisac-bearing females; all female populations are presumed to reproduce parthenogenetically or hermaphroditically, populations with some males are presumed to be androdioecious and populations that are approximately equal in sex ratio are presumed to be obligate outcrossing with separate sexes (gonochoric). The current study uses mitochondrial DNA sequences and microsatellite markers on two species of Triops from southern New Mexico with presumed different modes of reproduction: T. newberryi (androdioecious) and T. longicaudatus "short" (parthenogenetic or hermaphroditic). The genetic markers reveal a high degree of genetic structure between geographically proximal populations that is likely to represent a persistent founder effect and populations of both species have low genetic diversity. Population genetic theory predicts that an androdioecious species (T. newberryi) would have slightly elevated levels of genetic diversity due to the effects of outcrossing. In comparison to T. l. "short", T. newberryi did have higher nucleotide diversity, allelic richness, observed and expected heterozygosity, but the comparisons between species were not statistically significant. However, the level of inbreeding (FIS) and the selfing rate was higher in T. newberryi. Our results imply that either the degree of outcrossing between males and hermaphrodites does not alleviate accumulation of inbreeding or that T. newberryi is not androdioecious as assumed by previous authors. Additional work is in progress to analyze the mating system of these two species using a more direct approach of a progeny array. Genotypes of mothers and individual encysted embryos contained within their ovisacs will be used to better estimate outcrossing rates and to distinguish parthenogenesis from hermaphroditism.

When sex allocation theory and reality meet: Insights from size-specific reproductive investment in an androdioecious barnacle

Christine Ewers-Saucedo, *John P. Wares*

1D_206-Modes of Reproduction
Saturday, June 21, 2014 4:15 PM-4:30 PM

Why are species dioecious, hermaphroditic, sex changers or a combination of hermaphrodites and single-sex individuals? In other words, what determines how individuals allocate reproductive resources into the male and female sex?

Sex allocation theory explains the distribution of sexual systems by asking which sex allocation provides the highest fitness. These fitness maxima often differ for small and large individuals depending on the population-wide sex allocation-fitness relationship. Therefore we can use empirical measurements of size-specific reproductive investment to infer the population-wide relationship between sex allocation and fitness. However, being of a certain size may also convey direct fitness advantages. A common example is that large plants are able to disperse pollen further than small plants, even though both produce the same amount of pollen. In other words, large individuals have a higher fitness than small individuals, even though both have the same reproductive investment. In this case, size-specific reproductive investment does not accurately reflect the sex allocation-fitness relationship because fitness is increased in large individuals.

We can test if sex allocation theory is sufficient to explain an observed size-specific pattern of reproductive investment by comparing predictions made by sex allocation theory with empirical data.

Sex allocation theory predicts that androdioecy, the coexistence of males and hermaphrodites, is evolutionarily stable only under a very particular relationship between sex allocation and fitness. Comparing these predictions for androdioecy with inferences made from size-specific reproductive incestment shows that sex allocation alone cannot explain androdioecy in the commensal barnacle Chelonibia testudinaria. Instead, we conclude that males gain fitness through direct effects, which may be related to their dwarfed size and close proximity to hermaphrodites.

Patterns of gene expression underlying the extreme physiological remodeling of the Burmese python intestine upon feeding

Audra Andrew, *Daren Card, Drew Schield, Elizabeth La, Stephen Secor, Todd Castoe*

1D_301A-Evolution and Physiology
Saturday, June 21, 2014 3:15 PM-3:30 PM

The Burmese python (Python molurus bivittatus) has emerged as a premier model for studying physiological remodeling in vertebrates due to the massive changes in organ mass and physiological function observed in this species following feeding. Among these organ-specific responses, the small intestine experiences a doubling in mass, 6-fold fluctuations in microvillus length, and a up to 10-fold increases in nutrient uptake within 48 hours of feeding. We tested the hypothesis that these dramatic fluctuations in small intestine form and function temporally correspond to major fluctuations in intestinal gene expression. We sampled python small intestines for each of the 6 time points before (fasted) and after feeding (6h, 12h, 24h, 96h, 10d), with 2-5 replicates per time point, using RNA-seq to identify changes in gene expression associated with shifts in intestinal form and function. We identified genes that showed significant changes in expression across time points, as well as their magnitude and direction of change. We found a large number of genes that show significant differential expression with feeding, and multiple clusters of early and late-responsive genes. Our results indicate that there is a massive shift in gene expression that underlies large-scale rapid shifts in intestinal form and function upon feeding in the python, and that expression analyses have potential to identify the molecular mechanism and activated genetic pathways that facilitate this shift in intestinal function.

Physiological synergism and antagonism in the evolution of life histories

Goggy Davidowitz, *Derek Roff, Frederik Nijhout*

1D_301A-Evolution and Physiology
Saturday, June 21, 2014 3:30 PM-3:45 PM

Evolution acts on whole organisms and thus, on multiple traits simultaneously. We still, however, know little of how the underlying physiology enables or constrains the response to simultaneous selection on multiple traits such as body size and development time, which are often highly correlated with fitness. Previous work with insects has shown that these two life history traits are regulated by the interaction of the same three underlying physiological factors: growth rate, the timing of the cessation of juvenile hormone secretion and the timing of the secretion of the ecdysteroid hormones. Here we show how antagonism and synergism at the physiological level enables and constrains simultaneous selection at the phenotypic level of the two life history traits. After ten generations of selection on all four combinations of body size and development time (Big/Short, Big/Long, Small/Short, Small/Long) the three physiological and two life history traits differed significantly from the initial population.

The three physiological factors explained 93% of the response of development time to simultaneous selection and 99% of the response of body size. When the two life history traits were under synergistic selection, the response to simultaneous selection was due largely to juvenile hormone and the ecdysteroids and constrained by growth rate. When the life history traits were under antagonistic selection, the response to selection was due primarily to the change in growth rate and constrained by the two hormonal traits. The framework used here provides a bridge between too much mechanistic detail to allow for testable predictions on the mechanisms underlying the response to simultaneous selection and too little detail that ignores mechanism altogether. Evidence suggests that this framework has broad applicability to a diverse range of taxa including green algae, plants, amphibians and mammals and to other insects.

Cardiac myopathy and flight performance in starvation-selected Drosophila, or the case of the All-American flies

Allen Gibbs, Christopher Hardy, Michael Brewer, Ryan Birse, Matthew J. Wolf

1D_301A-Evolution and Physiology
Saturday, June 21, 2014 3:45 PM-4:00 PM

Previous studies have shown that selection for starvation resistance in Drosophila melanogaster results in populations that are extremely obese. We used high-speed videography and optical coherence tomography to investigate correlated changes in cardiac function. Hearts of starvation-selected flies had wider systolic and diastolic diameters and a smaller fractional shortening ratio, resulting in reduced cardiac output relative to fed control populations. These flies also exhibited low locomotor activity and flew poorly, due to increased wing loading. To investigate whether these phenotypes were genetically based, we made adult starvation-selected flies lean by withholding food for seven days. We also limited access to food late in the third larval instar, when excess lipids are accumulated. After either of these diets, the flies had the same mass and lipid content as controls. Cardiac parameters and flight performance were similar to those of control flies, indicating that the seven-day diet rescued these phenotypes. Our data are consistent with a model in which large lipid deposits cause a dilated cardiomyopathy. Thus, correlated responses to selection appear to be caused by physical interference with the heart rather than genetic differences in cardiac physiology. Supported by NIH award R15-GM100395.

Deeply conserved r-opsin phototransduction cascade genes may underlie a novel expansion response of chromatophores to light in isolated Octopus skin

Desmond Ramirez, Todd Oakley

1D_301A-Evolution and Physiology
Saturday, June 21, 2014 4:00 PM-4:15 PM

Understanding the evolutionary origins of novel traits, whether morphology, physiology or behavior, sheds light on the processes that help shape the exuberant diversity we see in life. A key question is the extent to which novel behaviors depend on new underlying components or arise through evolutionary “tinkering”, which may borrow and recombine existing components to produce new behaviors. Cephalopod mollusks like octopuses and squids dazzle prey, woo mates and seamlessly blend into the background by changing the color and pattern of their skin. Embedded in their skin are novel colored organs called chromatophores that they use to perform these astounding color-changing feats. While changes in body patterning are known to rely on eyesight, we have also found that bright white light causes the chromatophores in isolated Octopus bimaculoides skin to expand in the absence of eye or CNS input. We call this behavior Light-Activated Chromatophore Expansion or LACE. To identify potential molecular mechanisms that may underlie LACE, we found that r-opsin phototransduction genes are expressed in octopus skin, and identified peripheral sensory neurons in the skin that express r-opsin. LACE suggests that octopus skin is intrinsically sensitive to light, and that this dispersed light sense could contribute to their unique and novel camouflage abilities. Further, finding r-opsin phototransduction cascade genes expressed in octopus skin suggests that a common molecular mechanism for light detection in eyes may underlie LACE and may have thus been co-opted for light sensing in octopus skin.

Survival of the fattest? Indices of body condition do not predict fitness in the brown anole (Anolis sagrei)

Robert Cox, Ryan Calsbeek

1D_301A-Evolution and Physiology
Saturday, June 21, 2014 4:15 PM-4:30 PM

Measures of body mass and length are commonly used to derive indices of condition, which are often assumed to reflect the energetic state of an animal and, by extension, to predict its fitness. However, the relationship between condition and fitness is rarely quantified, and the appropriate method(s) for deriving indices of condition are frequently debated. We synthesized a decade of phenotypic selection studies involving over 4,600 individual lizards (Anolis sagrei) and 41 replicates of selection across seven populations to test the common assumption that body condition is a strong predictor of adult survival. We also compared inferences about natural selection using two indices of condition: the popular residual index (Ri), and the scaled mass index (Mi), which was recently proposed as a more robust alternative. Relative to variance in selection among replicates and to error associated with the estimation of selection gradients, variance due to the use of alternative condition indices was minor and effectively negligible. Contrary to the intuitive prediction that individuals in better condition should exhibit higher survival, we found no evidence for strong or consistent linear selection for higher condition in either males or females. Significant quadratic selection on condition was similarly rare in both sexes. Correlational selection favored combinations of large size and high condition in males, but not females. Collectively, our results indicate that inferences about natural selection may be robust to the choice between indices of condition, but that indices of condition can be unreliable as proxies for fitness, particularly when the relationship between fitness and condition is contingent upon interactions with other traits.

Computationally efficient estimation of the number of founders for colonized populations

Hua Chen

1D_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 3:15 PM-3:30 PM
Inferring the number of founding individuals for a colonized population, or quantifying the founder effect is important for population genetic studies. Existing approaches require intensive computation via simulations when the sample size is large. We adopt some recent theoretical results to improve the computational speed. Given the same computational capacities, the new approach can efficiently handle much larger samples, and has a significantly boosted performance characteristics than the existing methods. Simulation studies demonstrate that increasing sample size can greatly improve both accuracy and precision of the estimates. Therefore, this approach is expected to be useful for molecular ecological and evolutionary studies in the genomic sequencing era. The method is applied to a mtDNA data set with 352 Polynesian individuals, and estimate the number of founders of the Polynesian population to be 53 (95% CI (28.7, 77.5)) at 2500 years ago. The small number of founding individuals during the colonization of the Polynesian populations is consistent with former discovery of a severe founder effect and low genetic diversity in the Polynesian genomes.

Estimating F-statistics: Weir and Cockerham, Evolution 38:1358--1370 (1984) updated

Bruce weir

1D_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 3:30 PM-3:45 PM
In a highly-cited paper, Weir and Cockerham presented a method for estimating F-statistics, primarily Fst, from genetic marker data. They stated explicitly that their method was for data from a series of independent populations with similar histories: in effect a star phylogeny. Under this model, their weighting of allele frequencies by sample sizes when averaging over populations was appropriate and gave rise to estimates with low bias and low variance. Actual populations are neither independent nor similar of course and a more general approach was given by Weir and Hill (Annual Review of Genetics 36:721-750, 2002) but still using sample-size weightings for averages over populations. Following a recent paper by Bhatia et al (Genome Research 23:1514-1521, 2013), the earlier work has been re-cast in terms of unweighted averages of sample heterozygosities, but for any number of populations and any number of alleles per locus, and an emphasis given to the estimation of Fst-like measures within each population and between each pair of populations. The average of the within-population measure reduces to the original Weir and Cockerham estimator if populations are independent, or if the sample sizes are the same for each population. The numerical difference between the new and original estimators is generally small. This work will be illustrated with human SNP and STR data, and its use in detecting signatures of natural selection will be discussed. (Supported in part by NIH GM 075091).

A new test for positive selection with greatly improved power

Sarah Parks, Nick Goldman

1D_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 3:45 PM-4:00 PM
Finding positive selected genes, or sites in genes, is a key question in biology. A variety of maximum likelihood and Bayesian methods for testing for positive selection using omega, the ratio of the fixation rates of non-synonymous and synonymous mutations, have been developed. These are all very conservative when applied to real genes, and hence achieve a lower power than desired.

One of these tests, embodied in the SLR method (Massingham and Goldman, 2005), estimates the maximum likelihood value of omega for each site, and then tests whether this value is greater than one. This test is conservative because the null hypothesis assumes that all sites are either neutral or positively selected (omega >= 1), whereas in reality the majority of sites in genes are under purifying selection (omega

I will present a new method to test for positive selection that has greatly improved power whilst retaining control of the false positive rate. This involves a new site-wise likelihood ratio test, designed to have power and control when many of the sites in the gene are under purifying selection (as is typically the case), and a diagnostic for detecting certain situations in which the original SLR test should be preferred. The new test obtains improved power by fitting the null hypothesis to the data and then performing parametric bootstraps.

The method has been tested using simulations over a wide range of realistic conditions, including standard comparisons used in previous studies, and larger and more realistic examples modeled on real-life studies. I will show that, for those rare cases where all sites are either strictly neutral (omega=1) or positively selected (omega>1), the new method performs as well as SLR. More importantly, for genes where many of the sites are conserved, this method has much better power than other tests and a controlled false positive rate.

The shape of adaptive genetic covariance: Chromosome walking using population graphs

Rodney Dyer, Andrew Eckert, Brian Verrelli

1D_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 4:00 PM-4:15 PM
Throughout the genome, regions that have experienced selection can be identified by changes in structure and diversity. Indeed, outlier analyses have provided valuable insights into how selection has operated throughout the genome. Outlier status, while sufficient to hypothesize selection, is not necessarily the only physical signature that selection leave in the genome. Selection may change the covariance among populations yet not result in a net increase in divergence; there are many alternative neutral and adaptive histories that lead to the same exact Fst… Here I present work on quantifying the topographic shape of adaptive genetic covariance. Selection changes the shape of covariance defined in a population graph, deviating from neutral history in predictable ways. By focusing on the shape of covariance rather than the

amount of divergence, population graphs can be used to classify alternative 'outlier' genomic regions into groups based upon the way in which selection changed among-population covariance. A topological focus also allows the testing of hypotheses based upon external features such as genomic inferences (e.g., What else in the genome has covariance shaped like LCT?), phenotypic changes (e.g., What regions are congruent with among-population differences in morphology?), and environmental conditions (e.g., Where is covariance structured in a way that matches changes in altitude?). I close by discussing the general utility of adopting a topological approach to identifying and understanding putatively adaptive genomic regions and its utility in non-model systems.

Extending the Ewens Sampling Formula to structured populations: Recursive computation of exact probabilities of allele frequency spectra

Marcy Uyenoyama, Benjamin Redelings, Seiji Kumagai

1D_301B-Molecular Evolution and Evolutionary Genetics
Saturday, June 21, 2014 4:15 PM-4:30 PM

To accommodate the enormous amount of information available in a sample of entire genomes, many evolutionary analyses have relied upon summary statistics or data reduction methods that marginalize over full genealogical trees. An approach that appears to have received relatively little attention involves the Ewens Sampling Formula (ESF), which provides a closed-form expression for the probability of the allele frequency spectrum (AFS) observed in a sample of arbitrary size under the infinite-alleles model of mutation. We extend the ESF to accommodate population structure, here accommodating migration between two demes. We develop a recursion which relates a sample to its immediate ancestor sample (vertical in time). We then characterize properties of the next-sampled gene, given the AFS already observed (horizontal in time). While the AFS probabilities are fully determined by the vertical recursion, their derivation is greatly simplified by the horizontal argument. A rescaling of time or mutation rate that would permit the use in structured populations of the ESF for unstructured population does not exist, even in the case in which the sample is derived entirely from a single deme in a multideme population. For that case, we propose an approximate scaling, which interpolates between no migration and the high migration limit. This approximation provides a qualitative description of the AFS probabilities: higher migration rates increase the effective mutation rate. Under other sampling conditions and for applications in which the exact likelihood is required, our method provides the AFS probabilities through a double recursion that accommodates successively greater numbers of observed alleles and successively greater sample sizes.

The Genetics of Divergence Between Upland and Lowland Ecotypes of Panicum virgatum

Elizabeth Milano, David Lowry, Thomas Juenger

1D_302A-Local Adaptation
Saturday, June 21, 2014 3:15 PM-3:30 PM

Panicum virgatum (switchgrass) is an outcrossing C4 perennial grass native to most of North America. Wild populations are predominantly found in tall grass prairie and agronomic cultivars are being developed as a feedstock for cellulosic bioethanol. Because of its economic importance, there is interest in developing genomic tools for marker-assisted breeding programs and crop development. However there is abundant natural variation in Panicum virgatum that lends itself well to the study local adaptation. Two predominant ecotypes are found in overlapping ranges across the Midwestern United States. The northern upland ecotype is adapted to colder climates and shorter growing seasons, whereas the lowland ecotype is found in riparian areas and has a longer growing season. We have developed a 4-way outbred mapping population of 400 individuals that captures the variation observed between upland and lowland ecotypes to study the underlying genetic architecture of locally adaptive traits. Genetic markers were developed using a double-digest RAD scheme and assembled using both a reference-based and de novo approach. The population is currently growing in Austin, Texas but will be clonally propagated and planted at several sites spanning a latitudinal gradient across the Midwest. Thus far we have created a linkage map and found many QTL associated with traits measured in the initial field season. In future years we will compare QTL across environments to discover loci underlying trait divergence between locally adapted ecotypes.

The genetic architecture of local adaptation at fine spatial scales – a case study of three montane conifer species

Andrew Eckert, Christopher Friedline, Brandon Lind, D. Ethan Harwood, Erin Hobson, David Neale

1D_302A-Local Adaptation
Saturday, June 21, 2014 3:30 PM-3:45 PM

The structuring of genetic diversity within natural populations of forest trees results from the interplay of numerous evolutionary forces, such as genetic drift, migration, and natural selection. Landscape genomics is concerned with testing hypotheses about how these interacting evolutionary forces change over geographical space to shape naturally occurring patterns of this diversity. Here, a landscape genomic approach will be used to illustrate how genetic drift, migration, and natural selection interact to determine patterns of genetic diversity, including the genetic diversity underlying fitness-related phenotypes, at fine spatial scales within natural populations of forest trees. This task will be accomplished by providing evidence that populations of sugar pine (P. lambertiana Douglas), western white pine (P. monticola Douglas ex. Don), and whitebark pine (P. albicaulis Engelm.) are adapted to local site conditions within the Lake Tahoe Basin of California and Nevada. More specifically, I will test the hypothesis that local adaptation is apparent at local spatial scales (i.e. ~ 600 km2), despite large amounts of pollen-mediated gene flow among local populations. I will also highlight, however, several instances where clearly adaptive patterns of genetic diversity have been influenced by local demographic events. Building upon these results, I will then illustrate how the observed patterns of molecular genetic diversity for a varied set of functional genes are organized relative to the phenotypic variation used to highlight local adaptation. The drivers of these patterns are likely the multilocus aspects of molecular genetic diversity as it contributes to local adaptation at fine spatial scales. Lastly, I will draw upon an emerging example from foxtail pine (P. balfouriana Grev. & Balf.) to illustrate the promising role that species of Pinus subgenus Strobus can play in our understanding of the genetic architecture of local adaptation and the ability of this architecture to rapidly respond to environmental change within natural populations of forest trees.

The evolutionary interplay between dispersal traits and habitat specialization

Nancy Emery, *Elisabeth Forrestel*

1D_302A-Local Adaptation
Saturday, June 21, 2014 3:45 PM-4:00 PM
In spatially heterogeneous environments, patterns of gene flow have significant consequences for the evolution of specialization and phenotypic plasticity. Conversely, organisms that are restricted to patchy or isolated habitats will experience selection for local or more targeted dispersal. While the evolutionary interplay between dispersal traits and habitat specialization has been recognized in theory, few empirical studies have tested if these dynamics predict dispersal traits and habitat associations in natural systems. We tested the hypothesis that dispersal traits evolve in conjunction with habitat specialization in Lasthenia (Madieae, Asteraceae), a clade of herbaceous flowering plants that are widely distributed throughout the California Floristic Province of western North America. While many species of Lasthenia are broadly distributed throughout the region, others are endemic to geographically isolated ephemeral wetlands called vernal pools. Lasthenia seeds are predominantly wind-and gravity-dispersed, and vary substantially in fruit morphology and size as well as the presence/absence and length of the pappus (a tuft of hairs or bristles attached to the end of the seed that aid in wind dispersal). We predicted that species that are restricted to vernal pools have fruit traits that promote local dispersal, while the “habitat generalists” have traits that enhance dispersal over longer distances. First, we obtained fruits from all species in the genus and measured a suite of traits, including fruit weight, fruit length and width dimensions, and pappus length. Correlated measures of fruit size and shape were converted into independent variables using principal components analysis. Next, we released all fruits into a controlled wind current in a wind tunnel, measured their flight distances, and identified the fruit morphological traits that best predicted flight distance using ANOVA. Finally, we used comparative methods to evaluate the degree to which the flight-enhancing fruit traits evolved in conjunction with habitat affinity in Lasthenia. Results indicate that Lasthenia vernal pool specialists have smaller, shorter and wider fruits, as well as a drastically reduced (or absent) pappus, compared to their more widespread congeners, thus supporting the hypothesis that dispersal traits evolve in conjunction with habitat specialization.

Local adaptation to climate within a tree species range: the case of sugar pine, Pinus lambertiana

Aurore Bontemps, *Johanna Schmitt, Jessica Wright*

1D_302A-Local Adaptation
Saturday, June 21, 2014 4:00 PM-4:15 PM
Divergent selection among populations experiencing heterogeneous environments is expected to generate patterns of local adaptation. However, population evolution will depend on several factors such as gene flow that can either counteract selection by homogenizing gene pools or enhance response to selection by favoring the exchange of pre-adapted alleles. Assessing the extent of local adaptation is crucial in the current context of rapid climate change because locally adapted populations will be expected to lag behind their optimum. This is particularly true in long-lived species such as forest trees, where evolution by natural selection will be slowed by a longer generation time relative to projected climate change.

Provenance tests, in which individuals from multiple populations originating from different climates are grown in common experimental sites, can be used to dissect the role of climate in local adaptation. The studies of adaptation to climate usually rely on populations coming from latitudinal or elevation gradients. Our first expectation is that local adaptation would develop less easily in elevation gradients as gene flow is more likely between populations in contrasting environments. Yet, local adaptation can be observed in elevation gradients if selection is strong relatively to gene flow or if gene flow is prevented by phenological lags between populations. In general, latitudinal gradients should be better suited to highlight the broad imprint of climate on population adaptation, unless climate is not the main varying agent of selection.

In our study, we are characterizing patterns of local adaptation in sugar pine (Pinus lambertiana). We are focusing on two sets of sugar pine provenance tests. Both tests include sources from a wide variety of latitudes and elevations across the entire species range. We will assess whether there is local adaptation to climate in Pinus lambertiana. We will test the hypothesis that genotypes originating in climates similar to each test garden site will perform better than genotypes from dissimilar climates. Moreover, we will test the hypothesis that gene flow affects local adaptation by testing the effect of geographic and climatic distance between sites of origin on growth differences in transplantations, assuming that gene flow decreases with increasing geographical distance.

Using pooled sequencing and whole-genome environmental association analyses to study local adaptation in three Alpine Brassicaceae species

Christian Rellstab, *Martin C. Fischer, Stefan Zoller, Felix Gugerli, Rolf Holderegger, Andrew Tedder*

1D_302A-Local Adaptation
Saturday, June 21, 2014 4:15 PM-4:30 PM
Alpine regions are hot spots of biodiversity and ideal to study local adaptation of plants, because environmental conditions often change dramatically over small geographic distances, where gene flow is still present. Natural genetic variation is essential for the adaptation of organisms to their local environment and to changing environmental conditions. In recent years, the development of powerful nucleotide sequencing technologies, software that facilitates the analysis of large next-generation sequencing data sets, and climate databases with high spatial resolution have opened up new possibilities to study adaptation. Here, we used a pooled population sequencing (Pool-Seq) approach to study

genome-wide patterns of nucleotide variation in natural populations of three plant species of the Brassicaceae family in the European Alps (Arabis alpina, Arabidopsis halleri, Cardamine resedifolia), and to link this variation to abiotic factors that characterize the populations' environments. We first assembled the three genomes de novo, called up to 3.5 Mio single nucleotide polymorphisms (SNPs) per species, and identified FST-based outlier loci using a Bayesian method. We additionally linked all SNPs to high-resolution topo-climatic data (e.g., temperature, precipitation, radiation, and slope) using latent factor mixed models, a new and fast approach to identify loci associated with environmental factors while controlling for neutral background population structure. Finally, we compared the biological processes of the resulting candidate genes with the environmental factors they are associated with. We present (a) how Pool-Seq can establish a powerful data basis to study local adaptation in natural populations of non-model organisms, (b) topo-climatic factors that may drive local adaptation in the study species, and (c) candidate genes for adaptation to abiotic factors. Our results provide a genome-wide perspective on the distribution of adaptive genetic variation in natural plant populations from a highly diverse and heterogeneous alpine environment. We emphasize that the combination of genome-wide sequence data and precise habitat information, and the parallel study of several related species, present powerful approaches to study local adaptation. Our study may help unraveling the genetic basis of local adaptation and its interplay with climate change.

The predictors of avian song evolution: sexual selection and the trade-off between acoustic and visual signals

Christopher Cooney, Joseph Tobias, Nathalie Seddon

1D_302B-Sexual Selection
Saturday, June 21, 2014 3:15 PM-3:30 PM

Bird song, like many acoustic signals produced by species across the animal kingdom, plays a key role mediating, mate choice, resource defence, and species recognition trait. Identifying the factors that influence song divergence can therefore reveal the processes underlying the evolution of reproductive isolation between populations, and ultimately speciation. Yet, despite having clear implications for our understanding of species diversification, the mechanisms driving rates of song evolution—and their relative importance—remain poorly understood. Here, we analyse evolutionary rates of song divergence, using newly developed phylogenetic methods applied to a dataset of over 2500 songs from 235 pairs of closely related passerine bird species. Our results reveal that independent components of song structure (e.g. song frequency or duration) are influenced by unique combinations of physiological, ecological, and biogeographical factors. However, we find that overall levels of song divergence are most strongly predicted by the interaction between latitude and sexual dichromatism: rate of song divergence increases away from the tropics, but only amongst pairs that lack sex-differences in plumage coloration, supporting the existence of a trade-off between visual and acoustic signalling modalities. If the intensity of sexual selection increases with latitude, our results suggest that song divergence is most rapid when the focus of intense sexual selection targets acoustic, rather than visual, signals.

Evolution of female song production in Drosophila virilis group species

Kelly LaRue, Gordon Berman, Tristan Perez, Georgia Guan, David Stern, Mala Murthy

1D_302B-Sexual Selection
Saturday, June 21, 2014 3:30 PM-3:45 PM

Many species throughout the animal kingdom use acoustic communication for mate attraction. Typically, only males produce courtship song, as in the fruit fly model species Drosophila melanogaster, but in rare cases, females can acoustically participate in the courtship ritual. Female courtship song was previously observed in the twelve Drosophila virilis group species, who diverged from D. melanogaster approximately 40 mya. Using new high-throughput and quantitative methods for song recording and analysis, we confirm that D. virilis group females produce species-specific songs distinct from the primary courtship songs of their male counterparts. However, song features are highly correlated between female song and male secondary courtship song. This suggests that these song modes may share common neural elements. Specifically in D. virilis, we find that female song production is important for mating success and signals receptivity. Finally, we show that male and female courtship songs are temporally coordinated, which represents the first demonstration of predictable acoustic duetting in a Drosophilid species. Based on neurogenetic principles of coursthip song established in studies of D. melanogaster, we are developing genetic tools to evaluate the evolution of the song production neural circuitry in D. virilis males and females. These tools, combined with our behavioral analysis, lay the groundwork for establishing D. virilis as a useful model for comparative studies of acoustic communication systems.

Mate choice in European badgers (Meles meles): females choose males from neighbouring groups that have similar MHC

Simon Yung Wa Sin, Geetha Annavi, Chris Newman, Christina Buesching, Terry Burke, David Macdonald

1D_302B-Sexual Selection
Saturday, June 21, 2014 3:45 PM-4:00 PM

The major histocompatibility complex (MHC) plays a crucial role in the acquired immune system. It can be a target of mate choice, used to maximize offspring fitness, potentially mediated by olfactory cues. Under the genetic compatibility hypothesis, individuals are predicted to choose mates with maximal or optimal MHC divergence, to enhance the resistance of their offspring to pathogens. Studies of MHC-based mate choice in wild mammals are under-represented currently, and few investigate more than one class of MHC genes. Here we investigated mate choice based on the compatibility of MHC class I genes and MHC class II DRB genes in a wild population of group-living European badgers (Meles meles). We also investigated mate choice based on microsatellite derived pairwise relatedness, to distinguish MHC-specific effects from genome-wide effects. Using 6 years of data, overall we found MHC-assortative mating for neighboring-group, but not within-group parent-pairs, with yearly variations. This effect was due entirely to similarity at MHC class II DRB loci. Neighboring-group parent-pairs had similar DRB amino acid distances for both the entire exon 2 sequences and the antigen-binding site (ABS) in isolation. Our randomizations showed no evidence of genome-wide based inbreeding, based on 35 microsatellite loci; MHC class II DRB similarity was therefore the apparent target of mate choice. We propose that MHC-based mating studies should account for the class of MHC genes examined, mating system characteristics, and inter-annual variations.

Genetic and environmental contributions to a divergent plumage trait in barn swallows

Joanna Hubbard, Amanda Hund, Rebecca Safran

1D_302B-Sexual Selection
Saturday, June 21, 2014 4:00 PM-4:15 PM

A central theme of evolutionary research is to understand the source and function of phenotypic variation. For most phenotypic traits, sources of variation can be partitioned into genetic or environmental variation. Identifying the proportion of variance due to these components allows for predictions regarding phenotypic responses to variable environments and selection to be made. Barn swallow subspecies (Hirundo rustica) have divergent phenotypes and it appears that the focal trait for female preferences has also diverged. We examined at the sources of phenotypic variation of melanin-based ventral plumage in two populations of barn swallows: North America (Colorado: H.r. erythrogaster) and Europe (Czech Republic: H.r. rustica). In North America, male coloration is the target of sexual selection with darker males achieving higher reproductive success. However, it is unclear what role coloration plays in mate choice decision for our study population in the Czech Republic. In both populations, we found that coloration is explained by both genetic and environmental variation. The relative proportions of these sources of phenotypic variation may provide insight into how selection on plumage coloration has differed in these two phenotypically divergent populations and whether divergent sexual selection has contributed to divergence in phenotype.

Life history effects and demographic consequences of interacting QTL for flowering and seed dormancy in Arabidopsis thaliana

Johanna Schmitt, Martha Cooper, Peter Braun, Reena Sellamuthu, Mark Taylor

1D_302C-Demography
Saturday, June 21, 2014 3:15 PM-3:30 PM

Natural populations of the annual weed Arabidopsis thaliana exhibit natural variation at several major QTL for flowering time and seed dormancy. We conducted a demographic field experiment with selected recombinant inbred lines (RILs) segregating different combinations of late vs. early flowering alleles and strong vs. weak seed dormancy alleles. Seedlings of each line were planted in separate field cages in spring and allowed to disperse seed naturally to establish replicate populations. Each cage was monitored for germination, flowering, and fruiting of successive cohorts over 2 years. The life history effects of flowering time variation depended strongly upon the genetic background at seed dormancy loci, and vice versa. In particular, the combination of early flowering and weak dormancy alleles produced multiple summer-germinating rapid cycling generations. Expression of a single-generation winter annual life history required both late flowering and strong dormancy alleles. This experimental design allowed us to measure the interacting demographic effects of allelic variation at life history loci under natural field conditions.

Going with the flow: patterns of demographic divergence and connectivity in a Hawaiian stream goby.

Kristine Moody, Michael Childress, Johanna Wren, Donald Kobayashi, Michael Blum, Richard Blob

1D_302C-Demography
Saturday, June 21, 2014 3:30 PM-3:45 PM

Understanding the evolutionary processes contributing to population connectivity as a result of larval transport in marine environments is critical to determining how local adaptations arise in the face of gene flow. Differential, post-settlement selective pressures can reduce the amount of connectivity between populations, leading to population divergence. The waterfall-climbing Hawaiian fish, Sicyopterus stimpsoni, has a life cycle in which larvae hatch upstream but are swept to the ocean and develop for six months before returning to streams. Subsequent migration upstream requires climbing of waterfalls before reaching predator-free habitats. The environments to which juveniles return differ greatly between the youngest (Hawai'i, ~1 MY: waterfalls are close to shore, placing a premium on climbing ability to escape non-climbing predators) and the oldest (Kaua'i, ~5 MY: waterfalls are far inland, placing a premium on predator evasion as juveniles migrate upstream) islands. However, larvae from different islands may mix in the ocean, resulting in high gene flow and little differentiation between subpopulations.

We developed a spatially-explicit individual-based model (NetLogo) for the islands of Hawai'i, Kaua'i, and O'ahu coupled with a Lagrangian transport model using current data from a daily regional Hybrid Coordinate Ocean Model for the Hawaiian Islands. Using this coupled approach, we examined how topography, stream flow, predation, and immigration influenced population demography, optimal phenotype evolution, and the rate of evolution over the time period of ten years. The connectivity matrices from the transport model were derived from 51 release/recapture stream points and provided estimates of immigration, emigration, and local retention solely based on oceanographic currents.

Demographic differences between the islands were found with a greater number of resident adults on the islands of Hawai'i and Kaua'i than O'ahu. O'ahu's populations were sustained by juveniles through means of immigration and local retention, but did not contribute many larvae to other islands through emigration therefore, functioning as a sink. Furthermore, immigration and emigration is largely unidirectional with larvae moving with the currents from southeast to northwest (Hawai'i to Kaua'i). All levels of immigration resulted in diminished rates of evolution of optimal phenotypes across all streams and islands. However, phenotypes conferring improved climbing performance on Hawai'i and phenotypes conferring improved predator evasion on Kaua'i did evolve. Local retention within the islands of Kaua'i and Hawai'i was always present and maybe indicative of isolation by distance contributing to the potential for locally adapted phenotypes to evolve despite the high degree of gene flow between islands.

Reconstructing the Demographic History of Adélie Penguins (Pygoscelis adeliae) Using mtDNA and Coalescent Methods

Howard Ross, Alex Stuckey, Craig Millar

1D_302C-Demography
Saturday, June 21, 2014 3:45 PM-4:00 PM

Adélie penguins are distributed around coastal Antarctica and on nearby islands. Our goal was to infer how the population size has changed in response to global warming since the Last Glacial Maximum 23 - 19 ka before present (BP). An alignment of ~650 mitochondrial D-loop sequences of length 315 bp was assembled from sequences derived from modern and subfossil specimens collected from colonies around Antarctica, but predominantly from the Ross Sea. Analyses of the variation revealed no genetic structure beyond that previously identified as the ancient Ross Sea and Antarctica haplogroups. There is evidence for extensive gene flow among Ross Sea and adjacent colonies. Bayesian skyline plots indicate that the abundance of Adélie penguins began to increase ~10 ka BP, ~8 ka after the temperature began to rise, and reached a peak during the penguin "optimum" 4 - 2 ka BP. Changing availability of suitable sites for colonies arising from melting of the coastal ice sheet might explain the temporal dynamics of the species.

Using linked microsatellites to infer basic population decline parameters: a case study on a Mexican relict spruce

Juan Pablo Jaramillo-Correa, Sebastien Gerardi, Jean Beaulieu, F. Thomas Ledig, Jean Bousquet

1D_302C-Demography
Saturday, June 21, 2014 4:00 PM-4:15 PM

Estimating demographic parameters is fundamental for conservation programs. Such estimates are generally inferred from the variation of unlinked genomic regions, which are often unavailable for non-model threatened species. These limitations can be circumvented by using universal and highly polymorphic markers that can be transferred across taxa, such as cytoplasmic SSRs. These markers have been shown to be sensitive to population expansions, but no formal test has been conducted to explore if they can be used to infer and distinguish between competing bottleneck scenarios. Herein, we simulated the evolution of ten linked SSRs in populations submitted to different bottleneck regimes ($\theta_1/\theta_0 = 0.01, 0.1, 0.5$ and 0.90) at different times ($\tau = 0.5, 1$ and 10). The variation of these markers, as compiled with five summary statistics, allowed detecting severe population collapses independently of τ, and as long as stands kept roughly constant effective sizes after the size reduction. Mild declines became difficult to infer as τ increased, and small bottlenecks were virtually undetectable with these markers. More complex frameworks, such as bottlenecks followed by sudden expansions, were also difficult to infer. Comparisons with the chloroplast SSR variation of the relict Mexican spruce (Picea mexicana) suggested that this species went through a severe bottleneck that could be dated back to the last interglaciation (LIG, ~130,000 to 116,000 years ago). These results indicate that linked SSRs can be used as proxies to infer basic parameters of population decline in species that lack adequate genomic tools, particularly in emerging countries.

Independent origins of the avian Z chromosome reveal contrasting short- and long-term dynamics of sex-specific selection

Alison Wright, Peter Harrison, Stephen Montgomery, Marie Pointer, Judith Mank

1D_303-Sex determination/Sex chromosomes
Saturday, June 21, 2014 3:15 PM-3:30 PM

Sex chromosomes provide unique opportunities to study the role of sex-specific selection, and when contrasted with autosomes, can reveal the magnitude of sexual conflict acting throughout the genome. Birds are useful in studies of sex chromosome evolution for two reasons. First, they are female heterogametic, which makes it possible through comparisons with male heterogamety to identify the fundamental forces shaping sex chromosomes. Second, although avian sex chromosomes are orthologous throughout the clade, they have diverged multiple independent times, making it possible to identify convergence.

We first mapped out the fine-scale evolutionary history of the sex chromosomes in the Galloanserae (land and waterfowl) using a combination of genomic, transcriptomic and phylogenetic data. Our results indicate that independent inversions spread progressively across the sex chromosomes over long evolutionary periods. We then used this map of avian sex chromosome evolution to test the role of sex-specific selection in shaping gene expression evolution. Our results reveal that over long-term evolutionary history, the Z chromosome has been convergently and successively masculinized. Older regions of the Z chromosome are expressed more in males than females, indicating that masculinization accumulates over time. This is consistent with theoretical predictions that Z-linked genes should be more often selected for male-benefit alleles due to their unequal inheritance pattern. We next examined the role of mating system in driving masculinization of the Z chromosome over the short-term. Our results suggest that recent changes in mating system are less important in driving patterns of Z-linked masculinization, indicating that substantial lengths of evolutionary time are required to break down inter-sexual correlation in gene expression.

Do interpopulation crosses and genetic drift disrupt sex determination in Tigriopus californicus, a species with polygenic sex determination?

Barret Phillips, Suzanne Edmands

1D_303-Sex determination/Sex chromosomes
Saturday, June 21, 2014 3:30 PM-3:45 PM

Theory predicts that polygenic sex determination (PSD) should be unstable--it should be easily disrupted by the invasion of novel sex-determining and/or sexual conflict alleles, thereby providing a route of evolution from polygenic to chromosomal sex determination (CSD). One simple but elegant way this might happen would be through the hybridization of divergent lineages segregating different sets of sex determination alleles. Hybridization here would be predicted to lead to a short-term increase in family sex ratio variance, but might be expected to lead to the emergence of a single, dominant sex determiner (and thus, a reduction in family sex ratio variance) over longer timescales, especially if the hybridization event was associated with a reduction in effective population size. However, despite the recent documentation of PSD in an increasing number of species, the role hybridization might play in PSD-to-CSD transitions remains largely unexamined. With a wide distribution (Baja California to Alaska), high interpopulation divergence (up to 27% at mtCOI), and a short generation time (~1 month), the intertidal copepod Tigriopus californicus is poised to provide insight into how PSD is maintained over time and how PSD might respond to the introduction of novel sex-determining alleles via hybridization. We constructed a series of interpopulation crosses between inbred lines and measured survivorship and family sex ratios. Hybrids demonstrated increased variance in family sex ratios that was sometimes, but not always, accompanied by sex-biased mortality. Though this sex-specific mortality cannot be attributed to Haldane's rule, it may be a manifestation of the genetic discord caused by introducing novel sex-influencing alleles through hybridization. We also conducted population-diagnostic genotyping of a freely admixing laboratory population (comprised of an equal initial input of two highly divergent natural populations). The maintenance of heterozygosity across a single chromosome in females, but not males, suggests a putative transition to CSD in this hybrid swarm. We therefore measured family sex ratios and survivorship in the swarm and its wild source populations. If the hybrid population has transitioned to CSD, we would expect to see a reduction in the variance in family sex ratios. The sequencing of the hybrid swarm and wild source populations will provide detailed insight into the genetic mechanism of sex determination in each and into how sex determination mechanisms are perturbed by hybridization.

Sex Chromosome Dosage Compensation in Heliconius butterflies

James Walters, Thomas Hardcastle, Chris Jiggins

1D_303-Sex determination/Sex chromosomes
Saturday, June 21, 2014 3:45 PM-4:00 PM

Dosage compensation is the equalization of gene expression levels in response to differences in gene dose or copy number. It is classically considered to play a critical role in the evolution of heteromorphic sex chromosomes. As the X and Y diverge through degradation and gene loss on the Y (or the W in female-heterogametic ZW taxa), it is expected that dosage compensation will evolve to correct for sex-specific differences in gene dose. Although this is typically observed in male-heterogametic (XY) species, recent genome-wide expression studies in other taxa have revealed striking exceptions, especially in ZW taxa such as birds and snakes. In these taxa, the single Z of females is under expressed relative to males. These results fuel speculation that incomplete dosage compensation may be a defining characteristic of female-heterogamety. However, Lepidoptera (moths and butterflies) are also female-heterogametic, and evidence is accumulating that at least some moth species show balanced expression between sexes on the Z chromosome, contradicting the emerging consensus that ZW taxa lack complete dosage compensation. We report the first genomic assessment of sex chromosome dosage compensation in butterflies, focusing on the genus Heliconius. Our results show that Z chromosome global expression is significantly lower than autosomes in both sexes, similar to previous reports in Silkmoth, and suggesting a novel mechanism of dosage compensation may exist in the Lepidoptera. We additionally detect a significantly greater global Z expression in males over females, indicating dosage compensation is imperfect in this species. However, the magnitude of this dosage effect is much less than the magnitude of reduced Z expression in both sexes. Methodologically, we introduce mixed-model linear regression with a poisson error structure as a useful statistical framework for assessing sex-chromosome dosage compensation.

Molecular basis of protogynous sex change in fish

Hui Liu, Melissa Slane, John Godwin, Kim Rutherford, Neil Gemmell

1D_303-Sex determination/Sex chromosomes
Saturday, June 21, 2014 4:00 PM-4:15 PM

Socially-induced sex change is a common phenomenon in marine fishes. The Caribbean bluehead wrasse (Thalassoma bifasciatum), for example, exhibits female-to-male (protogynous) functional sex change based on social context: when the dominant male disappears, the largest female initiates sex change to replace him. This process entails a series of radical alterations at morphological, behavioral and physiological levels, which makes the bluehead wrasse a good experimental model for understanding plasticity of sexual development in response to the environment. Recent research suggests that, during sex change, social cues gathered by the brain are likely transduced into a cascade of physical signals that travel through the hypothalamic-pituitary-gonadal axis to the gonads, where they mediate steroid hormone synthesis and promote the gonadal transition. We still know little about the details, especially of how this process is regulated at the molecular level. My PhD research uses next generation sequencing approaches to detect what genes are expressed and at what level they are expressed in the brain and gonads at different time points across the sex change process in bluehead wrasses. By analyzing the expression pattern of these genes using downstream bioinformatics tools, we hope to gain a better understanding of how sex change is controlled at the most fundamental level in fish. In a more general sense, we anticipate this study will also provide important insights into the sex differentiation mechanisms, as well as behavioral and phenotypic plasticity in response to the environment.

Sexual co-adaptation or conflict: Are genes that interact with the mitochondria more often on the sex chromosomes?

Rebecca Dean, Fabian Zimmer, Judith Mank

1D_303-Sex determination/Sex chromosomes
Saturday, June 21, 2014 4:15 PM-4:30 PM
Asymmetrical inheritance patterns have the potential to invoke intra-genomic co-adaptation or conflict between females and males. In contrast with autosomal genes, which are inherited equally from both parents, mitochondria are only transmitted through the maternal line, and are selected primarily for female effects. Sex chromosomes, on the other hand, are either female-biased (the X) or male-biased (the Z) in their transmission, and this creates the potential for sex-specific intra-genomic conflict or co-adaptation dynamics between the sex chromosomes and cytonuclear genomes. Nuclear genes that interact with the mitochondria (mito-nuclear genes) may move onto or off of the sex chromosomes, depending upon whether co-adaptation or conflict dominates, resulting in non-random distributions of mito-nuclear genes. We explored the genomic distribution of mito-nuclear genes in multiple species with independently evolved sex chromosomes across a broad array of animals. Although therian mammals and C. elegans showed a deficit of mito-nuclear genes on the X chromosomes consistent with sexual conflict, other independent X chromosomes lacked significant deficits, and there was no converse over-abundance of mito-nuclear genes on Z chromosomes. Our findings suggest that sexual intra-genomic conflict does not broadly explain the distribution of mito-nuclear genes, and we suggest other potential causes related to haploid selection and sperm biology that may explain these observations.

Intrahost HIV Evolution During Early Infection

Sivan Leviyang

1D_304-Viral Evolution
Saturday, June 21, 2014 3:15 PM-3:30 PM
During HIV infection, immune response in the form of cytotoxic T lymphocytes (CTLs) creates a selective force on the infecting HIV population. HIV escape from this CTL mediated selection is complex and poorly understood, but occurs rapidly and throughout infection. In this talk, I will discuss some recent work focused on quantifying the strength of selection exerted by CTLs during early HIV infection.

Episodic nucleotide substitutions in seasonal influenza virus H3N2 can be explained by stochastic genealogical process without positive selection

Kangchon Kim, Yuseob Kim

1D_304-Viral Evolution
Saturday, June 21, 2014 3:30 PM-3:45 PM
Nucleotide substitutions in the HA1 domain of seasonal influenza virus H3N2 occur in temporal clusters, which was attributed to the effect of recurrent selective sweeps underlying antigenic drift. However, classical theory suggests that these episodic substitutions are mainly due to stochastic coalescent processes combined with the unique genetic structure of influenza virus: high cumulative mutation rate over a non-recombining viral segment. This explains why, while the effect of selective sweeps between segments is limited due to reassortment, high variance in the number of allelic fixations per year is observed at non-antigenic gene segments of H3N2 as well as antigenic (HA and NA) segments. Using simulation, we confirm that in the absence of selection allelic substitutions at non-recombining segments with high mutation rate are temporally clustered, the degree of which increases with per-segment mutation rate but dramatically decreases if sequences recombine freely. Addition of recurrent selective sweeps rather leads to reduced clustering in substitutions. We conclude that clustering of fixations in influenza H3N2 segments is a direct result of inherent randomness in genealogical process at linked sites, and that the role of positive selection in the tempo of sequence evolution in rapidly evolving asexual genomes needs to be carefully assessed.

Ecological competition drives viral host range evolution and adaptation

Lisa Bono, David Pfennig, Christina Burch

1D_304-Viral Evolution
Saturday, June 21, 2014 3:45 PM-4:00 PM
Competition for resources has long been thought to be a key driver of diversification. In a previous study, we found that competition alone promoted host range expansion in the bacteriophage phi 6. Generalists able to use both the original, standard host and a novel host rapidly increased when the supply of host cells were restricted. These generalists expanded their host range without diminishing their fitness on the standard host and thus competitively excluded ("swept") specialists with the ancestral host range (standard host only). However, in one population, both phenotypes coexisted, because generalists used the novel host more often, decreasing competition for the shared standard host (niche partitioning). Using the coexisting generalists and specialists, we initiated a new evolution experiment to test if the presence of a competitor can drive the generalists to adapt to novel faster than evolving alone with only the novel host. Specifically, we evolved the generalist with a competitor (specialist) in sympatry with both hosts. As a control, we evolved the generalist alone in allopatry with only novel host. Generalists evolved in both treatments maintained the same host range but varied in how often they used each host. Allopatric generalists used the standard host significantly less than the sympatric generalists. This can be explained by access to a particular host, even when there is competition for it, and/or gene flow with the competitor, which will be estimated in future. Taken together, these experiments show that competition can drive host range expansion and affect host use.

Metagenomic analysis of a ssDNA viral community

Victoria Pearson, Darin Rokyta

1D_304-Viral Evolution
Saturday, June 21, 2014 4:00 PM-4:15 PM
Every organism has at least one virus capable of infecting it, yet our knowledge of the Earth's virome is extremely limited. The development of high-throughput sequencing has made it possible to examine the community composition of viruses at a depth that was not previously possible. It is important that we increase our knowledge of the single-stranded DNA (ssDNA) viral group as it

contains agricultural pathogens, such as porcine circoviruses and cotton leaf curl viruses, and Microviridae, a family of viruses that is often used as a model system in experimental evolution studies. This study utilized size selection and Illumina MiSeq sequencing to analyze the genetic diversity of a community of circular ssDNA viruses from a wastewater treatment plant. Wastewater treatment plants can be seen as a reservoir for viruses, and by studying the diversity of viruses present in them we can learn about potential agricultural pathogens in the area. All of the genomes analyzed were found to be genetically distinct from any known virus, with all of them sharing identity with their closest match on GenBank. Of the 66 Circoviridae and Geminiviridae genomes examined, six were found to be mosaics of both families, 44 had one gene which could not be classified, and only 16 could be definitively classified as solely belonging to one of these families. Surprisingly, no Microvirinae were found and all Microviridae genomes belonged to the subfamily Gokushovirinae. Ongoing temporal sampling will aid our understanding of whether this population is stable or continually variable and the breadth of mutations allowable in these groups.

Endogenous hepdnaviruses, bornaviruses and circoviruses in snakes

Clement Gilbert, Jesse Meik, Daren Card, Todd Castoe, Sarah Schaack

1D_304-Viral Evolution
Saturday, June 21, 2014 4:15 PM-4:30 PM

Endogenous viruses from three major viral groups (hepdnaviruses, bornaviruses and circoviruses) have been identified in the genome of the speckled rattlesnake, Crotalus mitchellii, the first viperid for which such data are available. Analysis of the draft genome assembly reveals fragments from these three viral families have been inserted into the genome of this snake over the past 50 million years. We characterized sequences from each virus bioinformatically and validated their presence using PCR. Analysis of other whole genome sequences and PCR screens of other species were also used to determine the presence/absence of these endogenous viral elements (EVEs) in other lineages of snakes. Based on these data and known divergence times among snake species, we are able to estimate the date of endogenization events for each EVE. Circoviruses appear to have integrated most recently (within the last ~10 my), whereas bornaviruses and hepadnaviruses integrated much earlier (~30 and ~60 mya, respectively). We discuss the relationships of the endogenous viruses in snakes relative to endogenous viruses from other metazoans, as well as to their closest known exogenous relatives. Given the paucity of studies on endogenous viruses in vertebrates, despite the plethora of whole genome sequence data now available, our study provides new and valuable insight into the process and timing of viral endogenization, indicating that it has occurred on both recent and more ancient evolutionary timescales. This is, to our knowledge, the first report of endogenized viruses in non-avian reptiles and provides a window into the evolutionary dynamics of viruses in these host lineages.

The fates of rare beneficial lineages in hypermutable asexual populations.

Tanya Singh, Paul Sniegowski, Philip Gerrish, Kate Kerpen

1D_305A-Mutation in Evolution
Saturday, June 21, 2014 3:15 PM-3:30 PM

The fixation probability of a beneficial mutation that arises spontaneously in a population is dependent on the fitness benefit afforded by the beneficial mutation. In classical theory, this probability is approximately twice the size of the benefit for mutations of weak selective effect (Haldane, 1927). However, in an asexual population the spread of a beneficial mutation may be impeded by beneficial mutations arising on alternative genetic backgrounds (Gerrish and Lenski, 1998), and by deleterious mutations arising on the same genetic background. I have shown using simulations that the fixation probability of beneficial mutations in asexual populations with very high genomic mutation rates is considerably reduced below the classical expectation. Muller's Ratchet refers to the stochastic loss of the best genotype in an asexual population due to the accumulation of deleterious mutations. The lower probability of fixation of a beneficial lineage in an asexual population that possesses a very high mutation rate may be attributed to the fact that the lineage size of a new beneficial mutation is extremely small, and hence Muller's Ratchet operates at a much faster rate in this small lineage than in the rest of the population. Simulations confirm this idea, showing that a faster rate of accumulation of deleterious mutations in the small beneficial mutation lineage leads to a reduced fixation probability at higher mutation rates compared to lower mutation rates. I am pursuing experimental work with E. coli populations to test these ideas. The initial experimental results suggest that the beneficial mutation supply rate is extremely high in these populations and may overwhelm the predicted effect of deleterious mutations. Ongoing work is directed toward developing tests of the fixation of probability of a new beneficial mutation in populations in which the background beneficial mutation rate is greatly reduced.

Accurate detection of mutations from short read sequencing data

David Winter

1D_305A-Mutation in Evolution
Saturday, June 21, 2014 3:30 PM-3:45 PM

Spontaneous mutation is the ultimate source of all genetic diversity. The rate, fitness distribution and directional biases present in newly arising mutations are fundamental paramaters in theoretical evolutionary genetics. The rate of deleterious mutation has obvious relevance to the study of human disease, and is also a key parameter in models of conservation in small populations, the evolution and maintenance of sexual recombination and the evolution of aging. Mutation bias contributes to patterns of genomic evolution and the mutation rate is a key demographic parameter, and a labile evolutionary trait in its own right.

Determining the values of these important parameters in practice is difficult. Mutation-accumulation experiments require completely relaxing the effects of natural selection, which is both a technically challenging and laborious process. Detecting mutations from genetic data associated with these experiments is also difficult. Modern high-throughput sequencing methods make the generation of whole-genome data possible. However, the high per-base mutation rates of these methods, combined with biases in library perpetration and sequence assembly, mean typical approaches to variant detection produce many false positives.

The ciliate Tetrahymena thermophila provides an almost perfect model for the study of spontanaeous mutation. Individuals of this species contain distinct germline and somatic nuclei. During asexual reproduction the genes of the germline nucleus are not expressed, meaning germ-line mutations are not exposed to selection. When T. thermophila cultures are maintained in asexual growth otherwise lethal and highly deleterious mutations can accumulate in the germline genome. In order to take advantage of this remarkable system, we have developed a novel approach to detecting spontaneous mutations from short-read sequencing data. We model base-calls for a given site in an assembly using the Dirichlet-multinomial distribution, and sum over all possible genotypes and lineage-histories to calculate the probability a site contains a mutation in one line.

We are testing this model on a preliminary dataset arising from 10 mutation accumulation lines. These data, along with PCR validation of putative mutations, have allowed us to investigate properties of sequencing data associated with both false-negative and false-positive mutations calls. Our initial results suggest T. thermophila has a low single nucleotide mutation rate with strong directional biases.

Genetic constraints cause mutation rate catastrophe

Bingjun Zhang, Ricardo Azevedo

1D_305A-Mutation in Evolution
Saturday, June 21, 2014 3:45 PM-4:00 PM

As the fundamental sources of evolutionary innovations, mutations play an important role in the evolution of populations. Mutator alleles commonly occur as variants in DNA repair systems in many natural and experimental populations. Individuals with mutator alleles can possess mutation rates over 1000-fold greater than wildtype. The trade-off between acquiring beneficial mutations and avoiding accumulation of excessive deleterious mutations becomes an intriguing question for the evolution and maintenance of mutator alleles. Mutation rate catastrophe was found in previous theoretical study, where the mutation rates of populations can surge up to an extraordinarily high level. The populations experience huge mutational load due to the high rate of deleterious mutations. Thus, the population fitness suddenly declines after experiencing exponential fitness growth. Surprisingly, the mutation rates do not arrest but continue to soar during the fitness decline until it drop to an extremely low level when the population essentially go extinct. Here we employ a Wright-Fisher model of adaptive evolution of both asexual and sexual populations. Based on it, evolutionary simulations are performed through a selection-reproduction-mutation life cycle for populations. We found that the inability to efficiently remove mutators from the population can cause the mutation rate catastrophe. Specifically, low mutation rates to antimutators or antimutators with small effects to lower the mutation rates lead to mutation rate catastrophe. Moreover, recombination can facilitate the process of removing mutators from the population and prevent the catastrophe. We conclude that the genetic constraints that impede the process of eliminating mutators from populations can lead to the mutation rate catastrophe.

Experimental evidence for both upward instability and decline of the genomic mutation rate across isogenic asexual Escherichia coli populations.

Mitra Eghbal, Paul Sniegowski, Philip Gerrish

1D_305A-Mutation in Evolution
Saturday, June 21, 2014 4:00 PM-4:15 PM

Most mutations of any phenotypic effect are deleterious, yet mutations can serve as sources of evolutionary innovation. The evolution of the genomic mutation rate in asexual populations has been studied through both theoretical modeling and experimental evolution. A mutator allele may “hitchhike” to fixation in linkage with beneficial mutations. Recurrent mutator hitchhiking is possible because the deleterious mutational load accumulates gradually; other mutators may hitchhike before the deleterious effect of each mutator is fully realized. Theoretical calculations have predicted that such recurrent mutator hitchhiking events in asexual populations can lead to chronic upward instability of the mutation rate that may even culminate in extinction. I am conducting an experimental test of the idea that asexual populations are at risk for recurrent mutator hitchhiking. I have propagated 30 experimental populations of Escherichia coli that were initially fixed for one mutator allele (mutS-). These populations serve as a “detector array” for further mutator hitchhiking events. If one or more mutator populations spontaneously evolve a further increase in mutation rate, it is evidence that a mutator population can indeed undergo a spontaneous increase in mutation rate. After propagating these populations for approximately 900 generations, I isolated a random clone from each evolved population. I found that, relative to the ancestor’s mutation rate, the genomic mutation rates (measured by resistance to the antibiotic nalidixic acid) have significantly increased in clones from 2 populations, significantly decreased in clones from 9 populations, and did not differ significantly in clones from 19 populations. This is the first time that a spontaneous increase in mutation rate has been measured in an evolving asexual E. coli population already fixed for a mutator allele (assuming that the measurement at the genetic locus affecting nalidixic acid resistance is representative of the genomic mutation rate and assuming that the clones are representative of their respective populations). There are at least two potential explanations for the decreased mutation rate in 9 populations: pleiotropic direct fitness effects of new antimutator alleles, or fixation of new antimutator alleles due to reduction of the deleterious mutational load. In the former scenario, a new allele rises to fixation due to a beneficial phenotype unrelated to mutation rate, but the allele has the additional effect of lowering the mutation rate. I discuss ongoing research to test these possibilities.

Dynamics of evolutionary innovations in cancer

Kirill Korolev, Christopher McFarland, Leonid Mirny

1D_305A-Mutation in Evolution
Saturday, June 21, 2014 4:15 PM-4:30 PM
Cancer progression is an example of a rapid adaptive process where evolving new traits is essential for survival and requires a high mutation rate. Precancerous cells acquire a few key mutations that drive rapid population growth and carcinogenesis. Cancer genomics demonstrates that these few `driver' mutations occur alongside thousands of random `passenger' mutations---a natural consequence of cancer's elevated mutation rate. Some passengers can be deleterious to cancer cells, yet have been largely ignored in cancer research. In population genetics, however, the accumulation of mildly deleterious mutations has been shown to cause population meltdown.

Here we develop a stochastic population model where beneficial drivers engage in a tug-of-war with frequent mildly deleterious passengers. These passengers present a barrier to cancer progression that is described by a critical population size, below which most lesions fail to progress, and a critical mutation rate, above which cancers meltdown. We find support for the model in cancer age-incidence and cancer genomics data that also allow us to estimate the fitness advantage of drivers and fitness costs of passengers. We identify two regimes of adaptive evolutionary dynamics and use these regimes to rationalize successes and failures of different treatment strategies.We find that a tumor's load of deleterious passengers can explain previously paradoxical treatment outcomes and suggest that it could potentially serve as a biomarker of response to mutagenic therapies. Collective deleterious effect of passengers is currently an unexploited therapeutic target. We discuss how their effects might be exacerbated by both current and future therapies.

The origin of species by means of Dobzhansky-Muller incompatibilities

Ricardo Azevedo

1D_305B-Hybridization
Saturday, June 21, 2014 3:15 PM-3:30 PM
A central challenge in evolutionary biology is understanding the mechanisms by which reproductive barriers between populations evolve and are maintained. The Dobzhansky-Muller (DM) model posits that reproductive isolation is caused by incompatibilities between alleles at different loci. However, if the alleles involved in the DM incompatibility are neutral, the resulting reproductive isolation cannot be maintained in the presence of either mutation or gene flow. Here I ask two related questions. Can neutral DM incompatibilities involving more than two loci lead to the evolution of stable reproductive barriers between populations? And, if so, can those reproductive barriers be maintained in the presence of gene flow? I address these questions using an extension of the DM model to multiple loci. I show that, when it comes to multiple DM incompatibilities, the whole can be greater than the sum of its parts. Certain combinations of multiple DM incompatibilities can lead to the evolution of strong reproductive barriers between populations, provided the recombination rate is high relative to the mutation rate. Complex DM incompatibilities (i.e., those involving alleles at three or more loci simultaneously) are especially likely to promote the evolution of reproductive barriers between populations. Furthermore, some of the reproductive barriers generated by DM incompatibilities can persist in the presence of substantial gene flow. I consider the possibility that combinations of multiple DM incompatibilities play an important role during the early stages of speciation.

Genes vs. culture: song variation across an avian hybrid zone

Haley Kenyon, Darren Irwin, Miguel Alcaide, David Toews

1D_305B-Hybridization
Saturday, June 21, 2014 3:30 PM-3:45 PM
Song is one of the most widely recognized premating barriers to reproduction between avian species. In oscines both genetic and cultural inheritance contribute to an individual’s song phenotype, contributing to difficulty in predicting the role that song may play in reproductive isolation; interspecific song learning could promote interbreeding. Here I seek to better understand this phenomenon by studying song in a narrow hybrid zone between black-throated green (Setophaga virens) and Townsend’s warblers (S. townsendi). I use multivariate analyses to compare songs in the hybrid zone to those found in allopatry, predicting that if song is a strong barrier to interbreeding, then there should be a relationship between song and genotype in the hybrid zone. I employ a genotyping-by-sequencing (GBS) method to identify thousands of markers and develop a hybrid index. Playback experiments were carried out in the field to test responses to parental songs, and a cline analysis was conducted in order to compare transitions in genotype and song across the hybrid zone. I show that only parental song types are found in the hybrid zone, and furthermore, that there is little if any association between song and genotype in sympatric individuals; this suggests that song is not an important reproductive barrier. Allopatric individuals responded only to local songs, indicating that individuals may exhibit a learned response to songs that they are commonly exposed to. I observed discordance between the song and genotype clines; the song cline was much narrower indicating that song is under stronger selection. Taken together, these findings suggest that song is not a reproductive barrier in this hybrid zone, but is instead a cultural trait that is maintained by frequency-dependent selection. Thus, it may be more beneficial for males to sing a locally common song than to broadcast accurate species-membership information.

A simple two-locus hybrid incompatibility underlies inviability between sympatric Mimulus species

Matthew Zuellig, Amanda Kenney, Andrea Sweigart

1D_305B-Hybridization
Saturday, June 21, 2014 3:45 PM-4:00 PM
Recent studies have identified genes underling hybrid incompatibilities (HIs), shedding light on their molecular functions and the evolutionary forces that drove their evolution. However, we still know relatively little about the population genetic forces acting on HI alleles or how they are maintained once species come into secondary contact. To address these problems in a natural system, I have identified a simple two-locus hybrid incompatibility

that causes inviability in 1/16 of the F2 progeny in a cross between sympatric Mimulus guttatus and M. nasutus. I have fine-mapped both loci to small regions on chromosomes 13 and 14, respectively, and identified candidate genes in both regions. Additionally, data from additional crosses within and between species show that these HI alleles are polymorphic within M. guttatus. I discuss the implications of these findings and plans for future research.

Two-locus hybrid incompatibilities and the introgression of adaptive alleles

Derek Setter, Joachim Hermisson

1D_305B-Hybridization
Saturday, June 21, 2014 4:00 PM-4:15 PM
The sources of genetic variation and their relative contributions to adaptation is a central topic in the study of evolution, and mounting evidence points to an important role for variation introduced through hybridization between species. Adaptive alleles introduced through hybridization must overcome barriers to gene flow, particularly those due to epistatically incompatible alleles. Current models of introgression lack an explicit treatment of incompatibility loci. Here, we analyze the situation in which hybridization generates a beneficial locus that is linked to a two-locus genetic incompatibility using a multi-locus Moran-like model. We calculate both the likelihood of adaptive introgression and the likelihood that a linked incompatible variant hitchhikes to fixation. We contrast this model with one in which barriers to gene flow are due to extrinsically maladaptive loci. We determine that the influence of a genetic incompatibility on the probability of adaptive introgression depends strongly on the distances between the incompatible loci and the adaptive allele. Furthermore, we investigate the potential for adaptive introgression to erode barriers to gene flow between divergent populations. Our analysis supports the idea that the variation introduced through introgression is a potentially important source of adaptive alleles.

Placental gene expression and the evolution of extreme overgrowth in dwarf hamster hybrids

Thomas Brekke, Jeffrey M. Good

1D_305B-Hybridization
Saturday, June 21, 2014 4:15 PM-4:30 PM
Mammalian hybrids often show abnormal growth, indicating that disruption of early development may play an important role in mammalian speciation. We have shown that reciprocal crosses between two species of dwarf hamsters, Phodopus campbelli and P. sungorus, yield extreme and asymmetric growth of hybrid embryos and placentas. This parent-of-origin dependent form of hybrid inviability appears to be common in other mammalian hybrids and has been hypothesized to reflect the regulatory disruption of genes that show imprinted expression in the placenta. However, the generality of this model has not been determined. Here we use RNA-seq experiments to quantify genome-wide patterns of gene expression in the placenta of P. campbelli and P. sungorus and their reciprocal F1 hybrids. We use these data to test for differences in gene expression and imprinting status between reciprocal hybrids that show either normal or extremely overgrown placentas. We found an excess of differentially expressed genes involved in fetal growth that were highly upregulated in overgrown hybrid placenta. These data provide strong evidence that disrupted gene regulation plays an important role in the evolution abnormal growth in these mammalian hybrids.

Environmental stability, niche conservatism, and energetic constraints--explaining tropical biodiversity

Allen Hurlbert, James Stegen

1D_306A-Biodiversity and Niches
Saturday, June 21, 2014 3:15 PM-3:30 PM
Many different hypotheses have been suggested to explain why there are more species at tropical versus temperate latitudes. Among these are (1) the "species-energy hypothesis", in which species richness is a function of the energy or resources available in the environment, (2) the "tropical conservatism hypothesis", in which a tropical clade origin combined with highly conserved thermal niches results in fewer species dispersing away from the tropics with less time for diversification, and (3) the "tropical stability hypothesis", in which temperate regions have fewer species because of repeated extinction events related to global climate cycles. We use a novel eco-evolutionary simulation model to identify the spatial, temporal, and phylogenetic secondary patterns that might be diagnostic of these three hypotheses. The patterns examined include metrics of tree shape (acceleration or deceleration in branching events, imbalance) and how measures such as mean root distance and phylogenetic species variability vary across the latitudinal gradient. Empirical patterns of mammals in the New World are interpreted in the context of simulation results.

Testing the role of ecology and life history in structuring genetic variation across a landscape: A comparative ecophylogeographic approach

Andrea Paz, Roberto Ibáñez, Karen R. Lips, Andrew Crawford

1D_306A-Biodiversity and Niches
Saturday, June 21, 2014 3:30 PM-3:45 PM
Hypotheses to explain phylogeographic structure traditionally invoke geographic features, but often fail to provide a general explanation for spatial patterns of genetic variation. An organism’s intrinsic characteristics might play more important roles than landscape features in determining phylogeographic structure. We developed a novel comparative approach to explore the role of ecological and life-history variables in determining spatial genetic variation and tested it on frog communities in Panama. We quantified spatial genetic variation within 31 anuran species based on mitochondrial DNA sequences, for which hierarchical approximate Bayesian computation analyses rejected simultaneous divergence over a common landscape. Regressing ecological variables on genetic divergence revealed that body size, current landscape resistance, geographic range, biogeographic origin, and reproductive mode were significant predictors of spatial genetic variation. Our results support the idea that phylogeographic structure represents the outcome of an interaction between organisms and environment, and suggest a conceptual integration we refer to as ecophylogeography.

Incorporating Evolutionary History into Ecological Niche Modeling

Dan Warren

1D_306A-Biodiversity and Niches
Saturday, June 21, 2014 3:45 PM-4:00 PM

Many fundamental questions in ecology, evolution, and conservation biology require estimates of species' environmental tolerances. Environmental niche models (ENMs, sometimes referred to as species distribution models) use species occurrence data in order to construct these estimates. Recent advances have made these models more accessible and easier to use in a comparative framework, and as a result they are being used at a rapidly increasing rate across ecology, evolution, and conservation biology. Useful though these approaches are, there are fundamental limits to our ability to model the niche through presence-only data, as these data are subject to many phenomena such as biotic interactions, sampling bias, and dispersal limitation that limit their utility for niche estimation. Niche modeling is currently dominated by machine learning methods that treat species' responses to their environment as a "black box" phenomenon about which no prior information exists. Although these methods have been useful, there are other data sources that may, if incorporated appropriately into the modeling process, serve to partially overcome many of the limitations of presence-only data. One such data source is the evolutionary history of the species being modeled.

Spatial niches influence biodiversity during adaptive radiation

Jiaqi Tan, *Lin Jiang*

1D_306A-Biodiversity and Niches
Saturday, June 21, 2014 4:00 PM-4:15 PM

Adaptive radiation, through which multiple species emerge from a single evolutionary lineage to utilize various ecological opportunities, is a major contributor to biodiversity. While adaptive radiation has been observed in many natural communities, the role of spatial niches on biodiversity patterns during adaptive radiation has been rarely explored. The ecological theory of the storage effect suggests that variation of environmental conditions over space provides spatial niche opportunities for co-occurring species, potentially allowing more species to coexist. We hypothesize that spatial niches may also influence biodiversity patterns over evolutionary timescales.

We experimentally explored how spatial niches influence adaptive radiation, using the rapidly evolving bacterium Pseudomonas fluorescens SBW25 as the model organism. P. fluorescens undergoes rapid adaptive radiation under the static condition where specialized niches are available for new phenotypes to utilize, but not under the shaking condition where such niches are absent. By taking advantage of these characteristics, we constructed laboratory metacommunities each containing two local microcosms, incubated either under the same (shaking or static) conditions, or under different conditions. In addition, we also manipulated species dispersal, either allowing or not allowing exchange of individuals among the local communities.

Our results showed that spatial niches and dispersal interactively affected P. fluorescens diversity. When there was no dispersal, spatial niches had little effect on either alpha-diversity in local microcosms or beta-diversity among microcosms. By contrast, when dispersal was present, spatial niches increased alpha-diversity but reduced beta-diversity.

The spatial storage effect was responsible for the observed biodiversity patterns. Adaptation of P. fluorescens to different incubation conditions increased the niche difference between its phenotypes, promoting frequency-dependent selection among them in metacommunities with spatial niches. Such frequency-dependent selection facilitated phenotypic coexistence but weakened priority effects, resulting in the highest alpha-diversity and lowest beta-diversity in metacommunities characterized by both dispersal and spatial niches. These results highlight the importance of spatial niches in maintaining biodiversity in evolving metacommunities.

The coupling of niche divergence and lineage diversification at different spatial scales

Glenn Seeholzer, *Robb Brumfield*

1D_306A-Biodiversity and Niches
Saturday, June 21, 2014 4:15 PM-4:30 PM

The concept of the niche has played a fundamental role in our understanding of the origins of biological diversity. Specifically, the hypothesis that niche divergence drives speciation, such as in adaptive radiation. In this context, it is important to recognize that niche divergence may occur at both small and large spatial scales. At either spatial scale, ecological and evolutionary theories predict a positive relationship between the rate of niche evolution and the rate of lineage diversification. This predication has seldom be tested. At small spatial scales, species may diverge in morphological traits tied to resource partitioning within communities, which facilitates diversification by reducing competition and propelling incipient species into novel adaptive zones or environments. At large spatial scales, lineages may diverge in macro-habitat preferences or climatic tolerances thereby promoting local adaptation. In both scenarios, if gene flow is reduced sufficiently, speciation may occur. Because morphological divergence is often tied to niche divergence at large spatial scales, via the colonization of novel environments, we further predict a positive relationship between rates of niche evolution at small and large spatial scales. We tested these predictions using the morphologically and environmentally diverse South American bird family Furnariidae, one of the most species rich bird families in the world. We quantified the niche for all species at both large and small spatial scales with morphological measurements and climatic-niche data, respectively. We divided a time-calibrated phylogeny of the family into independent clades, for which we estimated rates of morphological and climatic-niche evolution and the rate of lineage diversification. Using phylogenetic regression, we found that both rates of climatic-niche evolution and rates morphological evolution predicted rates of lineage diversification yet this relationship was stronger for the climatic-niche. We also found a positive relationship between rates of morphological and climatic-niche evolution. These results suggest that morphological evolution relevant to resource partitioning at small spatial scales can be coupled with climatic-niche evolution promoting geographic isolation and population differentiation at large spatial scales. Rapid evolution in both niche axes, in turn, promotes rapid lineage diversification. This demonstrates that a holistic examination of niche evolution can connect disparate ecological and evolutionary processes to help understand the drivers of lineage diversification.

A tale of two lineages; contrasting patterns of diversification in saxicoline lizard lineages of the Australian monsoon tropics

Rebecca Laver, Paul Oliver, Tim Jessop, Jane Melville

1D_306B-Speciation and Diversification
Saturday, June 21, 2014 3:15 PM-3:30 PM

While Savannah biomes dominant large areas of the globe (around 20% of the earth's land area), the major climatic and topographic variables that have shaped diversification in these ecologically and economically important regions remain poorly understood. We are undertaking a project to understand diversification processes in a suite of ecologically divergent geckos from the vast savannahs of northern Australia. Multilocus work on the large saxicoline Oedura (velvet geckos) of the Kimberley region has revealed two divergent lineages with broadly overlapping distributions. Both are closely associated with outcropping rocks, and have a long history of intraregional diversification dating back well into the Miocene. However, one lineage is widespread, with an exceptional number of divergent parapatric mitochondrial lineages, while the other comprises two highly disjunct and morphologically distinct forms (including a recently discovered micro-endemic restricted to a single rocky range in the south Kimberley). Nuclear loci support the evolutionary distinctiveness of isolated populations in the latter lineage, but suggest a much more complicated and unresolved history of periodic fragmentation and geneflow in its more widespread congener. Our data support the hypothesis that rock outcrops and ranges within the savannahs of northern Australia have mediated long persistence and divergence of mitochondrial lineages, but also suggest differing ecological and physiological limitations of saxicoline lineages can result in contrasting evolutionary outcomes to this diversification process.

No divergence in sympatry on a remote oceanic island (Cocos Island, Costa Rica)

Javier Igea, Diego Bogarín, Vincent Savolainen

1D_306B-Speciation and Diversification
Saturday, June 21, 2014 3:30 PM-3:45 PM

Cocos Island is a small (24 km2) volcanic island located 550 km off the Pacific Coast of Costa Rica. It was formed 1.9 – 2.4 million years ago and constitutes the only island in the Eastern Pacific with tropical rainforest. It has 189 native vascular plant species, including 32 endemics. We categorized the modes of speciation for the plants on Cocos Island using a phylogenetic approach, including species from the source regions for the island's flora. Endemic species were only classified as products of a sympatric speciation event if they had a sister congeneric endemic on the island, and the divergence time between the two could be confidently dated to be younger than the age of the island. Despite having eight genera with more than one endemic species, no convincing case of sympatric speciation was found. A total of 73% of the species were the result of colonization events, while 12% were instances of allopatric speciation. A similar study carried out previously on another remote island, Lord Howe Island, presented a stark contrast with these results. In that case, as much as 8% of the species were found to be the result of sympatric speciation. Allopatric speciation accounted for 25% of the cases and only 55% of the species were a result of colonization. These results suggest that immigration is the main force shaping the flora of Cocos Island. In spite of the physical isolation, multiple independent colonizations from congeneric species followed by anagenesis seem to have occurred in the relatively short lifespan of the island. The prevalence of sympatric speciation on Lord Howe Island was not mimicked on Cocos Island. This may indicate that not only physical isolation, but other factors such as age, topological heterogeneity or the conditions of the surrounding regions play a significant role in island evolutionary processes. Together, these factors determine the relative importance of immigration and the different modes of speciation in the species composition of oceanic island floras.

Linking neotropical biomes in a spider web

Vera Solferini, Fernanda Fontes, Luiz Filipe Macedo Bartoleti, Elen Peres

1D_306B-Speciation and Diversification
Saturday, June 21, 2014 3:45 PM-4:00 PM

There is a general agreement that the evolutionary history of neotropical diversity is very complex and still poorly understood. More recently, phylogeographic approaches have been adding many valuable pieces to this great puzzle, providing inferences about the past events that shaped the species' present distribution. Most of phylogeographic studies focus on species endemic or restricted to one biome, but the study of species with broad geographic ranges can also provide interesting information. To conduct a comparative phylogeography study we choose three spider species that can be found in most part of Brazil: Araneus venatrix (Araneidae), Aglaoctenus lagotis (Lycosidae) and Nephila clavipes (Nephilidae). We aimed to cover the main biomes, sampling on 54 sites along the Brazilian Amazonia Rainforest, the Atlantic Rainforest and the Cerrado (Brazilian Savanna). We have analyzed partial sequences of nuclear ITS2 for A.venatrix and partial sequences of mitochondrial COI gene for the three species. The patterns found for A.lagotis and A.venatrix in the bayesian phylogenetic inference and haplotype network are remarkably similar, with three geographically structured clusters: a deep lineage split during the Pliocene or late Miocene, separating the populations of Southern Atlantic Rainforest from all others; later, an early Pleistocene split formed a clade that occurs in the South-Central region and another comprising populations from Amazonia, Cerrado and Northern Atlantic Rainforest. Nephila clavipes presented four clusters that have split on the Pleistocene, one along the Atlantic Forest, one in the Amazonia and two in the Central and South part of the country. For the three species the several terminal branches originated on Pleistocene, reinforcing this period as one of intense lineage diversification. Our results corroborate a subdivision between the Tropical and Temperate biota of South America, possibly associated with major events along Miocene and Pliocene, showing that the Amazonia, Northern Atlantic Forest and Cerrado are not evolutionary isolated units and that the histories of Neotropical biomes are not independent.

Ecological controls of mammalian diversification

Antonin MACHAC

1D_306B-Speciation and Diversification
Saturday, June 21, 2014 4:00 PM-4:15 PM

Mammalian diversity is generated by the process of evolutionary diversification, or amidst the pull of speciation and extinction. To study these dynamics, we combine several tools of modern diversification analysis and apply them to a state-of-the-art phylogeny of mammals. We find that mammalian diversification is remarkably directional, transitioning from unbounded clade expansion to diversification slowdowns and, eventually, equilibrium diversity. Each of these phases is controlled by different ecological processes. The most universal role plays species co-occurrence which induces steep diversification slowdowns, suggesting that competition might constrain clade expansion. We also find that clades of warm, humid, and productive climates saturate faster, which perhaps results in finer ecospace subdivision in the tropics. Our study is the first to show how diversification dynamics change with phylogenetic scale. It also lends support to the hypothesis of ecological limits on clade diversification and illustrates how these limits presumably operate.

Sequential speciation multiplicitively amplifies biodiversity across trophic levels

Glen Hood, Andrew Forbes, Thomas Powell, Scott Egan, Meredith Doellman, James Smith

1D_306B-Speciation and Diversification
Saturday, June 21, 2014 4:15 PM-4:30 PM

Diversity can beget diversity when speciation by one organism drives diversification of associated organisms in adjacent trophic levels. If organisms diverge and create new niches for others to exploit and catalyze a chain reaction of sequential speciation events, it is important to know the (1) frequency of such events in nature and (2) barriers to gene flow evolving between diverging populations that reinforce diversification. The apple maggot fly, Rhagoletis pomonella (Diptera: Tephritidae), is a classic example of sympatric speciation in action. Host races of hawthorn and apple flies and sibling species in the pomonella complex differ in eclosion timing, host odor preference and allele frequencies. Recently, the R. pomonella–attacking parasitoid wasp, Diachasma alloeum (Hymenoptera: Braconidae), has undergone sequential speciation as a result of diversification of its fly host. Paralleling the flies, wasps exhibit differences in allele frequencies, eclosion timing, and odor preference. We tested the hypothesis that sequential speciation is not simply linearly, but multiplicatively, amplifying biodiversity across trophic levels in the remaining members of Rhagoletis attacking parasitoid community. Two additional parasitoid wasps, Diachasmimorpha mellea and Utetes canaliculatus, also exhibited differences in eclosion timing, host odor preference and allele frequencies between sympatric populations. Ecological and genetic evidence supports the hypothesis that allochronic isolation via eclosion timing and behavioral isolation via host odor discrimination contributes to host-associated genetic structure in sympatry and is an important mechanism generating biodiversity and structuring parasitoid communities in this system.

Piscivorous fish in a fishless environment: predicting ecological and phenotypic differentiation of bigmouth sleepers in Bahamas blue holes

Ryan Martin, Matthew McGee, Brian Langerhans

1D_306C-Hybridization and Speciation
Saturday, June 21, 2014 3:15 PM-3:30 PM

Environmental variation drives ecological and phenotypic change. But how predictable is population differentiation in response to environmental change? We address this question in bigmouth sleeper (Gobiomorus dormitor) populations following the colonization of inland blue holes differing in the availability of fish prey. We develop and test predictions of differences in population demographics, habitat use, diet, locomotor and trophic morphology, and feeding kinematics and performance between bigmouth sleeper populations inhabiting blue holes with and without potential fish prey. We found that populations of G. dormitor independently diverged between prey regimes, with broad agreement between observed differences and a priori predictions. For instance, in populations lacking fish prey, we observed male-biased sex ratios, greater use of shallow-water habitat, and larger population diet breadths owing to greater individual diet specialization. We further found predictable differences in aspects of body shape, mouth morphology, suction generation capacity, strike kinematics, and feeding performance on different prey types, consistent with G. dormitor adaptation to piscivory when coexisting with fish prey and to feeding on small invertebrates in the absence of fish prey. Our results suggest great promise in our ability to predict population responses to changing environments, an increasingly important capability in a human-dominated, ever-changing world.

Positive selection drives frequency increase of a young chromosomal inversion

Cheng-Ruei Lee, Tom Mitchell-Olds

1D_306C-Hybridization and Speciation
Saturday, June 21, 2014 3:30 PM-3:45 PM

Chromosomal inversions play important roles in species divergence as well as adaptive evolution, and genetic elements controlling important traits are often mapped within inversions. Without effective recombination, chromosomal inversions that are fixed among lineages suppress gene flow, thereby allowing the accumulation of neutral as well as adaptive divergence. It is still unclear, however, what are the forces that contribute to the initial frequency increase of young inversions. Since adaptive mutations may arise before or after the establishment of chromosomal inversions, studies on young inversions is necessary. Three hypotheses explain the spread of young inversions: Under the ‘neutral hypothesis’, genetic drift governs the evolution of young inversions. For the ‘direct advantage hypothesis’, an inversion has direct advantage over local non-inverted (standard) haplotypes due to meiotic drive or genetic changes caused by the inversion event. Under the 'introgression hypothesis', while both local inverted and standard haplotypes contain adapted alleles in multiple loci, the inversion gains advantage over local standard haplotypes by suppressing recombination with non-adaptive introgressing standard haplotypes. Here we provide one of the first empirical and extensive investigations of these hypotheses by examining a young chromosomal inversion in Boechera stricta. This inversion is at high frequency in a local population in the hybrid zone between East and West subspecies. While genomic microsatellites show high polymorphism in both inverted and standard individuals, inversion-linked markers are less polymorphic in inverted than in standard individuals. This is consistent with the selective sweep of a young mutation and does not support the 'neutral hypothesis'. Between local inverted and standard West genotypes, we observed no inversion-related genetic or phenotypic effects, nor altered expression of seven genes near the breakpoints of this rearrangement, hence the 'direct advantage hypothesis' is not supported. To test the 'introgression hypothesis', we performed quantitative trait locus (QTL) mapping between inverted-West and standard-East genotypes. The inversion has significantly higher fitness than the introgressing standard haplotype. In addition, analysis of standard West and East haplotypes identified two separate QTL in the inversion region controlling phenology, an ecologically important trait under strong selection in the natural environment. Together, these results support the 'introgression hypothesis'. This study is one of the first to test a range of hypotheses explaining the origin and establishment of chromosomal inversions, which have fundamental importance in species divergence and local adaptation.

Missing snowball in house mice? Evidence against the faster-than-linear accumulation of hybrid incompatibilities between Mus musculus subspecies

Richard Wang, White Michael, Bret Payseur

1D_306C-Hybridization and Speciation
Saturday, June 21, 2014 3:45 PM-4:00 PM

Distinct species in nature exist because of reproductive isolation, a collection of barriers impeding gene flow between individuals of different species. Postzygotic isolation, the class of barriers that act after fertilization, is theorized to evolve according to the Dobzhansky-Muller (DM) model. The DM model proposes that postzygotic isolation emerges from negative epistatic interactions between mutations that arose in allopatric populations. The "snowball effect" is a prediction from the DM model that has received substantial attention; it describes an acceleration in the rate at which hybrid incompatibilities accumulate between two species with respect to the time since their divergence. Evidence in favor of the "snowball" has been found in fruit flies and tomatoes, but the generality of this phenomenon remains unclear. We tested the "snowball" hypothesis in a recently diverged group of subspecies that show partial reproductive isolation: house mice. We used a statistical approach we developed that directly incorporates phylogenetic history and considers whether incompatibilities are shared or unique between hybrids. We compared QTL for hybrid male sterility phenotypes, including testis weight, sperm count, and sperm morphology, mapped in two F2 intercrosses. The subspecies tree was constructed by summarizing 43,000 gene trees estimated from whole genome sequence data. In contrast to the "snowball" prediction, a model postulating a linear increase of incompatibilities with time received the most support. This result raises the prospect that alternative genetic mechanisms were responsible for the evolution of hybrid male sterility in house mice and draws attention to interpretative challenges with comparative genetic mapping.

Ecological divergence across two North American biodiversity hotspots in the Yellow-Bellied Kingsnake (Lampropeltis calligaster)

Alexander McKelvy, Frank Burbrink

1D_306C-Hybridization and Speciation
Saturday, June 21, 2014 4:00 PM-4:15 PM

Biogeographic barriers that have been examined across many taxa in the eastern Nearctic (ENA) appear to reduce gene flow in populations in predictable ways. To determine the location and understand how these barriers generate species requires estimates of divergence dates and degree of gene flow among emerging lineages. Importantly, we address the question of whether speciation events in extant taxa at barriers in the ENA were common during the Pleistocene by using a multilocus statistical phylogeographic approach to examine diversity within a North American snake, Lampropeltis calligaster, to reveal mode and timing of speciation at two main biodiversity hotspots in Eastern North America. We recovered three well-supported species inhabiting distinct ecological niches with divergences dating to the mid- and early-Pleistocene with subsequently stable or increasing effective population sizes, further implicating the Pleistocene as an important driver of diversification in North America. These taxa likely diverged ecologically across environments associated with the Mississippi River and at the Florida peninsula. Delimited taxa in allopatry necessarily occupy a subset of the range of the larger species complex, and likely have distinct ecologies with independent evolutionary trajectories. Ecological niche models suggest that by the end of the century, changes in climate may negatively alter habitat suitability and, barring adaptation, substantially reduce the suitable range of two of the three species

---

Using genome-wide single nucleotide polymorphisms to estimate patterns of gene flow and population structure in Crotalus atrox

Drew Schield, Daren Card, Jacobo Reyes Velasco, Carol Spencer, Tereza Jezkova, Todd Castoe

1D_306C-Hybridization and Speciation
Saturday, June 21, 2014 4:15 PM-4:30 PM

How the dynamics between gene flow and selection shape the genomic landscape of natural populations is a major question in evolutionary biology. Interpreting how local selection acts upon populations is important for understanding how species adapt to local climate and habitat, and for understanding how speciation occurs. The Western Diamondback Rattlesnake (Crotalus atrox) is a species of North American rattlesnake with an expansive distribution that is subdivided by distinct biogeographic regions, making it a prime system for addressing questions about the influence of local selection on populations in the face of other evolutionary forces (e.g., gene flow). A previous study using mitochondrial DNA sequences found evidence for two anciently diverged lineages of C. atrox, which have since integraded, leading to a region of their range that contains populations showing mixed mitochondrial ancestry. Here, we generated a substantially more thorough mitochondrial DNA data set to test previous estimates of gene flow and population genetic structure. We also used restriction-site associated DNA (RADseq) libraries to obtain nuclear-genome-wide estimates of population genetic patterns. Our estimates from both nuclear and mitochondrial data sets were largely congruent. Using these complementary data sets, we estimated historical demography and inferred population structure, and have been able to characterize the population genetic framework of this system, enabling further study of local selection and adaptation.

An improved approximate-Bayesian model-choice method for estimating shared evolutionary history

Jamie Oaks

1D_402-Ernst Mayr Symposium
Saturday, June 21, 2014 3:15 PM-3:30 PM

To understand the processes that generate biodiversity, it is important to account for large-scale processes that affect the evolutionary history of entire communities of co-distributed populations of organisms. Such events predict temporally clustered divergences times, a pattern that can be estimated using genetic data from co-distributed species. I introduce a nonparametric, approximate-Bayesian method of comparative phylogeographical model choice that estimates the probability of shared divergence histories across taxa using DNA sequence data. Using analyses of biological and simulated data, I compared the performance of the new approach to the current state-of-the-art method implemented in the software msBayes. The results show the new method has improved robustness, accuracy, and power for estimating shared evolutionary history across taxa. Compared to msBayes, the new model better estimates posterior uncertainty, which greatly reduces the chances of incorrectly estimating biogeographically interesting scenarios of shared divergence events. The results demonstrate the improved performance of the new method is due to (1) more appropriate priors on divergence-time and demographic parameters that avoid prohibitively small marginal likelihoods for models with more divergence events, and (2) the Dirichlet-process providing a flexible prior on divergence histories that does not strongly disfavor models with intermediate numbers of divergence events. The new model is implemented in the freely available software package dpp-msbayes. This tool will allow evolutionary biologists to better leverage comparative genetic data to assess the affects of regional and global biogeographical processes on biodiversification.

Temporal evolution of coral reef fishes: global patterns and disparity in isolated locations

Jennifer Hodge, Lynne van Herwerden, David Bellwood

1D_402-Ernst Mayr Symposium
Saturday, June 21, 2014 3:30 PM-3:45 PM

Understanding the complex history of earth's endless forms, how they came to be and how they are sustained, has been a fundamental facet of biology since the dawn of evolutionary theory. This presentation examines the evolution of coral reef fish species, specifically the chronology and geography of extant species divergence. Many coral reef regions have a history of isolation and extinction. My aim was to test whether the disparate evolutionary and biogeographical histories of the world's coral reef regions have significantly impacted temporal patterns of speciation within regions. In essence, do assemblages in peripheral locations contain the youngest coral reef fish species? The evolutionary histories of species belonging to multiple genera from four common coral reef fish families: the Chaetodontidae (butterflyfishes), Labridae (wrasses), Pomacanthidae (angelfishes), and Serranidae (groupers) were reconstructed based on molecular data. Resultant phylogenies were temporally calibrated using palaeontological data. Species' distributions were quantified using IUCN maps. The ages of species with different biogeographical extents were compared using two approaches. The full-phylogeny approach considered estimated divergence times for all extant species in the phylogeny, excluding outgroup and fossil calibration taxa, as indicators of species' ages. The sister-species approach considered estimated divergence times as indicators of species' ages only for the species with the smallest geographical range area between two sister-species, for all sister-species pairs. The sister-species approach minimized the effects of extinction and ancestral persistence on the estimation of divergence times and eliminated the co-variance of species' ages. Model fitting was also used to compare the distribution of species' ages across the whole phylogeny with age distributions of species restricted to the Red Sea and Hawaiian Islands. Temporal patterns of coral reef fish divergence were similar among major marine realms and regions. However, notable differences were recorded between the Red Sea and Hawaiian Islands. Red Sea endemics have diverged consistently throughout the last 16 Myr, whereas endemic species colonized the Hawaiian Islands in two distinct waves (0–3 Ma and 8–12 Ma). Differences in the proportions of allopatric and sympatric sister-species between Red Sea and Hawaiian endemics were also detected. Despite differing geological histories, marine realms and regions have all experienced comparable and relatively recent divergences of extant coral reef fish species. Differences in age distributions and spatial relationships of endemic species in the Red Sea and Hawaiian Islands suggest that markedly different processes have shaped patterns of diversification in two prominent, peripherally isolated locations.

Author contributions to the published version of the paper: J.R.H and D.R.B. conceived the ideas; J.R.H. compiled and analysed the data; and J.R.H, D.R.B and L.vH contributed to the writing and intellectual discussion.

Comparative population genomics of island endemic reedfrogs: dispersal and diversification in the Gulf of Guinea

Rayna Bell, Robert Drewes, Kelly Zamudio

1D_402-Ernst Mayr Symposium
Saturday, June 21, 2014 3:45 PM-4:00 PM

The ecological theory of island biogeography describes species richness on islands as an equilibrium between colonization and extinction, yet many lineages undergo extensive diversification within islands and these in situ speciation events contribute significantly to total island biodiversity. Classic investigations of island biogeography have focused on relatively young and remote archipelagos with focal species that are either good dispersers across saltwater barriers or that have radiated extensively within a particular archipelago. Here we examine these same mechanisms within the Gulf of Guinea islands, a relatively old archipelago located a few hundred kilometers from West-Central Africa that hosts numerous endemic species from groups that are considered poor dispersers across saltwater barriers. Among the islands' "poor dispersing" vertebrates, reedfrogs (genus Hyperolius) are thought to be the only lineage that diversified within a single island and also dispersed between islands in the archipelago. Therefore, this group presents an opportunity to jointly investigate colonization routes from the mainland, dispersal within the island chain, and in situ diversification. The prevailing hypothesis for the presence of amphibians on the Gulf of Guinea islands is assisted dispersal via vegetation rafts that are swept down major river drainages into the gulf following large rain events. We employ a multi-locus phylogeography approach with range-wide sampling of the most closely related mainland taxon of the island endemics (H. cinnamomeoventris) to confirm that Hyperolius in the Gulf of Guinea result from a single colonization event originating from either the Ogooué or Congo River basins in West-Central Africa. Using a species tree approach with genome-wide SNPs (RADseq) we recover three distinct lineages in the archipelago (one on Príncipe island and two on São Tomé) that correspond to two currently recognized species (H. molleri, which is found on both islands and H. thomensis, which is only present on São Tomé). Estimates of historical population demography confirm that Hyperolius first colonized São Tomé, that H. molleri subsequently dispersed to Príncipe, and that migration between populations of H. molleri on the two islands is not ongoing. Hyperolius thomensis and H. molleri are considered distinct species based on a number of phenotypic and life history differences, yet where the two species' ranges overlap on São Tomé we identify a secondary contact zone with unidirectional hybridization from H. thomensis to H. molleri. Combined, these results reveal a complex history of dispersal, in situ divergence, and gene flow in generating biodiversity in the Gulf of Guinea.

Lessons for phylogenomics analyses based on 48 bird genomes

Siavash Mirarab, Shamsuzzoha Bayzid, Bastien Boussau, Tandy Warnow

1D_402-Ernst Mayr Symposium
Saturday, June 21, 2014 4:00 PM-4:15 PM

Reconstructing the history of rapid radiations is one of the most challenging problems in phylogenetic reconstruction, at least partly due to rampant incomplete lineage sorting that is caused by short divergence times. Some have argued that genome-scale data can solve such problems. A recent phylogenomic project sequenced and analyzed 48 bird species representing every generally accepted order of Neoaves, a group hypothesized to have undergone a rapid radiation. Analyzing this huge dataset presented many challenges, and in particular, coalescence-based analyses of the genome-scale data using summary methods such as MP-EST proved challenging. One major issue was that many gene trees had extremely poor resolution, a problem that is typically addressed by filtering out such genes. We developed new ways of addressing this problem through a statistical binning approach that divides the genes into groups called supergenes. Multiple genes are put into the same group if no statistically meaningful conflict between their gene trees is detected. We then used a concatenation approach to build supergene trees, and applied a coalescence-based summary method, such as MP-EST, to these supergene trees. We showed in simulation and biological studies that this binning approach resulted in improved accuracy. A statistical binning analyses of the avian data produced trees that were broadly congruent with concatenation results, but also had interesting differences with it. Here, we present these and other advancements in application of coalescence-based summary methods to genome-scale data.

Evidence for early adaptive divergence in Malagasy primates: niche filling and mass extinction

James Herrera

1D_402-Ernst Mayr Symposium
Saturday, June 21, 2014 4:15 PM-4:30 PM

Ecological divergence in adaptive radiations may be the primary mode of speciation generating biodiversity. Rapid speciation and trait diversification due to selection and niche divergence characterize adaptive radiations. The primates of Madagascar, lemurs, are monophyletic, speciose, and ecologically diverse, suggesting they may have diversified in an adaptive radiation. If lemurs diversified in an adaptive radiation, then phenotypic traits, especially body mass, are predicted to have diverged adaptively early in lemur evolution. I used a total evidence tip-dating approach to infer the first near-complete phylogeny of extant and extinct lemurs as well as living and fossil relatives (115 taxa). I compared models of body mass evolution under gradual, rapid, and adaptive evolution and estimated the magnitude and tempo of body mass change through time. The divergence time estimates for the initial splits of main clades are older than previous studies that used molecular data and node calibration by up to 20 million years. Models of body mass evolution suggest that divergences towards large- and small-bodied optima occurred rapidly within clades. This pattern is apparent across multiple lineages, consistent with a model of character displacement during early radiation. These results suggest that lemur phenotypes diverged early in their evolution, as predicted if early lineages filled unique niches to avoid competition. Crucially, the extinction of giant lemurs has changed the evolutionary and phenotypic structure of lemur diversity substantially, and including the extinct forms is necessary for understanding the patterns of lemur evolution.

Recurrent recent dispersal accounts for treefrog diversification in hotspots of biodiversity in South America

Mariana Vasconcellos

1D_402-Ernst Mayr Symposium
Saturday, June 21, 2014 4:30 PM-4:45 PM

Although the Neotropical region encompasses a large fraction of global biodiversity, knowledge about the origin and diversification of its biota is still limited, particularly in dry forest and savanna regions. The Cerrado savanna in Central Brazil, one of the 25 global hotspots of biodiversity, is remarkable for the high endemicity level of frogs and plants, among other organisms. Yet, the evolutionary processes responsible for this great diversity are largely unknown. We studied the diversification pattern and biogeographic history of a lineage of 33 treefrog species in the Hypsiboas pulchellus group with several endemics of the Cerrado savanna and other South American hotspots such as the Andes and the Atlantic Forest. This treefrog lineage originated in the Miocene, most likely in the area comprising the Andes and the Cerrado savanna. Surprisingly, we found no support for the hypothesized origin of this group in forested regions. Diversification was not constant, but rather followed a logistic density dependent model with a burst of speciation coinciding with the origin of C4 grasslands and expansion of savannas worldwide. All but one biogeographic units comprised multiple clades, highlighting the importance of dispersal in the radiation of this group rather than long-term in situ diversification in those areas. Our range reconstruction indicates an interesting pattern of recurrent dispersal events in a stepping stone mode among distinct ecoregions in South America (including open and forested regions). This highlights the dynamic historical interchange between the Cerrado savanna and the surrounding ecoregions in South America.

Phylogenomics and Next-Generation Inferences: the Future of Phylogenetics in an Era of Big Data

L. Lacey Knowles, Stephen Smith, Laura Kubatko

1E_BalC-SSB Presidential Address
Saturday, June 21, 2014 -

Rapid shifts in taxonomic scope and numbers of loci are transforming phylogenetics. However, the awe of the scale of Big Data itself stands in the way of the field taking full ownership of this revolution, with opportunities currently being overshadowed by a number of challenges. These new challenges include a consideration of the tradeoffs surrounding data capture (especially, sampling of loci relative to taxa) and this impact on phylogenetic analyses, as well as an emphasis on broad objectives and future interoperability (as opposed to ease of data capture) as phylogenomic priorities. Because of the myriad of compromises researchers make in response to new data types, more data is not equal to better inference. I discuss how next-generation inferences – with reference to both examples of estimating evolutionary relationships and addressing biological questions in phylogenetic frameworks – are key to the future of phylogenetics in an era of big data.

Comparative transcriptomic analyses of venoms from the Cottonmouth (Agkistrodon piscivorus) and Copperhead (Agkistrodon contortrix)

Karalyn Aronow, Darin Rokyta, Kenneth Wray

2A_201-Venom
Sunday, June 22, 2014 8:30 AM-8:45 AM

Studies of adaptation aim to explain the links between genotypes, phenotypes, selection, and fitness. However, teasing apart these connections in natural systems is often difficult. Snake venom, which is necessary for feeding in those species that possess it, allows research that clearly links genotypes and phenotypes to fitness and can illuminate patterns of selection on traits directly related to fitness. Venoms are complex phenotypes with both intra- and interspecific variation, usually thought to have evolved within the context of predator-prey arms races. Venom-gland transcriptomes are a powerful tool for addressing questions concerning an ecologically critical and complex phenotype and allow for near-complete characterization of not only high abundance toxin genes, but also nontoxin housekeeping genes. Here, we compare venom gland transcriptomes between two sister species, Agkistrodon piscivorus and A. contortrix. These species have different ecological niches; A. piscivorus has evolved a unique generalist diet, including being the only member of Viperidae to include fish in its diet, while A. contortrix possess a more traditional mammal and invertebrate-based diet.

Transcriptome analyses and differential gene expression in the cone snail Conus miliaris: Effects of predator-prey interactions on venom evolution.

David Weese, Thomas F. Duda, Jr

2A_201-Venom
Sunday, June 22, 2014 8:45 AM-9:00 AM

Species interactions represent fundamental ecological processes that can have significant impacts on the evolutionary trajectories of species. However, the contribution of predator-prey interactions to genetic and phenotypic divergence within and between species remains largely unknown. In this context, predatory marine snails of the genus Conus exhibit considerable variation in venom composition, a phenomenon that may be due to the evolution of conotoxins in response to predator-prey interactions. It has been hypothesized that geographic differences in prey utilization drive the evolution of conotoxnis in cone snails and that the diversity of conotoxins is positively associated with prey diversity. To test if differences in predatory-prey interactions are associated with differences in venom composition, we sequenced and compared venom duct transcriptomes from 22 individuals of Conus miliaris from three geographic populations differing in dietary breath. Preliminary analyses resulted in a reference transcriptome of ~28,000 annotated transcripts, including >700 transcripts representing known or suspected venom peptides. Differential expression analyses revealed a total 4,729 differentially expressed transcripts between individuals of C. miliaris. When analyzed as a whole, individuals did not cluster according to populations. However, when only toxin transcripts were analyzed, samples clustered according to populations/diets, suggesting functional differences in the venom composition of these populations.

The extremes of toxin expression variation revealed in two sympatric snake species

Darin Rokyta, Mark Margres, James McGivern, Kenneth Wray

2A_201-Venom
Sunday, June 22, 2014 9:00 AM-9:15 AM
The proteomic content of snake venoms determines their efficacy in feeding and defense and therefore the fitness of the animals wielding them. Optimization of venom for local prey species could proceed through qualitative changes, such as fixation of new alleles, or through quantitative changes in the amounts of particular venom components by means of changes in gene expression or post-transcriptional regulation. We investigated the prevalence of expression variation by characterizing range-wide patterns of proteomic variation in the venoms of two sympatric species: the eastern diamondback rattlesnake (Crotalus adamanteus) and the eastern coral snake (Micrurus fulvius). For each species, we constructed a genotype-phenotype map between the venom-gland transcriptome and the venom proteome to link expression differences to specific gene sequences. We then analyzed the contents of hundreds of individual venom samples. Not unexpectedly, geographic variation in expression patterns was detectable and extensive for C. adamanteus. We also detected significant ontogenetic variation and geographic patterns in both adult and juvenile venoms. In contrast, Micrurus fulvius showed no evidence for variation of any kind in their venoms.

Expression of venom homologs in the python suggest a model for venom gene recruitment and question the definition of a venom toxin

Jacobo Reyes Velasco, Kyle Shaney, Drew Schield, Audra Andrew, Cassandra Modahl, Nick Casewell, Stephen Mackessy, Todd Castoe, Daren Card

2A_201-Venom
Sunday, June 22, 2014 9:15 AM-9:30 AM
The evolution of snake venom genes has been studied intensively over the past several decades. Essentially all previous studies, however, have lacked the context of complete snake genome data. We took a novel approach to studying snake venom evolution by leveraging the complete genome of the Burmese python, including extensive information on tissue-specific patterns of gene expression. We identify the orthologs of snake venom genes in the python genome, and conduct detailed analysis of patterns of gene expression of these venom orthologs in the python to identify patterns of gene expression that differentiate snake venom gene families from all genes in the python. Under the hypothesis that the python may largely represent an ancestral state (prior to the evolution of substantial venom gene family radiations), we argue that these data provide novel insight into biases in which genes were recruited in venom production in snakes. We also use data from an oral gland (the rictal gland) as a vignette to understand the pros and cons of using transcriptomic data alone to define “venoms” in snakes

---

Inferring phylogenetic relationships and understanding venom evolution in cone snails (genus, Conus) using venom duct transcriptomes.

Mark Phuong, Michael Alfaro

2A_201-Venom
Sunday, June 22, 2014 9:30 AM-9:45 AM
Rapid evolution of venom genes is thought to play a crucial role in the diet specialization and diversification of cone snails (genus, Conus). Poorly resolved phylogenetic relationships within Conus and an incomplete understanding of venom gene diversity prevent full examination of the interplay between venom evolution and cone snail diversification. To address these issues, I sequenced the venom duct transcriptomes of 12 species distributed throughout the depth of Conus, identified 500 common cellular genes suitable for phylogenetic reconstruction, and inferred a maximum likelihood phylogeny. Markers identified from transcriptome sequencing provided greater resolution and higher support values at every node compared to markers obtained through traditional Sanger sequencing. In addition, I conducted a preliminary analysis of venom gene evolution across these 12 species. I plan to design a sequence capture array to target the 500 phylogenetic markers and all venom genes across the entire group to understand the impact of venom gene diversification on the evolution of Conus.

Genomic tests of Pleistocene aggregate island complexes as drivers of divergence: differentiation across local geographic scales in Caribbean crickets

Anna Papadopoulou, L. Lacey Knowles

2A_206-Island Biogeograhy
Sunday, June 22, 2014 8:30 AM-8:45 AM
Sea-level oscillations between Pleistocene glacial maxima and interglacial periods have caused repeated cycles of island connections and isolation in many archipelagos. In the Caribbean, the coalescing-island paradigm has been applied to explain diversification patterns that formed during the Miocene or the Pliocene. However, tests of recent population divergence across Pleistocene aggregate island complexes are still lacking, reflecting the limited resolution of traditional markers used in phylogeography (mtDNA or a few microsatellite loci) to distinguish among alternative evolutionary scenarios in such recent and dynamic systems. Harnessing the power of genomic scans, we estimate fine-scale biogeographic affinities among the Caribbean Virgin Islands – an archipelago with a history of repeated island reconnections during the Pleistocene, providing an ideal system to study genetic divergence due to sea-level oscillations, over short geographic distances and uniform climatic conditions. Specifically, with an average of 37,000 SNPs from the genome of 136 individuals from ten populations of an endemic flightless ground cricket species (Amphiacusta sanctaecrucis) we assess genetic differentiation and reconstruct population histories to make inferences about population connections and persistence in this geologically dynamic system. Despite the recent island connections fostered by sea-level changes and the small geographic scale separating islands, we nonetheless find high levels of population divergence with largely discrete genetic clusters on each present-day island and a strong geographic structure across the archipelago. We infer a stepping-stone pattern of colonization with long-term population persistence on most of the present-day islands, including the smaller islets. However, the genomic data

supports a model involving an over-sea colonization of Saint Croix (the only island that has been disconnected since at least the Pliocene) and a strong population bottleneck on the coral atoll of Anegada. We discuss these findings in the broader context of Caribbean biogeography and the role of Pleistocene aggregate island complexes as drivers of divergence across local geographic scales.

Biogeography, range size and body size evolution in North American minnows

Samuel Martin, Ronald Bonett

2A_206-Island Biogeograhy
Sunday, June 22, 2014 8:45 AM-9:00 AM

Body size is one of the most important traits influencing an organism's ecology and is often a major axis of evolutionary change. Among freshwater fishes, body size may influence patterns of biogeography and macroevolution. Fishes with larger bodies are better dispersers, inhabit larger streams and rivers, and may have larger ranges. Conversely, smaller fishes can inhabit smaller streams, are generally poorer dispersers, and are thus more likely to become isolated among drainages. We tested for a relationship between body size and range size in the highly speciose endemic clade of North American minnows (Cyprinidae), which exhibit diverse body sizes and ecologies. We developed a novel species level phylogeny based on 7 mitochondrial genes and 10 nuclear genes. We used this phylogeny to reconstruct ancestral body sizes, range sizes, and geographical range. We also examined regional trends in trait disparification, and body size at reconstructed dispersal and vicariance events. Lastly, after accounting for phylogenetic relatedness and uncertainty, we tested whether range size is related to body size. We discuss our results in the context of environmental stability, dispersal ability, and species diversity.

Caribbean biogeography: multiple arachnid lineages reveal the role of dispersal and geology in forming a biodiversity hotspot

Ingi Agnarsson, Matjaz Kuntner, Greta Binford

2A_206-Island Biogeograhy
Sunday, June 22, 2014 9:00 AM-9:15 AM

The importance of islands in revealing evolutionary processes was already highlighted by Darwin's work on the Galapagos and Wallace's work in the Malay Archipelago. Island biogeography has provided many elegant examples of the evolutionary mechanisms involved in generating biodiversity. These include geological processes such as plate tectonics and volcanism, and traits of organisms such as their size, generation time, and dispersal ability. Dispersal was an early focus of biogeography and is enjoying a renaissance as a key biogeographical player after a brief period of post-plate-tectonic reticence. Nevertheless, the focus on dispersal has long revolved around its role as an alternative to vicariance in explaining distributions. Here we focus on the role of dispersal abilities in the formation of biodiversity in the Caribbean hotspot. The West Indies form a remarkable archipelago for biogeographical studies. They consist of a dizzying number of islands, most of which are sufficiently old and isolated to have generated endemic forms, yet the islands are situated close enough to three continental landmasses to allow a more active biotic interchange between continents and islands than possible on more isolated archipelagos. It is thus an ideal 'laboratory of biogeography and evolution' serving to evaluate how dispersal abilities impact colonization and diversification on archipelagos. By investigating multiple arachnid lineages spanning a large spectrum of dispersal propensities (two scorpion genera, two pseudoscorpion genera, the amblypygid Phrynus, and numerous spider lineages), and their genetic and species diversity over the archipelago, we find that dispersal ability is of fundamental importance in shaping both distribution and diversity of taxa. The degree to which phylogenetic patterns reflect geological history is inversely related to dispersal ability of taxa, with patterns ranging from predictable in poorer dispersers to highly stochastic in excellent dispersers. Diversification peaks at relatively intermediate dispersal abilities with stretches of ocean permitting rare colonization but acting as effective barriers to gene flow. By looking across multiple lineages that differ in key traits such as dispersal, we are beginning to capture some fundamental components of Caribbean biogeography and the key role of dispersal ability in shaping taxon history and diversity.

Island and continental biogeography dynamics in the assembly of the Western Ghats (India) avifauna

Sushma Reddy, V. V. Robin, C. K. Vishnudas, Pooja Gupta, Uma Ramakrishnan

2A_206-Island Biogeograhy
Sunday, June 22, 2014 9:15 AM-9:30 AM

The Indian subcontinent is a biogeographic enigma with high species richness yet low endemism, despite a long history of isolation before reaching its current geographic position. The origins of montane species in the Western Ghats, a biodiversity hotspot in southwestern India, have long been debated. The prevailing hypothesis for birds is that Himalayan taxa were able disperse to the Western Ghats at a time when peninsular India was covered in moist forest and later these populations were isolated as the subcontinent dried up. We analyzed a majority of Western Ghats endemic species by examining phylogenetic relationships and ancestral area reconstructions to decipher potential routes of colonization. Western Ghats endemics have their closest relatives in different geographic regions and appear to have colonized India from all four possible source directions and at different times. The assemblage of the Indian avifauna is driven as much by island biogeography dynamics as vicariance events.

New perspectives on Sunda Shelf biogeography

Jacob Esselstyn, Anang Achmadi, Maharadatunkamsi None, Thomas Giarla, Kevin Rowe

2A_206-Island Biogeograhy
Sunday, June 22, 2014 9:30 AM-9:45 AM

The Sunda Shelf is an expansive region of shallow water encompassing many islands, large and small. These islands were united by dry land with the Asian mainland numerous times during the Pleistocene and earlier periods. This historical geographic template once provided a seemingly intelligent model for estimating rates of extinction and processes of community disassembly as land area was reduced by rising sea level. However, recent genetic studies of multiple terrestrial vertebrate groups reveal deep inter-island genetic isolation and within-island speciation, raising questions regarding past assumptions of a once homogeneous biological community of on the Sunda Shelf. We will discuss the implications of these findings in a context of an improving understanding of the systematics of shrews and rodents in the region.

Broad host ranges in fungal parasites of anciently asexual bdelloid rotifers

Christopher Wilson, *Tim Penny*

2A_301A-Coevolution
Sunday, June 22, 2014 8:30 AM-8:45 AM

The evolution of sex is an enduring puzzle. One hypothesis posits that antagonistic coevolution favors sexually produced offspring because they possess rare or novel genotypes that are resistant to parasites and pathogens. A corollary prediction is that obligate asexuality will persist when antagonistic coevolution is relaxed: if parasites are scarce, for example, or if hosts disperse so rapidly and independently of parasites that the two become decoupled in time and space. The latter scenario accords with studies of bdelloid rotifers, aquatic microinvertebrates that have been obligately asexual for tens of millions of years. Bdelloids disperse frequently and broadly in a desiccated state that is not tolerated by their major enemies, parasitic fungi. However, it remains unclear how strongly this dispersal ecology relaxes antagonistic coevolution, because the relevant models also hinge on the specificity of parasites to hosts, which is unknown in the bdelloid-fungus system. We conducted cross-inoculation experiments to determine the host range of twenty fungal parasites across seven species of bdelloid rotifers in two genera, incorporating phylogenetic effects by molecular barcoding of all taxa. We found broad intra- and even intergeneric host ranges, in contrast to the narrow ranges assumed in many coevolutionary models. However, all hosts resisted at least one parasite, and parasites varied considerably in the degree of infectivity against hosts within their range. This 'anciently asexual' lineage therefore shows variation in susceptibility to infection, probably maintained in part because rapid migration relaxes coevolution and preserves diversity. To clarify this interpretation, coevolutionary models of sex in metapopulations should be updated to consider more generalised host-parasite interaction matrixes.

HOW SPECIFICITY AND EPIDEMIOLOGY DRIVE THE COEVOLUTION OF STATIC TRAIT DIVERSITY IN HOSTS AND PARASITES

Mike Boots

2A_301A-Coevolution
Sunday, June 22, 2014 8:45 AM-9:00 AM

There is typically considerable variation in the level of infectivity of parasites and the degree of resistance of hosts within populations. This trait variation is critical not only to the evolutionary dynamics but also to the epidemiology, and potentially the control of infectious disease. However, we lack an understanding of the processes that generate and maintain this trait diversity. I discuss a series of models that examine how epidemiological feedbacks and the characteristics of the interaction between host types and parasites strains determine the coevolution of host-parasite diversity. The interactions include continuous characterisations of the key phenotypic features of classic gene-for-gene and matching allele models. We show that when there are costs to resistance in the hosts and infectivity in the parasite, epidemiological feedbacks may generate diversity but this is limited to dimorphism, often of extreme types, in a broad range of realistic infection scenarios. For trait polymorphism, there needs to be both specificity of infection between host types and parasite strains as well as incompatibility between particular strains and types.

Does sociality modulate co-phylogeny between social shrimps and their host sponges?

Tin Chi Solomon Chak, *J. Emmett Duffy*

2A_301A-Coevolution
Sunday, June 22, 2014 9:00 AM-9:15 AM

Intimate biological associations comprise a large part of biodiversity and clarifying the nature and the evolution of these associations has been a fundamental quest in ecology and evolution. Here we study the evolutionary relationships between ~20 species of Caribbean sponges and ~40 species of snapping shrimps in the genus Synalpheus that live only inside sponge canals. The species of Synalpheus range from strict host specialists to relative generalists and include the only know marine eusocial animals, as well as species that live in small groups or in heterosexual pairs. The evolutionary trajectory of Synalpheus is likely linked closely to differences in their host sponges because the host, offering a protective and stable environment, governs the shrimps' geographic distribution, density, species assemblage and diet. Therefore, we tested for congruence between the evolutionary histories of Synalpheus shrimps and their sponge hosts, and asked whether the strength of congruence varies with social organization. We found that Synalpheus species did not evolve independently of their hosts, which suggests phylogenetic conservatism in their host use patterns. Moreover, eusocial species are the main contributor to the significant co-phylogenetic pattern. This suggests that phylogenetic conservatism of host use is stronger for eusocial than non-social Synalpheus species. Many eusocial invertebrates and vertebrates evolved under stringent habitats. In eusocial shrimps, the stronger association with closely related host sponges might lead to stronger habitat constrains and promoted the evolution of eusociality.

Eco-evo dynamics of mutualism decline in response to nitrogen fertilization

Katy Heath, *Dylan Weese, Christie Klinger, Benjamin Gordon, Patricia Burke, Jennifer Lau*

2A_301A-Coevolution
Sunday, June 22, 2014 9:15 AM-9:30 AM

Mutualisms are predicted to be evolutionarily unstable and sensitive to environmental change. Given the importance of mutualisms in nature, understanding how mutualisms evolve in response to global changes such as nitrogen (N) deposition, and how these evolutionary responses feed back on ecological processes, might be important for predictions of community and ecosystem-level responses. Such feedbacks are particularly likely for ecologically-important mutualisms, such as the legume-rhizobium symbiosis, in which traded benefits play a roles in structuring the plant community and mediating nutrient cycles. In the legume-rhizobium resource mutualism, symbiotic rhizobia provide their legume hosts with fixed N in return for plant photosynthates. Theory predicts that increased N availability should favor the evolution of less-beneficial rhizobium symbionts. We isolated clover-associated Rhizobium from replicated N-fertilized and control plots in the Kellogg Biological Station LTER and tested these strains in controlled greenhouse experiments to study how 22 years of N fertilization have influenced the stability of the legume-rhizobium mutualism. We found that fertilization led to the evolution of rhizobia that are less-beneficial for clover hosts, as evidenced by smaller plants with lower chlorophyll content. Genetic analyses implicate microevolution, and horizontal gene transfer of genes on the symbiosis plasmid, in this phenotypic change. Moreover these evolutionary effects are not limited to the mutualist partners themselves. In a community mesocosm experiment, inoculation with N-adapted rhizobia shifted plant community composition to favor grasses and forbs, at the expense of clover species, and also caused soil nitrate and ammonium pools to decline. The results of several experiments thus suggest that the evolution of benefits in the legume-rhizobium mutualism, and ultimately mutualism stability, depend on N availability. Moreover these microevolutionary responses scale up to influence ecological interactions in the plant community, shifting the abundance of functional groups, and altering ecosystem-level processes (soil N-availability). Mutualism evolution might play a surprisingly important role in predicting community and ecosystem responses to global environmental change.

Helpful allies or suffocating friends? Evolution in a mutualism constrains adaptive change

Levi Morran, McKenna Penley, Victoria Byrd, Andrew Meyer, Timothy O'Sullivan, Farrah Bashey-Visser

2A_301A-Coevolution
Sunday, June 22, 2014 9:30 AM-9:45 AM
Mutualistic coevolution is vital to many species and can dictate the evolutionary trajectory of a population. Nonetheless, the long-term consequences of mutualistic coevolution are largely untested. We tested the effects of evolution within a mutualism on the bacteria Xenorhabdus nematophila by disassociating the mutualism between X. nematophila and the nematode Steinernema carpocapsae and experimentally evolving the bacteria either apart from the nematode or with the nematode. Disassociated bacteria exhibited adaptation in response to selection, but the coevolved bacteria did not. Additionally, the disassociated bacteria evolved a phenotype that disrupted the mutualism upon reintroduction. Therefore, mutualistic interactions imposed phenotypic restrictions and constrained rates of adaptation in the mutualist bacteria relative to the disassociated bacteria. Thus, the dynamics of natural selection are fundamentally altered by mutualistic interactions.

Quantitative trait locus analysis under osmotic and thermal stress in an intertidal copepod, Tigriopus californicus

Helen Foley, Suzanne Edmands

2A_301B-Adaptation
Sunday, June 22, 2014 8:30 AM-8:45 AM
As natural habitats are exposed to increasing environmental change, species must adapt to new conditions in order to survive. When Tigriopus californicus, a copepod adapted to the high intertidal zone, was challenged with high temperature and high and low salinity stress, we observed that more individuals from southern populations are likely to survive high thermal and salinity stress, while the northern populations have an advantage under low salinity. We hypothesized that some parts of the genome associated with survivorship would vary between crosses and between stressors, indicating a stress-specific response, while some loci would associate with more than one stressor, indicating a general or shared response.

We generated two hybrid F2 groups from one southern population (San Diego, CA) crossed to two northern populations (Santa Cruz, CA and Friday Harbor, WA). F2 adults were assayed for tolerance to the three stressors, and genotyped for 61 Single Nucleotide Polymorphisms (SNPs) across the genome. Using Quantitative Trait Locus (QTL) analysis, we examined the genetic loci associated with survivorship under each of these stressors for males and females.

Putative QTL were found to differ between stressors and crosses, indicating populations may employ different mechanisms for the same stress, and that different loci confer an advantage under different stressors. In a dynamic environment, subjected to many stressors, a diverse range of stress-responses may be advantageous and contribute to overall survivorship.

Behavioral Diversity in Malawi African Cichlid Fishes

Emily Moore, Jonathan Tufts, Reade Roberts

2A_301B-Adaptation
Sunday, June 22, 2014 8:45 AM-9:00 AM
The adaptive radiation of cichlid fishes in Lake Malawi has resulted in a species flock that is ideal for studying diversity among many phenotypically divergent but closely related species in a natural context; wild-derived cichlid fish can be examined in a controlled laboratory setting, while interpretations of results can be informed by ecological studies. Because of this unique feature, laboratory lines of African cichlids can be used to examine the genetic basis of a variety of morphological and ecologically relevant phenotypes, including fundamental differences in how species use and investigate their environment. In order to identify behavioral differences between cichlid species, I modified classical behavior tests to quantify individual responses to novel environments, objects, and individuals in five wild-derived cichlid lines representing two genera. Four sister species of the rock-dwelling genus Metriaclima were used to provide a picture of the behavioral differences between recently diverged lineages, and were compared to Aulonocara baenchi for more distant evolutionary context. Recorded videos of each assay were analyzed with computer software to generate measures of movement (such as speed) and exploration (such as number of approaches to a novel object). Preliminary findings suggest that both open field speed

and novel object investigation differs by species, providing exciting prospects for future genetic studies.

Host-associated differentiation as a midpoint in a total host shift: Loss of adaptation to a native host in Florida soapberry bugs

Meredith Cenzer

2A_301B-Adaptation
Sunday, June 22, 2014 9:00 AM-9:15 AM

Host-associated differentiation is often studied with the goal of understanding the early stages of speciation. However, local adaptation to distinct hosts will not always result in the emergence of reproductive isolation, as many components of spatial, temporal, and ecological isolation and stability may contribute to gene flow in spite of strong differential local selection.

The soapberry bugs (Hemiptera:Rhopalidae: Serenithinae) have been well-studied for their remarkably rapid, repeated adaptation to novel host plants throughout the world. In the early 1990s, Scott Carroll and colleagues demonstrated that populations of Jadera haematoloma had locally adapted to the invasive host plant golden rain tree (Koelreuteria elegans) in Florida after its introduction and spread in the mid-1990s, and that a trade-off existed between ability to use the invasive and the native host (balloon vine, Cardiospermum corindum), leading to two distinct sets of host-associated populations with fitness peaks on their local host. Key morphological adaptations, namely differences in beak length optimized to feed on each host, also showed clear differentiation.

However, this no longer seems to be the case. Returning to these populations almost 25 years after the original work, both morphological measurements and cross-rearing experiments demonstrate that populations on both hosts are now more well adapted to the invasive host plant. Compared to previous measures, populations using the invasive host appear to have changed relatively little in the past 25 years. However, populations on the native host are now very similar to those on the invasive host morphologically and have similar survival when reared on the invasive host. When reared on the native host, all populations show dramatically reduced survival, but populations from the native host still out-perform those on the invasive host.

Although what has driven this loss of local adaptation has not yet been explicitly studied, it seems likely that the much larger populations supported by the invasive host, and their expansion since its introduction, have contributed to increased gene flow swamping out adaptation to the native host. Given the variable nature of host abundance and stability in many systems in the field, this should serve as a cautionary tale to those of us interested in extrapolating from local adaptation to speciation.

Genome-wide evidence of evolution and adaptation in the invasive Florida python population

Daren Card, Drew Schield, Kristen Hart, Margaret Hunter, Todd Castoe

2A_301B-Adaptation
Sunday, June 22, 2014 9:15 AM-9:30 AM

Analyzing how natural selection exerts its effects on a genomic scale is difficult because substantial evolutionary changes often happen over long time periods in most species. Invasive species, however, represent a promising model for analyzing the processes of evolution and adaptation on timescales that are tractable for study, and have been shown to demonstrate rapid evolutionary responses over short or ‘ecological’ timescales. Such recent invasive introductions often demonstrate rapid responses to this shift in environmental conditions and habitat (from native to introduced), and present ready opportunity to test the genome-wide effects of natural selection and putative adaptation. The Burmese python (Python molurus bivittatus) is ideal for this work due to its recent establishment and proliferation in Florida, a location with climatic conditions much different from those in the species' native range of Southeast Asia. A 2010 freeze event in Florida led to a large (>50%) die-off of snakes in the Florida python population (FPP), and likely catalyzed selection-driven evolution in the FPP. We used discrete population-level sampling of the FPP before (2007) and after (2013) the freeze event and genome-wide marker sequencing (RADseq) to test the hypothesis that large fluctuations in allele frequencies (i.e., evolution) have occurred in the FPP as a result of the freeze event. We found multiple regions of the genome that appear to show major fluctuations in heterozygosity, indicating in situ evolution in the FPP, and we used the Burmese python genome to identify genes and associated functions linked to these putatively selected loci.

Swimming with the Red Queen: adaptive evolution of a ZP-domain glycoprotein in galaxiid fishes

Graham Wallis, Lise Wallis, David Winter, Luca Jovine

2A_301B-Adaptation
Sunday, June 22, 2014 9:30 AM-9:45 AM

We describe protein sequences for a uromodulin-like larval glycoprotein (LGP) from 21 species of galaxiid fishes, with a MRCA about 30 Ma. These have been derived from both genomic DNA and cDNA, by conventional and Roche 454 sequencing. LGP shows a fast rate of evolution and an exceptionally strong signal of positive selection over the entire coding region, as evidenced by $dN/dS > 1$. Across all sequences, 182/336 (54%) of residues are variable; many substitutions are profound/non-conservative and include in-frame indels. Genetic distances are, on average, 2.4x larger for coding region (996 bp) than introns (1459 bp). We identify 20–30 positively-selected ($dN/dS > 4$) amino acid sites using a variety of approaches. By homology modelling, we show that these proteins can fold following the recently-elucidated structure for ZP3, and that the positively selected amino acids occur in loop regions of both ZP-N and ZP-C domains. The high rate of evolution is further accelerated in lineages that have lost the marine larval phase.

Like other ZP-domain proteins, which are categorized as members of the immunoglobulin superfamily, LGP shows properties expected of an extracellular polymeric cell-surface protein and appears to be highly glycosylated. Taken together, these features make it likely that LGP is an immune protein. This idea is supported by initial gene expression analysis showing that the gene is active in developing skin and gill arches, which are likely conduits for pathogens. These fish, therefore, appear to be engaged in a Red Queen arms race, which further accelerates when larvae adopt a freshwater environment through a change in life-history, exposing themselves to a new range of pathogens and parasites.

Centromere-associated drive and the maintenance of fitness variation in Mimulus

Lila Fishman

2A_302A-Plant Evolution
Sunday, June 22, 2014 8:30 AM-8:45 AM

Centromeres, which mediate chromosomal segregation, may act as selfish genetic elements by gaining excess transmission to the egg pole during asymmetric female meiosis (a process termed female meiotic drive). Female meiotic drive may have profound effects on the maintenance of individual fitness variation within populations, the evolution of species barriers, and karyotypic diversification. However, little is known about the incidence and effects of centromeric drive in natural populations. Previously, we characterized a novel centromere-associated female meiotic drive system within the yellow monkeyflower Mimulus guttatus, and demonstrated that a balance of drive and male fitness costs (pollen inviability) were sufficient to maintain intra-population polymorphism for drive. Here, we investigate additional fitness consequences of drive genotype with five years of field data on fruit number, seed production, and seedset per fruit, and also use bulk genome sequence data from multiple seedling cohorts to evaluate changes in drive haplotype frequency indicative of effects of survival. We observed an overall consistent negative effect of homozygosity for the driving haplotype on seedset (despite tremendous year-to-year variation in fecundity), but relatively little effect on other fitness components. This suggests that female fitness costs may also contribute to balancing selection on the drive locus, and, conversely, that drive contributes to the maintenance of standing variation for both male and female fitness. We discuss possible mechanisms of reduced seedset in drive homozygotes, including reduced pollinator attraction, reduced self-fertilization, and meiotic defects. In addition, we demonstrate that the drive locus is polymorphic in a neighboring population, but that fitness costs appear different there, suggesting that they reflect hitchhiking by deleterious recessive alleles rather than an intrinsic cost of homozygosity for the driving centromere.

Sexy signals: gamete recognition is a reproductive mechanism and isolating barrier in wild tomato species (Solanum sect. Lycopersicon)

Cathleen Jewell, Leonie Moyle

2A_302A-Plant Evolution
Sunday, June 22, 2014 8:45 AM-9:00 AM

Recognition and chemoattraction between male and female gametes has been observed in a broad range of sexually reproducing organisms, including both internally and externally fertilizing species. Gamete recognition is thus thought to be a widespread, fundamental mechanism that facilitates fertilization. Conversely, misrecognition of gamete chemical cues can disrupt interspecific mating events; the resulting gamete isolation is a potentially powerful, though relatively poorly understood reproductive isolating barrier between species. Here we demonstrate that active gamete recognition occurs within species in the wild tomato clade—consistent with other plant and animal systems—and can also act as a strong postmating, prezygotic isolating barrier between some species. Using an in vitro assay that allows gamete interactions between male pollen tubes and female ovules to be observed directly, we quantified gamete recognition both within and between three tomato species (Solanum lycopersicum, S. pimpinellifolium and S. pennellii). In conspecific assays, growing pollen tubes actively reorient toward and make contact with conspecific ovules, indicative of an active behavioral reaction by pollen tubes in response to an ovule-secreted chemoattractant. In vitro tests of heterospecific gamete interactions between species that are very closely related (S. lycopersicum and S. pimpinellifolium) indicate equally high gamete recognition and no evidence for gamete isolation. In contrast, in vitro gamete interactions between more distantly related species (diverged ~2 MY) show a reduction in pollen tube recognition of heterospecific ovules, consistent with the evolution of partial gamete isolation. These data indicate that gamete recognition can act as a postmating, prezygotic reproductive isolating barrier in the wild tomato clade. These results provide the basis for ongoing studies to identify the molecular basis of divergent heterospecific gamete signaling, based on biomolecular features of known gamete chemoattractants in other systems.

The role of adaptive introgression in a case of incipient speciation in Mimulus

Joshua Bahr, Matt Streisfeld

2A_302A-Plant Evolution
Sunday, June 22, 2014 9:00 AM-9:15 AM

Identifying the source of the adaptive alleles responsible for trait divergence and fitness variation in nature is a long-standing goal of evolutionary biology. Typically, this involves distinguishing whether selection acted on new or pre-existing variation. However, natural hybridization between recently diverged lineages also may play a significant, yet underappreciated role in this process. Through a process known as adaptive introgression, an allele that has high fitness in a novel environment can pass readily across a taxonomic boundary even if hybrids are relatively unfit. In this study, we use phylogenetics, genomics, and functional genetic approaches to demonstrate that historical hybridization between divergent taxa has led to the spread of an adaptive allele conferring red flowers in Mimulus aurantiacus. Moreover, because this allele has been demonstrated to be under strong divergent selection as a consequence of differences in pollinator visitation, the introgression of this adaptive allele also has important implications for the evolution of reproductive isolation and the subsequent origins of new species. Therefore, despite a rich history of debate about hyrbidization's role in evolution, our results suggest that it can be seen as a prolific source of the alleles that contribute to both adaptation and speciation.

Local Adaptation Drives Intraspecific Reproductive Isolation in Iris atropurpurea

Gil Yardeni

2A_302A-Plant Evolution
Sunday, June 22, 2014 9:15 AM-9:30 AM

Ecological speciation is a process in which local adaptation causes diverging selective pressure that consequently creates reproductive isolation (RI) between populations. RI can also arise between geographically distant populations due to stochastic processes. The two processes are not mutually exclusive and can cause outbreeding depression in crossings from different populations, representing the forming process of incipient speciation. Theory suggests that due to combined effect of inbreeding and outbreeding depression, RI will be the lowest in an intermediate distance between crossed populations. However, this was tested only for geographical, and not for ecological, distance.

In this study, we tested the role of geographical and ecological distances in creating reproductive isolation between populations of Iris atropurpurea, an endangered plant endemic to Israeli coastal plain. We performed crosses between populations at different geographical and ecological distances and tested for association of geographical and ecological distances with fruit-set, seed number and seed viability. We tested the effect of these distances on RI, which was calculated using the relative reproductive success of crosses between populations, compared to crosses within population.

RI calculated based on fruit-set was positively influenced by both geographical and ecological distances, but RI estimations based on seed number and viability were not. Total RI did not show an intermediate geographical distance of low RI, as expected; instead, a maximum RI was observed in this distance. Total RI increased with ecological distance, and the combined effect of ecology and geography on RI was overall a non-linear increase with increase of both distances. Individual edaphic and climatic factors were correlated with RI, suggesting specific role in local adaptation. Overall, our findings suggest that RI between populations of Iris atropurpurea is driven by local adaptation, rather than by isolation by distance. These results are relevant for both understanding ecological speciation and creating conservation programs of genetic rescue for endangered species

Rapid evolution and duplication of a key centromeric protein in Mimulus, a genus with female meiotic drive

Findley Finseth, Yuzhu Dong, Lila Fishman

2A_302A-Plant Evolution
Sunday, June 22, 2014 9:30 AM-9:45 AM

Centromeres mediate faithful segregation of chromosomes and are defined by the centromere-specific histone, CENH3. In all eukaryotes, CENH3 assembles the kinetochore, the proteinaceous structure that links chromatin with spindle microtubules to organize chromosomal movement. Despite its essential and conserved function, CENH3 evolves rapidly and adaptively across plants and animals. Female meiotic drive of selfishly evolving centromeres has been hypothesized to explain this pattern. Under this model, the fundamental asymmetry of female meiosis fuels an evolutionary ‘arms-race’ between centromeres and kinetochore proteins (such as CENH3), the byproduct of which is extreme sequence divergence. Although theorized to be a widespread and potent evolutionary force, there is scant empirical evidence of centromeric drive and much remains unknown about the nature and consequences of antagonistic coevolution between centromeric DNA and kinetochore proteins. Here, we investigate the molecular evolutionary patterns of CENH3 across Mimulus, the genus with the empirical model for centromere-associated meiotic drive, Mimulus guttatus. We sequenced CENH3 genus-wide and, intriguingly, discovered a duplication that dates to a period of dynamic chromosomal and centromere evolution. We find that 1) the two copies are expressed and highly divergent, with most divergence concentrated in the meiosis-specific N-terminal, 2) there are signatures of long-term positive selection acting on both duplicates, 3) both inter- and intra-specific patterns of variation suggest the paralogs are under different selective regimes and are on distinct evolutionary trajectories. Our results show that centromere-associated drive can have profound effects on the pattern of genetic variation at key kinetochore proteins, and may directly play a role in promoting diversity at centromeres and centromeric proteins.

Dimorphic development in Streblospio benedicti: genetic analysis of morphological differences between larval types

Christina Zakas, Matthew Rockman

2A_302B-Trait Evolution
Sunday, June 22, 2014 8:30 AM-8:45 AM

The marine polychaete Streblospio benedicti exhibits two distinct larval types, making it a model for the study of developmental evolution. Females produce either large eggs or small ones, which develop into distinct lecithotrophic or planktotrophic larvae with concomitant morphological and life-history differences. Here, we investigate the inheritance of key morphological traits that distinguish the larval types. We use genetic crosses to establish the influence of maternal and zygotic differences on larval phenotypes. We find a large maternal effect on larval size and the number of larval chaetae, while the number and length of these chaetae are also strongly influenced by zygotic genotype. Interestingly, the distribution of larval phenotypes produced by these crosses suggests traits intermediate to the two parental types should not be uncommon. Yet, despite gene flow between the types in natural populations, such intermediates are rarely found in nature, suggesting that selection may be maintaining distinct larval modes.

Modeling underwater light and visual sensitivity in the estuarine diamondback terrapin (Malaclemys terrapin)

Abby Dominy, Ellis Loew, Harold Avery, James Spotila

2A_302B-Trait Evolution
Sunday, June 22, 2014 8:45 AM-9:00 AM

We measured the absorbance spectra of oil droplets and visual pigments in retinal photoreceptors, as well as the ocular media (i.e. lens, cornea) in the diamondback terrapin (Malaclemys terrapin) to model physiological visual ability against measured ambient irradiance spectra. Terrapins have a tetrachromatic visual system that matches well with the visual system measured in the closely related freshwater turtle, the red-eared slider (Trachemys scripta elegans). The four single cone photoreceptors responsible for this visual system have visual pigment sensitivities with λmax = 370 nm (UV), 457 nm (blue), 527 nm (green), and 610 nm (red), as measure by microspectrophotometry. The oil droplets associated with each of the visual pigments act as long-pass spectral filters of light that alter the sensitivity of each visual pigment. The ocular media measured in other visual ecology studies is usually found to transmit light equally between 400 and 700 nm. However, the ocular media measured in the terrapin maximally absorbs at 505 nm, causing the ocular media to act as both a short-pass and long-pass filter of light before it reaches photoreceptors in the retinal epithelium. This results in a dramatic shift in spectral sensitivity with λmax = 356 nm (UV), 427 nm (blue), 572 nm (green), and 630 nm (red). The measured ambient irradiance spectrum at the surface of the water column demonstrates relatively low photonic irradiance—and relatively low photon capture probability—around 500 nm, which suggests that the filtering effects of the ocular media are forcing maximal sensitivities in the terrapin to match maximal light availability. Given that the closely related red-eared slider turtle does not have the same ocular media absorbance as measured in the terrapin in this study, we suggest that the terrapin visual system has adapted to the unique light environment that occurs in dynamic estuarine ecosystems.

Genetic effects and behavioral plasticity of winner and loser effects in baboons

Mathias Franz, Jenny Tung, Jeanne Altmann, Susan Alberts

2A_302B-Trait Evolution
Sunday, June 22, 2014 9:00 AM-9:15 AM

Winner and loser effects commonly occur when individuals compete aggressively for access to limited resources such as food and mates. These effects are used to describe the phenomenon in which winners tend to become more likely to win in subsequent interactions, and losers tend to become more likely to lose. Winner and loser effects are predicted to evolve when individuals are uncertain about their relative fighting ability; in these situations, the outcome of a given agonistic interaction provides information on an individual's relative fighting ability, which can be used to adjust future agonistic behavior. However, current work on winner and loser effects ignores the fact that the relative fighting abilities of individuals change over time, e.g. due to growth or aging. We hypothesize that temporal changes in relative fighting ability lead to the evolution of behavioral strategies that flexibly adjust the strength of winner and loser effects to expected age-specific changes in fighting ability. To test this hypothesis we investigated agonistic behaviors in a population of wild baboons that consists primarily of yellow baboons (Papio cynocephalus) with some admixture from a closely related taxon, anubis baboons (P. anubis). We analyzed a total of 16,821 agonistic interactions among 152 adult males living in 5 social groups over a total time period of 54 group-years. In agreement with our hypothesis, we found that winner effects were stronger than loser effects in young males, who undergo growth-related increases in fighting ability. In contrast, winner effects were weaker than loser effects in old individuals, who undergo aging-related decreases in fighting ability. In addition to testing for effects of age, we investigated whether winner and loser effects were related to admixture-based genetic variation. Genetic hybrid scores were assigned to all individuals based on genotypes at 14 microsatellite loci. Our results show that increasing anubis admixture was associated with weaker winner and loser effects. Taken together our findings suggest a genetic basis for winner and loser effects in baboons and a flexible adjustment of these effects to temporal changes in relative fighting ability. More generally, our study points to the importance of temporal variation in individual fighting ability and social context as a driver for the evolution of agonistic behavior.

Old World fruit bats (Pteropodidae) vary in pollinator importance and selection exerted on night-blooming plant species

Alyssa Stewart, Michele Dudash

2A_302B-Trait Evolution
Sunday, June 22, 2014 9:15 AM-9:30 AM

Given their relative immobility, reproduction can be challenging for plants. Many flowering plant species overcome this obstacle by relying on animals to transfer their gametes. As these pollinating animals directly impact plant fitness, they can be major drivers in the floral and fruit evolution of the plant species they visit. For instance, different foraging behaviors can select for different traits in a plant species. Old World fruit bats (Pteropodidae) are typically classified as one functional group, implying that they interact with flowers in similar ways and exert similar selective pressures on plants, despite the diversity of this bat family. To study the potential selection exerted by different pollinators in this system, we examined the foraging behaviors of the seven most common pteropodid species in southern Thailand. We hypothesized that pollinator importance would vary among pteropodid bat species due to their different foraging behaviors, and vary by plant species as well. Specifically, we predicted that the diverse group of bats within this family would exhibit preferences for different plant resources and subsequently carry different pollen loads. We mist-netted at six focal bat-pollinated plant species to determine the foraging times and visitation rates of each bat species. We also collected and identified pollen from the fur of netted individuals to assess the pollen loads carried by each bat species. Our data reveal significant differences in the foraging times, visitation rates, and pollen loads of pteropodids. These findings indicate that pollinating bat species do exhibit preferences for different plants species and likely exert different selective pressures on their food resources. Our results suggest that Old World fruit bat species interact with floral resources in different ways and may belong to different functional groups. Studying the unique selective pressures placed by different pollinator species is necessary to fully understand the evolutionary past and future of biotically-pollinated plants.

Local adaptation of Metrosideros polymorpha along a steep elevation gradient

Tomoko Sakishima, Abby Cuttriss, Don Price, Elizabeth Stacy

2A_302B-Trait Evolution
Sunday, June 22, 2014 9:30 AM-9:45 AM

Elevation gradients are important drivers of divergence in plants, yet little is known about which abiotic factors along these gradients are responsible for divergence. The endemic Hawaiian tree, `ōhi`a lehua (Metrosideros polymorpha), which dominates the forest canopies of Hawai`i Island, has diverged along elevation gradients in the forms of two pubescent varieties; M. polymorpha var. incana occurs in monotypic stands on young substrates at lower elevations, M. polymorpha var. polymorpha is monotypic at higher elevations, and purported hybrids are found in between. Previous studies revealed differentiation between early-successional var. incana and its late-successional counterpart, glabrous var. glaberrima, in light requirements at the seedling stage (at low to middle elevations). To better understand the abiotic factors that drive divergence in tree populations along elevation gradients, we are conducting field, greenhouse, and growth-chamber experiments on open-pollinated seedlings from six populations (20 families per population) of pubescent M. polymorpha spanning the full elevation range of this species (from near sea level to 2,470 m above sea level) on Hawai`i Island. The field experiment involves reciprocal transplants of seedlings from each sampled population into plots at each of the six elevations with mortality recorded monthly. Preliminary results indicate increased mortality of low and mid elevation seedlings compared to high-elevation seedlings at the highest-elevation site. Next, the greenhouse experiment exposes seedlings from the six elevations to three UV light levels to understand how UV light intensity affects survivorship at the seedling stage. Early results reveal significantly greater mortality under high-UV light of seedlings from the two highest-elevation populations, in contrast with expectations. Lastly, stress response tests are being done under extreme environmental conditions in a growth chamber (i.e., high UV radiation, low temperature, high temperature, and drought). Oxidative damage is visualized by leaf staining with nitro blue tetradium for detecting O2-, and 3,3’-diaminobenzidine for H2O2. We will discuss the results of these experiments in the context of divergence of long-lived tree populations along elevation gradients.

Constraints on the evolution of sex-biased gene expression in Drosophila serrata

Scott Allen, Steve Chenoweth

2A_302C-Sexual Selection
Sunday, June 22, 2014 8:30 AM-8:45 AM

Sexual antagonism is an inevitable phenomenon arising from sex-specific selection on genetically correlated traits. The evolution of sex-biased gene expression is one mechanism that may alleviate sexual antagonism. Although sex-biased transcripts are common, it is unclear whether extant levels of sexual dimorphism reflect fully or only partially resolved sexual conflicts, or have arisen via other evolutionary processes. While positive genetic covariances between the sexes may generate considerable constraint to the evolution of sexually dimorphic gene expression, further constraints likely arise due to the multidimensional nature of gene expression. For example, sex-specific responses to selection depend not only genetic (co)variances between genes within a sex, but also genetic covariances between genes, both within and between the sexes, for many other genes. To examine the extent of these constraints, we have assayed sex-specific fitness and genetic (co)variation in gene expression in a panel of 40 wild-derived lines of Drosophila serrata.

When mito-nuclear epistasis looks like genomic and sexual conflict

Michael Wade, Devin Drown

2A_302C-Sexual Selection
Sunday, June 22, 2014 8:45 AM-9:00 AM

We show how a gene’s eye view of simple mito-nuclear epistasis can give the appearance of mother’s curse acting on the mitochondrial genome or of intra-locus sexual conflict acting on the nuclear genome. We also show how either single-gene view misses important aspects of the inter-genomic co-evolutionary dynamic, including the potential for run-away co-evolution, the influence of inbreeding on mitochondrial evolution, and the potential for transient mito-nuclear disequilibria. We suggest that, in some instances, the perception of genetic conflict may be an ‘evolutionary spandrel;’ an adaptive single-gene interpretation of an essentially multi-locus adaptive process.

“Broad-Sense” Sexual Conflict: A New Model of Evolution of Resistance to Sexual Violence

Samuel Snow

2A_302C-Sexual Selection
Sunday, June 22, 2014 9:00 AM-9:15 AM

Current models of sexual conflict over mating largely conflate mating preference and resistance to forced copulation, and thus have focused narrowly on the direct fitness costs that females incur by mating with males that harm them. Recent work on antagonistic genital coevolution in waterfowl suggests that indirect fitness “opportunity” costs to females associated from forced copulation by non-preferred individuals may be key to understanding the evolution of traits such as female vaginal complexity that control rates of forced fertilization but not sexual attack. While the processes of behaviorally choosing mates and cryptically “choosing” them via genital complexity both affect male mating success, their effects are not additive. We propose a new, broader framework that treats behavioral preference and resistance to forced fertilization as explicitly independent traits. Using four-locus theoretical population genetic models, we show that female genital complexity can evolve via conflict over mate choice due to its role in enhancing females’ ability to retain attractive mates. Females that manage to resist coercion and mate with attractive males pass on those advantages to their offspring. Our broader concept of sexual conflict that incorporates indirect costs and multiple simultaneous forms of mate choice is necessary for understanding the evolution of traits that enhance sexual freedom of choice, and applies widely in natural systems.

Dissecting an intersexual genetic correlation for fitness using whole genome sequence data

Adam Reddiex, Steve Chenoweth, Thomas Gosden, Scott Allen

2A_302C-Sexual Selection
Sunday, June 22, 2014 9:15 AM-9:30 AM

The intersexual genetic correlation for fitness, rw(m,f), is a key parameter describing the evolutionary potential of sexual populations. For example, the independent evolution of males and females can be impeded when rw(m,f) is negative owing to a preponderance of sexually antagonistic genetic variation. Because rw(m,f) summarises the combined effects across all fitness-affecting loci in the genome, there are many potential combinations of alleles that could underlie a given value of rw(m,f). Alleles may vary in frequency, and their degree of pleiotropy on male and female fitness. To date, these parameters remain unknown for any organism. In this talk I will share our most recent attempts to address this shortcoming, using sex-specific fitness assays in a panel of over 100 fully sequenced lines of Drosophila serrata derived from a natural Australian population.

Between-sex genetic covariance constrains the evolution of sexual dimorphism in (everyone's favourtite) Drosophila melanogaster

Fiona Ingleby, Paolo Innocenti, Howard Rundle, Ted Morrow

2A_302C-Sexual Selection
Sunday, June 22, 2014 9:30 AM-9:45 AM

Males and females share much of their genome, and as a result, intralocus sexual conflict is generated when selection on a shared trait differs between the sexes. This conflict can be partially or entirely resolved via the evolution of sex-specific genetic variation that allows each sex to approach, or possibly achieve, its optimum phenotype, thereby generating sexual dimorphism. However, shared genetic variation between the sexes can impose constraints on the independent expression of a shared trait in males and females, hindering the evolution of sexual dimorphism. Here, we examine genetic constraints on the evolution of sexual dimorphism in Drosophila melanogaster cuticular hydrocarbon (CHC) expression. We use the extended G matrix, which includes the between-sex genetic covariances that constitute the B matrix, to compare genetic constraints on two sets of CHC traits that differ in the extent of their sexual dimorphism. We find significant genetic constraints on the evolution of further dimorphism in the least dimorphic traits, but no such constraints for the most dimorphic traits. We also show that the genetic constraints on the least dimorphic CHCs are asymmetrical between the sexes. Our results suggest that there is evidence both for resolved and ongoing sexual conflict in D. melanogaster CHC profiles.

Using fossils, ecology, and molecules to understand the mechanisms shaping dry forest bird species diversity and distributions

Jessica Oswald

2A_303-Macroevolution
Sunday, June 22, 2014 8:30 AM-8:45 AM

The historical processes that drive endemism, speciation, and community composition are important in understanding the mechanisms that underlie the spatial structure of species diversity. Neotropical dry forests are characterized by low diversity yet high endemism, and we combined survey methods with fossil and molecular analysis to evaluate the relative importance of the Neogene Andean uplift and Quaternary climate change had on shaping the diversity and distributions of birds in dry forests over time. To evaluate the effects of these two abiotic processes we censused six modern bird communities in NW Peruvian dry forests that are separated by the Andes Mountains, the Marañon Valley and the Tumbesian region. In addition, we studied one late Pleistocene community in the Tumbesian region with fossil data. We used genetic analyses to date relative divergence times in subspecies found across the region. Fossils indicate more extensive dry forests and a non-analog community at the Tumbesian site in the recent past. Therefore, historical climate change had a significant role in shaping distributions and community compositions. We predicted that the climatic instability through time in the Tumbesian region would result in more homogeneity in community composition across space as species track resources compared to the more stable Marañon Valley. To test this, we determined the betadiversity and phylobetadiversity across the bird communities with both presence-absence and abundance data. Each species was assessed as being significantly over- or underrepresented across sites to investigate which species were driving these patterns. Bird communities subjected to more climatic instability during the Pleistocene (the Tumbesian region) tended to be more similar to each other than those of more climatically stable areas (Marañon Valley). Based on species abundance, a majority of the 217 species of birds recorded were overrepresented in two or fewer communities. This indicates that there is a propensity for species to become specialized to various patches of forest across NW Peru. Bird communities differed significantly between the Tumbesian region and the Marañon Valley, suggesting that geologic barriers have significantly structured communities at a regional scale both in terms of species and phylogenetic composition. To determine how long the Andes have been a barrier to the movement of species we determined relative divergence time in mitochondrial genes between subspecies unique to Tumbes and the Marañon Valley. Our results suggest that historical climate change, Andean barriers, and specialization to local conditions have led to the high endemism found in NW Peru.

Macroevolutionary consequences of chemical defence in amphibians

Kevin Arbuckle

2A_303-Macroevolution
Sunday, June 22, 2014 8:45 AM-9:00 AM

Predators have driven the evolution of chemical defences such as poisons in a wide range of species. Although often costly to produce, such defences can relax behavioural constraints imposed by predators and allow prey species to exploit more ecological opportunities. Consequently, we might expect chemical defences to influence macroevolutionary processes such as speciation and extinction via their effects on niche space. Amphibians provide an ideal system in which to test these predictions due to the large number of extant species and variation in the presence or absence of chemical defences, mostly toxins. I therefore used trait-dependent diversification models to investigate whether chemical defence explains differences in speciation and extinction rates, as well as rates of gain and loss of chemical defence across the amphibian tree of life. These analyses reveal strong effects of chemical defence on diversification that help us understand the macroevolutionary consequences of antipredator mechanisms, the impact of predation in evolution, and could potentially inform conservation planning via knowledge of differential extinction risks.

Differences in evolutionary patterns and rates of general cognitive ability compared to neuroanatomical indicators in the primate phylogeny

Heitor Barcellos Ferreira Fernandes, *Michael Woodley*

2A_303-Macroevolution
Sunday, June 22, 2014 9:00 AM-9:15 AM

Various neuroanatomical indicators (NIs) are frequently used as proxies for general cognitive ability (g) in comparative studies, however their evolutionary patterns and rates have never been compared. With a sample of 174 primate species from all superfamilies, we tested the following predictions based on recent findings involving coefficients of additive variance in the homininan lineage: (1) evolutionary rates for g will be faster than those for NIs, (2) g will less phylogenetically conserved, and (3) evolutionary models fitted to g and to NIs will present at least moderately distinct parameter values. We obtained species means for g and for the most-used NIs in comparative studies: neocortex ratio (neocortex size/size of rest of brain), neocortex residualized (and phylogenetically residualized) against body size, brain size likewise residualized both ways, absolute brain size, and absolute neocortex size. Evolutionary rates (sigma-squared, with log-transformed values) were significantly faster for g than for NIs residualized against body size (four to twelve times, Cohen's d ranged from .5 to 1.3, depending on the evolutionary model fitted), and than for absolute NIs and for body size (two to three times, Cohen's d .4 to 1.1). Phylogenetic signal (PS) was significantly different from zero and from unity for g and for residualized NIs using Pagel's lambda but was smaller for g, and was equal to unity for absolute NIs and body size. Using Blomberg and colleagues' K, PS was nonsignificantly different from zero only for g, suggesting g is not importantly more similar among closely-related primate taxa than among distantly-related ones, whereas K surpassed unity only for absolute NIs and body size, indicating phylogenetic conservatism. To test prediction three we analyzed the fit of each variable to the Brownian-motion, lambda (PS smaller than unity), delta (acceleration), Ornstein-Uhlenbeck (stabilizing selection), and Early-Burst (exponentially decreasing niche-filling) models. Although relative AICc model weights for g did not differ strongly from those for body size-corrected NIs (with the lambda model as best fit), g presented a delta parameter-estimate around ten times larger, indicating stronger rate acceleration. The relative model weights for absolute brain and neocortex sizes greatly differed from the other variables however, and strongly conformed to the patterns presented by body size (Early-Burst and Brownian-motion models fitted best). Finally, g presented selection regime shifts in different nodes from NIs. Predictions were largely corroborated; the limitations and benefits of using the various NIs as proxies for g in comparative studies are discussed.

Using genetic variation to infer the comparative demographic history of avian populations in the West Indies

Maria Pil, *Robert Ricklefs*

2A_303-Macroevolution
Sunday, June 22, 2014 9:15 AM-9:30 AM

The sizes and distributions of populations vary over time, and episodes of expansion and contraction create characteristic patterns of genetic variation. Consequently, contemporary patterns of genetic diversity open a window onto demographic history. Here, we employ population genetics approaches to infer the demographic history of three tanager-like bird species in the West Indies: Coereba flaveola, Loxigilla noctis, and Tiaris bicolor. We analyzed genetic variation in two mitochondrial genetic markers for up to 33 individuals of each species on each of nineteen islands in the West Indies. Understanding the causes of change in population size requires a large sample of populations to determine statistical relationships between demography and attributes of islands and species. In addition, comparisons across multiple islands allow one to distinguish regional effects, for example related to climate fluctuations, and island-specific effects caused by localized environments or biological interactions. We used several indicators of population size change, including Tajima's D, Fu's FS, and mismatch distributions, to infer demographic history of the three species on each island, supplemented by Approximate Bayesian Computation (ABC), and signature shapes in haplotype networks to infer relationships among populations. All three species showed evidence of dynamic demographic histories, including genetic indicators of expansion in several island populations. Patterns of genetic variation and population expansion differed between species, but tended to correlate with island size. Island populations of C. flaveola and L. noctis were more differentiated over the archipelago than those of T. bicolor. Populations of all three species on Puerto Rico harbored higher genetic variability than on other islands and exhibited signatures of recent population expansion.

The combination of population genetic approaches used here can provide detailed insight into the demographic and geographic history among discrete island populations. By comparing several species from the same geographic area, one can disentangle species characteristics from regional effects to better understand factors that cause demographic change. The Caribbean experienced a cool, arid late Glacial, which progressed to a moister climate in middle-late Holocene. Following changes in habitat extent, as well as direct effects of climate on population parameters, bird populations could contract and expand in response to broad-scale environmental change. In contrast, populations could experience idiosyncratic changes related to specialized biotic interactions that are independent of general environmental conditions. With historical demographic data acquired by the analyses mentioned above, we determine whether populations these three species exhibit similar patterns and timing of expansion phases throughout the archipelago.

A bird's eye view of habitat fragmentation: comparing the effects at ecological and evolutionary timescales in two sister species

Kin Han, Garth Spellman, Rebecca Kimball

2A_303-Macroevolution
Sunday, June 22, 2014 9:30 AM-9:45 AM

Habitat loss and fragmentation is considered to be one of the greatest threats to biodiversity today. As habitats become more fragmented, populations become more isolated as gene flow between them decreases. We used microsatellites to examine the effects of habitat fragmentation at two different timescales, ecological and evolutionary. We compare genetic structure of brown-headed nuthatches (Sitta pusilla), which occupy (formerly contiguous) pine forests of the southeastern US that have been fragmented on an ecological timescale, to their closely related sister species, pygmy nuthatches (S. pygmaea). Pygmy nuthatches occupy ponderosa pine forests in sky islands of western North America and have been fragmented on evolutionary timescales. We genotyped 290 brown-headed nuthatches from 12 Florida populations and 120 pygmy nuthatches from 11 populations throughout their range. Although we would expect to see much greater structure in pygmy nuthatch populations due to the large geographic range sampled and presumably greater isolation, that was not the case. Instead, analyses indicate similar genetic structure between the two species. We test several hypotheses, both biological and artefactual, to explain our observations, including higher than expected rates of dispersal or by recent postglacial expansion of a large population into the present range with insufficient time for divergence. Alternatively, the low level of structuring in pygmy nuthatches could be an artefact of the lower sample sizes for this species.

Experimental Measures of the Costs of Complexity for Horizontal Gene Transfer

Artur Romanchuk, Corbin Jones, Christina Burch

2A_304-Microbial Evolution
Sunday, June 22, 2014 8:30 AM-8:45 AM

The addition of a gene to a genome, whether by duplication or horizontal gene transfer, imposes energetic and functional costs. Functional costs are predicted to increase with connectivity (protein-protein interactions), whether the costs arise from gene mis-regulation or from a failure of divergent homologues to make normal protein-protein interactions. I will discuss two experimental approaches that we used to disentangle the costs associated with gene misregulation and with protein interaction failure. We used existing plasmid libraries that enabled the transfer into E. coli and overexpression of 4102 E. coli genes, 90 S. aureus genes, and 90 V. cholerae genes, and measured the cost of transfer using a combination of pairwise (2 strains) and bulk (4102 strains) competition assays. Our data recapitulate the comparative observation that informational genes are less transferable than other genes, and reveal a strong dependence of the cost of connectivity on the degree of divergence between the transferred and native homologues. The cost of overexpression unexpectedly decreased with connectivity among the non-divergent E. coli genes, but increased with connectivity among the most divergent S. aureus genes. Thus, the cost of complexity differed depending on the mechanistic basis of the cost -- gene misregulation or protein interaction failure.

Fitness Effects of Cell-to-Cell Expression Heterogeneity in Saccharomyces cerevisiae

Christopher Morales, Isaak Heon, Kashyapa Bandaralage, Joshua Rest

2A_304-Microbial Evolution
Sunday, June 22, 2014 8:45 AM-9:00 AM

A small fraction of proteins show significant cell-to-cell heterogeneity in their expression levels among clonal, well-mixed Saccharomyces cerevisiae cells. It is known that the fitness effects of variation in protein expression levels among populations of cells are highly nonlinear; cells may be tolerant to wide variation in the expression level of a protein, or sensitive to even small changes. However, the consequences of cell-to-cell expression differences have not been widely studied. Here, we separate populations of cells into fractions expressing high, medium, and low levels of a single gene at a time, based on the intensity of a fused fluorescent tag. We find that extreme cell-to-cell heterogeneity in the expression level of highly expressed proteins results in dramatic differences in cellular growth rate. We also assess growth patterns of heterogeneous cells across various stress environments in order to evaluate the hypothesis that these differences in growth rate, as well as the underlying heterogeneity in protein expression, are part of a bet-hedging strategy. In bet-hedging, individuals within a population take on phenotypic states that are sub-optimal in the current environment, but well suited to other commonly encountered environments, thereby increasing the overall fitness of the population in the face of environmental change.

Genetics of Ecological Specialization and Incipient Speciation in an Experimental Population of E. coli

Zachary Blount, Richard Lenski

2A_304-Microbial Evolution
Sunday, June 22, 2014 9:00 AM-9:15 AM

In the absence of sexual reproduction, microbial species concepts emphasize ecological divergence rather than reproductive isolation as in Mayr’s Biological Species Concept (BSC). Cohan’s Ecotype Species Concept (ESC) identifies bacterial speciation with niche discovery mutations (NDMs) that permit invasion of a novel niche. In the new niche, a mutant lineage can pursue an evolutionary trajectory independent of its parent. This trajectory may involve the accumulation of mutations that improve fitness in the new niche while reducing fitness in the ancestral one. These niche-specific adaptive mutations (NSAMs) promote ecological specialization. Because NSAM fitness benefits are dependent upon the presence of the NDM, they can also present barriers to successful inter-ecotype horizontal gene transfer analogous to reproductive isolation.

After 31,000 generations of an ongoing long-term evolution experiment (LTEE) with E. coli carried out in glucose-limited medium that also contains a large amount of citrate, we observed the evolution of an aerobic citrate-using (Cit+) phenotype. This Cit+ phenotype transcends the accepted range of variation for E. coli, and permitted access to a large, previously unavailable resource. The Cit+ subpopulation rose to numerical dominance of the population, but a Cit– subpopulation persisted. Extensive whole genome sequencing has confirmed that the two subpopulations are divergent ecotypes.

We have previously shown that the Cit+ lineage improved markedly in its fitness in DM25 through 40,000 generations while also losing fitness on glucose. This pattern strongly suggested that niche-specific adaptive mutations (NSAMs) have been accruing in the Cit+ lineage. We identified a number of candidate NSAMs in evolved Cit+ genomes. We then used recombineering to move these candidates into Cit+ and Cit– genetic backgrounds, and examined their background-dependent fitness effects. We identified a number of NSAMs that improve fitness in a Cit+ background, but reduced fitness in a Cit– one, including mutations in the citrate synthase, gltA, and isocitrate lyase, aceA, genes. These NSAMs provide a genetic basis for the ecological specialization observed in the Cit+ lineage, and further suggest that Cit+ is an incipient species under criteria that fit both the ESC and BSC.

Ants show distinct gut microbiome convergence at opposite ends of the trophic scale

Jacob Russell, Piotr Lukasik, Yi Hu, Benjamin Rubin, Corrie Moreau

2A_304-Microbial Evolution
Sunday, June 22, 2014 9:15 AM-9:30 AM

Ants are among the world's most abundant terrestrial animals, with dominant roles in many ecosystems. While known as symbiotic creatures, symbioses with bacteria have not been explored in a systematic fashion across this diverse group. Our research aims to uncover the drivers and implications of such associations. Through a combination of molecular screening and next generation sequencing, we have characterized microbial communities and symbiont distributions across ants from four geographic locations, spanning much of the family phylogeny and much of the trophic scale. We find notable convergence among ants from herbivorous and predatory ends of the food chain, with unrelated ants from the same trophic extremes harboring overlapping communities of specialized gut bacteria. Ants from distinct herbivore or predator groups seem to harbor taxon-specific communities, suggesting impressively long-term evolution between some host taxa and their gut bacteria. In summary, these trends reveal a great importance for diet and ecological niche in favoring the origin of specialized symbiotic associations, while also suggesting an importance for particular bacteria within such niches. Our findings, thereby implicate bacteria as substantial players in the evolution of some ants. Yet the lack of such specialized associations across many ant groups hints that such symbioses may be a defining feature at the very ends of the food chain.

Ecological diversification of Vibrio fischeri during the planktonic phase and subsequent consequences for squid host colonization

Michele Nishiguchi, William Soto, Michael Travisano

2A_304-Microbial Evolution
Sunday, June 22, 2014 9:30 AM-9:45 AM

Stable microcosm experiments with bacteria have become model systems for studying microbial ecological diversification, whereby standing liquid cultures founded by planktonic, water-column inhabiting cells that form smooth colonies (smooth morphs) on agar plates differentiate into alternative types due to resource competition as a result of mutations. These variant cell types can either establish pellicle and/or benthic populations in structured, undisturbed, and heterogeneous microcosms. When grown on agar plates, the derived cell types can form wrinkled and fuzzy colonies (wrinkly-spreaders and fuzzy spreaders). Bacteria in the family Vibrionaceae are gram-negative bacteria living in marine and brackish waters as planktonic cells and biofilms attached to abiotic surfaces or eukaryotic host cells. In particular, Vibrio fischeri is a marine bioluminescent microbe that exists mutualistically with sepiolid squids and monocentrid fishes. Although V. fischeri has been well studied as a beneficial bacterium during host colonization, adaptive radiation during the free-living phase due to mutations and the accompanying effects on animal host colonization are poorly understood. V. fischeri wrinkly-spreaders that evolve in stable microcosms as free-living cells are competitively superior during squid colonization relative to their smooth morph ancestors, indicating that simple de novo mutations can significantly affect symbiosis. Understanding how bacteria are capable of adapting to fluctuating conditions in the environment may provide insight to how organisms accommodate these changes to their dual life history between planktonic and symbiotic states.

Comparing Patterns of Molecular Evolution in Nuclear-Encoded Mitochondrial Genes in Sexual and Asexual Lineages of a New Zealand Freshwater Snail

Michelle Sullivan, Joel Sharbrough, Jeffrey Boore, John Logsdon, Maurine Neiman

2A_305A-Molecular Evolution
Sunday, June 22, 2014 8:30 AM-8:45 AM

Nuclear-encoded mitochondrial (NEM) proteins directly interact with mitochondrial-encoded (MT) proteins to form multi-subunit enzymes necessary for mitochondrial function. The cooperative nature of NEM and MT proteins suggests that the genes that encode these proteins may coevolve and raises the question of how these cooperative relationships are maintained despite the fact that these two critical sets of genes are housed in two very different genomes. NEM and MT coevolution might itself be profoundly influenced by reproductive mode (sexual vs. asexual reproduction) because 1) NEM and MT genes are transmitted in complete linkage disequilibrium in asexuals but bi-parental inheritance and recombination of nuclear genes breaks down NEM and MT gene linkage in sexuals, 2) nuclear mutations may counter or compensate for harmful mtDNA mutations that often accumulate in asexuals at higher rates than related sexuals, and 3) the particularly tight coevolution between NEM and MT genes encoding subunits of mitochondrial enzymes in asexual vs. sexual lineages may reduce the potentially harmful effects of mutation accumulation. Here, we use Potamopyrgus antipodarum, a New Zealand freshwater snail, to address these possibilities. Potamopyrgus antipodarum is ideally suited for evaluating how reproductive mode influences coevolution of mitochondrial and nuclear genes because sexual and asexual P. antipodarum often coexist and compete in nature and because there have been multiple independent transitions to asexuality, allowing for direct comparisons between sexuals and asexuals without introducing potentially confounding effects of genetic background or source population. We are currently sequencing NEM genes in 26 asexual and nine sexual P. antipodarum lineages to compare patterns of molecular evolution in NEM genes and all 13 MT genes across reproductive modes. While data collection and analyses are ongoing, we have already detected polymorphisms at nucleotide sites at the NEM-MT interface, suggesting the potential for compensatory evolution. Regardless of outcome, the data we are collecting will provide new insights into how reproductive mode influences patterns of molecular evolution in coevolving genes, and more broadly, how the lack of sex affects molecular evolution in the nuclear vs. the mitochondrial genome.

Analysis of six gene sets in the chimpanzee lineage illustrates the differential action of natural selection upon coding and non-coding sequences

Arcadi Navarro, Gabriel Santpere, Elena Carnero-Montoro, Natalia Petit-Marty, Francois Serra, Christina Hvilsom, Jordi Rambla, Txema Heredia, Daniel Halligan, Hernan Dopazo, Elena Bosch

2A_305A-Molecular Evolution
Sunday, June 22, 2014 8:45 AM-9:00 AM

We investigate the selective forces acting in the coding and non-coding regions of six different functional and evolutionary gene sets: i) two reference sets presenting accelerated and slow rates of protein evolution (Complement and Actin pathways), ii) a set of genes with evidence of accelerated evolution in at least one of their introns; and iii) three gene sets related to neurological function (Parkinson, Amyloid and Presinilin). To that effect, we combine human-chimpanzee divergence patterns with polymorphism data obtained from target resequencing 20 central chimpanzees. By using the DFE-alpha extension of the McDonald-Kreitman test, we reproduce inferences of rates of evolution previously based solely on divergence data on both coding and intronic sequences and also obtain inferences for other classes of genomics elements (UTRs, promoters and trailers). We confirm that the accelerated rates of divergence previously inferred in coding and non-coding elements can be attributed to positive selection and not to relaxation of purifying selection and find consistent trends of recent evolutionary constraint in the coding sequences from all three neurological pathways. Interestingly, particular genes and introns that in our reference sets i) and ii) did not present accelerated rates of divergence do show high rates of adaptive substitution when combining polymorphism and divergence data. Such a pattern suggests that each class of genomic element tends to evolve under particular adaptive forces within the same pathway or evolutionary gene set. On the contrary, the adaptive history of coding and non-coding sequences within each dataset analyzed seems to be decoupled.

Molecular evolution of anthocyanin pigment genes during flower color transitions

Winnie Ho, Stacey Smith

2A_305A-Molecular Evolution
Sunday, June 22, 2014 9:00 AM-9:15 AM

Understanding the predictability of genetic changes associated with phenotypic evolution is a main focus of evolutionary biology. In the Iochrominae clade (Solanaceae), losses of floral anthocyanin pigments have resulted in multiple transitions from blue to white or yellow phenotypes. This repeated evolution of floral color presents an ideal opportunity to determine if repeated phenotypic transitions involve similar genetic changes and have consistent consequences for subsequent evolution of pathway genes. Here, we test the hypothesis that pigment pathway genes experience changes in selective pressure during and following losses of floral pigmentation. Focusing on three genes (CHI, F3H, DFR), we find that white-flowered lineages have maintained full coding length sequences with no clear evidence of pseudogenization. However, maximum likelihood analyses reveal that all of the genes have higher ratios of non-synonymous and synonymous substitutions (dN/dS) in white vs. blue lineages, consistent with relaxed constraint or selection for new functions following the color shifts. These results support the hypothesis that transitions from blue to white flowers, and the associated losses of anthocyanin production lead to predictable changes in selection pressures on pigment pathway genes.

Molecular evolution of the selfish sex-ratio X-chromosome in Drosophila neotestacea

Kathleen Pieper, Kelly Dyer

2A_305A-Molecular Evolution
Sunday, June 22, 2014 9:15 AM-9:30 AM

Sex-ratio (SR) is a selfish X-chromosome that kills Y-bearing sperm in carrier males. In Drosophila neotestacea, SR is found in wild populations at stable frequencies of up to 30%. I sampled SR and standard (ST) X-carrying males from across the geographic range for DNA sequence polymorphism at 12 X-linked markers and 7 autosomal markers. I found that SR is derived from ST, and inversions on SR limit gene flow between them to cause genetic differentiation. The ratio of nucleotide polymorphism between SR and the autosomes is lower than for ST but higher than expected given SR's average species-wide frequency, which could result from occasional recombination between SR and ST. High, stable frequencies of SR, clear evidence of genetic differentiation, and potential long term-maintenance through recombination strongly suggests that SR has had a large impact on genome evolution in this species.

Structure and function of sites under positive selection

Greg Slodkowicz, Nick Goldman

2A_305A-Molecular Evolution
Sunday, June 22, 2014 9:30 AM-9:45 AM

Selective pressure acting on a protein-coding gene can be estimated by comparing the ratio of non-synonymous substitutions per non-synonymous site to synonymous substitutions per synonymous site (dN/dS). Values of dN/dS larger than 1 are indicative of positive selection, whereas dN/dS

Most analyses of selective constraint to date were conducted without regard for functional and structural characteristics or were limited to a small set of genes. Here, we attempt a global characterisation of selective pressures, taking into account the impact of structural and functional features. Using a method previously developed in the group, Sitewise Likelihood Ratio, we obtain estimates of selective constraint in the coding genome (9 million sites in total) in different mammalian species groups. These data indicate that the selective pressure on a site is strongly affected by structural features such as relative solvent accessibility and secondary structure. We also identify the pathways and domain types enriched in regions under positive selection. In addition to providing insight into the evolutionary history of mammals, these findings have implications for development of more powerful methods of detecting positive selection.

Gene expression explains patterns of evolution in tRNA synthetase genes interacting with mitochondrial and cytosolic tRNAs

Jeffrey Adrion, P. Signe White, Kristi L. Montooth

2A_305B-Gene Expression
Sunday, June 22, 2014 8:45 AM-9:00 AM

Mitochondrial translation requires physical interactions between tRNAs encoded by the mitochondrial genome and aminoacyl tRNA synthetase (aaRS) proteins encoded by the nuclear genome. In animals, it has been suggested that mitochondrial tRNAs (mt-tRNAs) experience higher rates of mildly deleterious nucleotide substitutions relative to their nuclear-encoded counterparts (cyt-tRNAs). This dynamic provides an opportunity for elevated rates of compensatory evolution of aaRS proteins interacting with mt-tRNAs (mt-aaRS), relative to aaRS proteins interacting with cyt-tRNAs (cyt-aaRS). We demonstrate that mt-aaRS genes do evolve at significantly higher rates (exemplified by higher dN and dN/dS) relative to cyt-aaRS genes, across mammals, birds, Drosophilids, and the Nasonia group of parasitic wasps. While these results are consistent with a compensatory evolution hypothesis, a more universal predictor of protein evolutionary rate is the level of gene expression. To attempt to disentangle these competing hypotheses, we 1) relate levels of gene expression (FPKM) with dN/dS across a set of aaRS genes, 2) test whether individual sites in aaRS genes are under positive selection, and 3) evaluate patterns of polymorphism and divergence in Drosophila. We show that FPKM explains much (19-49%) of the variance in dN/dS across aaRS genes; cyt-aaRS genes are more highly expressed and have lower values of dN/dS relative to mt-aaRS genes across all taxa analyzed. Moreover, we are unable to detect any individual sites under significant positive selection in either class of aaRS genes, and the neutrality index of all aaRS genes is indicative of genes experiencing purifying selection. We thereby conclude that the level of gene expression may be the most parsimonious hypothesis for the rates of substitution observed in proteins interacting with mitochondrial versus cytoplasmic factors.

Gene expression alterations trigger adaptve diffusion after recurrent allopolyploidization in Dactylorhiza (Orchidaceae)

Ovidiu Paun, Francisco Balao, Maria Teresa Lorenzo, Daniel Jacob Diehl, Bao-Hai Hao, Mikael Hedren

2A_305B-Gene Expression
Sunday, June 22, 2014 9:00 AM-9:15 AM

Hybridization and whole-genome duplication have been central to angiosperm evolution, but early-generation allopolyploids need to accommodate two divergent genomes into a single nucleus by adjusting organization and function, thereby influencing the adaptive success and the evolutionary fate of resulting lineages. Most allopolyploids have multiple origins, but the long-term significance of iterative allopolyploid evolution is not fully understood. Ecologically-divergent allopolyploids Dactylorhiza majalis and D. traunsteineri (Orchidaceae) have been independently formed through unidirectional hybridization between the widespread diploids D. fuchsii and D. incarnata. By using over 6,000 informative SNPs filtered from restriction site associated DNA sequencing (RADseq) we document a genome-wide absence of genetic differentiation between these allopolyploid lineages despite the visible phenotypic divergence. In addition, we bring evidence of frequent gene flow between the polyploids in sympatry, which points toward a very strong divergent selection required in order to maintain the observed phenotypic divergence. We discuss the reduced efficiency of drift to altering gene frequencies in polyploid populations, and the apparently limited homoeolog repatterning that affected these allopolyploid genomes, a mechanism that has been elsewhere reported to result in reproductive isolation between recurrently formed allopolyploids. By using the sibling allopolyploids of different ages we investigate with RNAseq the progression through time of gene expression alterations after allopolyploidization, and their importance to the ecological properties of the polyploids. We observe a trend of increased overexpression of genes in the younger polyploid D. traunsteineri in comparison to D. majalis, whose transcriptome generally resembles more closely those of the diploid parents. The differential expression between the polyploids is mainly driven by a general parental dominance in opposite directions, a pattern retained in part also at the level of transgressively expressed genes. We discuss the importance of qualitative versus quantitative expression alterations in allopolyploid genomes, and their role for diversification and evolution in general.

Detecting relationships between integrated thermal environments & current gene expression profiles in corals

Megan Morikawa

2A_305B-Gene Expression
Sunday, June 22, 2014 9:15 AM-9:30 AM

Organisms are constantly responding to changes in environment. Many have evolved acute stress responses to deal with environmental extremes, for example the heat shock response in coral prior to bleaching. Yet over longer periods of time, organisms have also evolved mechanisms to integrate sub-lethal changes in environment, leading to an eventual physiological response. Notable examples include chilling hours required for bud breaking in plants as well as light & temperature durations to trigger leaf senescence. In this study, we focus on sub-lethal thermal integration in coral. Evidence for coral thermal integration is most notably summarized in the Degree Heating Week cumulative heat stress metric utilized by the NOAA Coral Reef Watch program to predict bleaching susceptibility on a global scale. Yet the index is based only on deviations in sea surface temperatures and the biological underpinning of thermal integration has not yet been extensively explored. In other organisms, microarrays and RNAseq have been used to elucidate patterns of gene expression associated with integrated thermal stress, (i.e. increase in expression of metabolic pathways after a duration and degree of chilling hours before bud breaking in plants). This study focuses on utilizing nearly continuous temperature data experienced by individual coral colonies from American Samoa up to six months prior to transcriptome collection to assess gene expression clusters that best describe integrated thermal profiles, similar to that in bud breaking plants. We do so by assessing the temperature threshold and integration of exposure that seems to best describe contemporary expression of pathways. Doing so may refine our understanding of coral thermal integration in the face of climate change.

Thermal reactionome of the temperate forest ants Aphaenogaster rudis and A. picea

John Stanton-Geddes, Andrew Nguyen, Nicholas Gotelli, Sara Helms Cahan

2A_305B-Gene Expression
Sunday, June 22, 2014 9:30 AM-9:45 AM

Temperature plays a prominent role in structuring biological diversity from molecular to macroecological scales. While thermal reaction norms at the level of organismal phenotype have been characterized in hundreds of insect species, little is known about how these are manifested at the level of genes underlying thermal tolerance, or how gene expression profiles respond evolutionarily to environmentally mediated selection. To characterize global gene expression in response to thermal stress (the "thermal reactionome"), we performed RNAseq analysis using a novel response-surface sampling design at 3.5°C temperature intervals across a 40°C temperature range in two closely related eastern North American ant species, Aphaenogaster rudis and A. picea, which have more southern and northern distributions, respectively. We identified over 8,000 transcripts, ~8% of the total, that were thermally responsive in the two species. Candidate genes such as heat shock protein 90, heat shock protein 20 and heat shock protein 30 were upregulated at high temperatures. Gene set enrichment analysis found six gene ontology (GO) terms that were enriched at high temperatures including “gene expression” and “regeneration”. 60 GO terms were enriched at low temperatures including 16 “metabolic process” terms. 11 GO terms were enriched at intermediate temperatures including 6 terms involved in lipid biosynthetic or metabolic processes. Overall comparisons of the thermal reactionomes between the two species revealed that about 90% of the differences were due to changes in the slope and curvature, rather than the means, for the reaction norms of gene expression. Many of the responsive genes would have been missed if a reaction norm approach had not been used. While both species activated about the same number of genes in response to heat stress, the northern species A. picea activated about 36% more genes in response to cold temperatures than A. rudis. In addition, both species activated 3-4x more genes in response to cold then warm temperatures. Together, these results suggest there is a genetic basis to the observation from phenotypic studies that critical maximum temperatures are less variable than critical minimum temperatures in Aphaenogaster and other ecototherms. A key implication of this conclusion is that temperate ant species may have a constrained potential to acclimate and adapt to global warming.

FlatNJ: A novel network-based approach to visualize evolutionary and biogeographical relationships

Monika Balvociute, Andreas Spillner, Vincent Moulton

2A_306A-Methods for Migration
Sunday, June 22, 2014 8:30 AM-8:45 AM

We introduce FlatNJ, a new method for producing a special type of phylogenetic networks known as planar split networks. Properties of these networks will be discussed by showing a few application examples followed by an overview of the method itself, which generalizies the popular NeighborNet method.

Planar split networks are a type of phylogenetic networks that can be drawn in the plane without edge crossings, facilitating exploratory data analysis. They can be used to detect and visualize potential relationships between sequence evolution and other aspects of a data set such as, for example, the geographic distribution of the corresponding organisms as well as indicate possible conflict in the data (e.g., in case of recombination). The main advantage of using planar split networks instead of phylogenetic trees is their ability to provide a more complete overview of the data when a single tree is not appropriate.

MIGRATE 4.0: many loci, divergences, and assignments

Peter Beerli

2A_306A-Methods for Migration
Sunday, June 22, 2014 8:45 AM-9:00 AM

New development of the Bayesian inference program MIGRATE (version 4.0; http://popgen.sc.fsu.edu) extend the available population models to divergence time estimation among populations. The new divergence model can handle situations that require an indpendent ancestral population and also situations where one of the sampled populations is also ancestral, resulting in models with fewer parameters. All models (migration, divergence) can be mixed and can be compared and ordered according to the marginal likelihood. Additionally, an assignment module was added. This module allows probabilistic assignment of individuals with unknown population-labels. The assignment is model-based and integrated with the other models available in MIGRATE; it assumes a particular migration/divergence model of which some or most individuals have known population-labels. Such assignment problems arise, for example, when we want to calculate the assignment probability of invasive species to known native populations.

General extensions of Qst/Fst for detecting adaptation in quantitative traits

Jeremy Berg, Graham Coop

2A_306A-Methods for Migration
Sunday, June 22, 2014 9:00 AM-9:15 AM

Understanding how adaptation has shaped variation across populations for a wide array of traits is a topic of great interest in evolutionary biology. One commonly used tool to aid in this endeavor is the Q_st/F_st comparison. In the simplest version, one measures the fraction of additive genetic variance for a quantitative trait that is among populations rather than within (Q_st), and then compares that value to F_st, an identical measure for neutral genetic variation. Under a set of restrictive assumptions, Q_st will be equal to F_st on average if the trait is neutral, and the distribution of their ratio will be chi-squared.

In the last decade, there has been a resurgence of statistical methods development work focused on expanding the general Q_st/F_st framework to use more of the available data, either incorporating information about the genetic covariances among multiple traits which one may wish to examine concurrently, or about patterns of population structure which are not adequately captured by the univariate measure F_st.

Building on this work, we show that the Q_st/F_st comparison can be see as a special case of a very general multivariate hypothesis testing framework. Using theory and simulations, we show how this generalized Q_st/F_st framework admits wide flexibility for investigators to chose specific hypotheses about the data they wish to test, providing increased statistical power and resolution to identify traits or populations which may be of further interest.

Evaluating methods for estimating effective population size in the presence of migration

Kimberly Gilbert, Michael Whitlock

2A_306A-Methods for Migration
Sunday, June 22, 2014 9:15 AM-9:30 AM

Effective population size (Ne) is a fundamental and useful metric in population genetics and evolutionary biology. Estimating Ne from genetic data has increased with the rise of affordable genotyping technology, however, the assumptions that multiple genetic methods rely on may be violated in natural situations, resulting in inaccurate estimates. We simulated various demographic histories of populations including ideal, isolated populations and various migration scenarios to assess the ability of different methods to estimate true effective population size. We find variation in the performance of methods across our different scenarios with no single method appearing to function universally. Our results also show that the majority of methods perform poorly at the largest effective population sizes. The linkage disequilibrium method (LDNe) performed well in the majority of scenarios, but is outperformed in scenarios with higher migration rates by a method accounting for migration (MLNe).

Parallel MCMC and Inference of Ancient Demography under the Isolation with Migration (IM) Model

Arun Sethuraman, Jody Hey

2A_306A-Methods for Migration
Sunday, June 22, 2014 9:30 AM-9:45 AM

The Isolation with Migration (IM) model has been utilized extensively for the inference of ancestral demography using putatively neutral genomic data. Among the parameters inferred under this model, are pair-wise migration rates, effective population sizes, and divergence times. The most widely used framework employs Markov-Chain Monte-Carlo (MCMC) based sampling of genealogies (Nielsen and Wakeley 2001). However such MCMC-based genealogy samplers suffer some from a state space that grows super exponentially with the size of the data (i.e. # of individuals and # of loci) and from a slow approach to stationarity for larger data sets (i.e. poor mixing). For example the IMa2 program (Hey and Nielsen 2007, Hey 2010) is difficult to use for large numbers of loci because of these issues. We addressed these problems by extending the current code using a parallel algorithm for MCMC, following Altekar et al (2004). The parallel version of IMa2 is capable of running multiple chains on each processor or node, and Metropolis coupling between independent MCMC spaces is invoked by swapping temperatures of chains, also known as (MC)3. We implement both the global and point to point exchange schemes as proposed by Altekar et al (2004), and explore efficiency and speed of the algorithm with a large data set from human hunter gatherer populations. Parallel IMa2 is written in C++, with OpenMPI, and both serial and parallel versions of the software, and source code will be made available through the Hey Lab website (https://bio.cst.temple.edu/~hey/software/software.htm).

Accelerated Anchored Phylogenomics: A new paradigm enables 10-fold increase in throughput and 10-fold decrease in cost for phylogenomics.

Alan Lemmon, Michelle Kortyna, Felipe Grazziotin, Lisa Barrow, Emily Lemmon

2A_306B-Methodology
Sunday, June 22, 2014 8:30 AM-8:45 AM

Targeted hybrid enrichment is quickly becoming one of the dominant forms of phylogenomic data collection, because of its broad application, utility for poor-quality samples, and low cost relative to other approaches. Previous improvements in laboratory and bioinformatic workflows produced a pipeline with a throughput of ~5000 samples per year per laboratory. Here, we present a new paradigm-shifting approach that has the potential to accelerate data collection by a factor of 5-10, thereby enabling a single laboratory to collect hundreds or thousands of loci for ~50,000 taxa in a single year. For example, this level of throughput could facilitate one research laboratory to collect phylogenomic-scale data for every vertebrate species in just over one year, or for every insect species in ~20 years. The new method also reduces costs by up to an order of magnitude, thus bringing phylogenomic-scale data collection within reach of all researchers working in phylogenetics, phylogeography, and population genomics.

Anchored Phylogenomics in Angiosperms: Maximizing Data Compatibility Through Coordinated Locus Selection

Chris Buddenhagen, Alan Lemmon, Emily Lemmon, Austin Mast

2A_306B-Methodology
Sunday, June 22, 2014 8:45 AM-9:00 AM
Targeted enrichment of DNA libraries prior to next generation sequencing permits the assembly of datasets with 100s or 1000s of putatively orthologous loci from across the genome for sophisticated species tree inference. A potentially transformative goal for the angiosperm phylogenomics community is agreement on a common set of target loci, since it would potentially remove the marker development step and maximize data combinability across studies. With collaborators we have identified and validated the candidate set of loci suitable for target enrichment across angiosperms. We began with the 959 genes previously identified by other researchers as apparently single-copy in the genomes of Arabidopsis, poplar, grape, and rice, identified the corresponding exons in Arabidopsis, found that 3050 of the exons were above a threshold size necessary for enrichment, and narrowed these down further to 1721 exons that are ≥55% similar between Arabidopsis and rice. Using these two taxa as a reference we then identified orthologous regions from 33 complete angiosperm genomes (representing the phylogenetic breadth of angiosperms, including Amborella) and nine low-coverage genomes that we produced for non-model angiosperms. 499 of the exons had an average copy number ≤1.2 and occurrence in ≥85% of the genomes. The sequences for those 499 exons in 26 genomes were used to produce a custom Agilent SureSelect Target Enrichment Kit. We enriched genomic libraries for 50 angiosperms, representing orders from across the phylogeny (Poales, Brassicales, Dipsacales, Caryophyllales, Proteales, and Magnoliales). The kit had an average enrichment success of 93.6% of the targets across the 50 species (range = 82.4–98.2%), and the assembled locus length averaged 903 bases (range = 428–2766) for the 50 species. Variability in the 499 target regions (the exons; with an average pairwise distance of 75.3%) produced a phylogeny for 91 taxa (the 50 enriched species, the 33 angiosperms with complete genomes used in the earlier step, and nine non-model angiosperm with low-coverage genomes) that was broadly consistent with previously published whole plastid phylogenies when those agreed with previous functional-nuclear-phylogenomics results, but it echoed (mostly) the latter when the previous plastid and nuclear results did not agree. We will discuss utility of the flanking regions at shallow levels of the phylogeny in a second talk.

Is the general time-reversible model bad for phylogenetics?

Barbara Holland, Jeremy Sumner, Peter Jarvis

2A_306B-Methodology
Sunday, June 22, 2014 9:00 AM-9:15 AM
The general time-reversible (GTR) model has been the workhorse of molecular phylogenetics for the last decade. GTR sits at the top of the ModelTest hierarchy of models (Posada and Crandall 1998) and, usually with the addition of invariant sites and a gamma distribution of rates across sites, is currently by far the most commonly selected model for phylogenetic inference. However, a recent publication (Sumner et al. 2012) shows that GTR, along with several other commonly used models, has an undesirable mathematical property that may be a cause of concern for the thoughtful phylogeneticist.

In mathematical terms, the problem is simple: matrix multiplication of two GTR substitution matrices does not return another GTR matrix. It is the purpose of this talk to give examples that demonstrate why this lack of closure may pose a problem for phylogenetic analysis and thus add GTR to the growing list of factors that are known to cause model misspecification in phylogenetics.

A history of arrivals and subsequent diversification in Madagascar: A case study from the myrrh genus, Commiphora Jacq. (Burseraceae).

Morgan Gostel, Andrea Weeks

2A_306C-Phylogenetic Systematics
Sunday, June 22, 2014 8:30 AM-8:45 AM
The myrrh genus, Commiphora Jacq. (Burseraceae), is the most species rich in the Burseraceae, yet its diversity is poorly understood. We have sampled approximately 61% of species in the genus and over 90% of species from Madagascar. A nearly comprehensive sampling of Madagascan Commiphora has contributed to a molecular phylogeny based on two nuclear (ETS and ITS) and three chloroplast spacers (ndhF–rpl32, psbA–trnH, and trnD–trnT). Previous studies have suggested that Commiphora has resulted from two dispersal events from continental Africa to Madagascar; however, we report a minimum of four such dispersal events. We have estimated the timing of these dispersal events and propose areas of endemism using species range and geographic information. Using this information, we perform ancestral area reconstruction to test three biogeographic hypotheses for each of the four radiations of Madagascar Commiphora. We identify shortcoming for understanding diversification in Madagascar and suggest mechanisms to overcome such challenges.

Phylogenomics and the Evolution of Paedomorphism in the Cyprinidae

Milton Tan, Carla Stout, Alan Lemmon, Emily Lemmon, Jonathan Armbruster

2A_306C-Phylogenetic Systematics
Sunday, June 22, 2014 8:45 AM-9:00 AM
The phylogenetic relationships of paedomorphic members of the Cyprinidae (species in the genera Paedocypris, Danionella,

Sundadanio) have been challenging to infer. Morphological studies suggest that these paedomorphic taxa form a single clade, while multiple molecular studies have presented conflicting relationships with high support. Molecular phylogenetic studies that included mitochondrial sequences unite Paedocypris and Sundadanio as sister genera, while a study that included only nuclear loci place these three genera in disparate parts of the phylogeny. To address this difficult phylogenetic problem, we utilized sequence capture to enrich 393 loci in these fishes for a phylogenomic-scale study. Preliminary analysis of 99 single-copy loci revealed that Paedocypris, Danionella, and Sundadanio do not form a clade, and thus are convergent in their paedomorphism; however, the recovered relationships present a novel hypothesis for the placement of Paedocypris.

Diversification of Horseshoe Bats

Sebastian Bailey, Xiuguang Mao, Joe Parker, Georgia Tsagkogeorga, Stephen Rossiter

2A_306C-Phylogenetic Systematics
Sunday, June 22, 2014 9:00 AM-9:15 AM

Horseshoe bats (Rhinolophidae) are one of the most speciose families of mammals (~100spp). They exhibit highly specialised, species-specific constant frequency echolocation calls, which correspond to a narrowly tuned frequency range of the inner ear. Due to this auditory specificity, horseshoe bat calls are thought to play a dual role in prey detection and communication. Such traits that influence both ecology and mate choice could facilitate speciation and, therefore, may underpin the diversification of this group.

To test if this unusual system of echolocation has contributed to the radiation of horseshoe bat species (call frequency range 20 kHz – 120 kHz), we screened for evidence of positive selection in sensory genes across the group. RNAseq was used to obtain the coding genes of nine horseshoe bat species. From ~10,000 single copy orthologs, we identified ~80 genes with known roles in hearing. These were then sequenced through a novel targeted capture approach (MyBaits) in a further 13 horseshoe bat species. We were able to identify 22 ‘hearing genes’ under selection within the horseshoe bat clade, both on the branch leading to horseshoe bats and within the horseshoe bat phylogeny. This result supports our hypothesis that hearing has played a crucial role in the evolution and diversification of these bats.

Origin and evolution of Oceanic pelagic communities

Francesco Santini

2A_306C-Phylogenetic Systematics
Sunday, June 22, 2014 9:15 AM-9:30 AM

In order to investigate the origin and evolution of communities of large pelagic predators in today's Oceans I generated megaphylogenies for three major fish groups (Scombriformes, Istiophoriformes, Clupeiformes) and dated the molecular trees using the rich fossil record of each of these groups. Together with previously available time−calibrated trees of cetaceans, cephalopods and sharks, these new phylogenies reveal for the first time the pattern of origination and diversification of all the major groups of pelagic inhabitants of the world's major Oceans. The result show two major bursts of origination and diversification: the first spanning the late Cretaceous/Early Paleogene, in some cases slightly predating the KPg extinction events, and a second one spanning the Late Miocene/Early Pliocene. The first burst of origination and diversification gave origin to many lineages that are currently assigned familial status, while the second episode saw the origin of most of the specific diversity of some of the largest pelagic predators, such as marlins and sailfishes, and tunas. I will discuss what factors may have been responsible for these two separate bursts of diversification in these clades, and how the radiation of these groups led to the present−day diversity of pelagic communities

Phylogenetic investigation of green algae that symbiose with spotted salamander eggs

Louise Lewis, Crystal Xue, Mark Urban

2A_306C-Phylogenetic Systematics
Sunday, June 22, 2014 9:30 AM-9:45 AM

The green alga Oophila amblystomatis Lambert ex Wille was described in 1909 for green algae that symbiose with salamanders in the egg stage. These algae were shown to provide oxygen and carbon to the developing salamanders. The source of the algae is under debate. Early studies concluded that the algae enter the eggs from the surrounding water once they are laid. Yet, an intimate association of green algae and their salamander partners has been described in which the algae occur inside tissues and even cells of embryonic salamanders, suggesting that there could be a maternal contribution. It is also known that male salamanders deposit spermatophores on pond substrate, after which the spermatophores are taken up by females for internal fertilization. We investigated the possibility of maternal contribution and spermatophore contribution by examining phylogenetic relationships and levels of sequence variation of algae within and among multiple egg clutches in seven small ponds in Connecticut, U.S.A. We also studied algae cultured from spermatophores and cloacal swabs of salamanders. In general, the algae associated with salamanders represented several phylogenetic lineages. Algae from the two largest (and most closely related) lineages were present in all studied ponds and in 18/20 clutches. Most clutches contained algae allied with one or the other, but not both, of these lineages. On average clutches had algae from 2 lineages. The greatest variation in the algae was found among clutches in a pond, not among eggs of individual clutches. This suggests that females contribute algae to eggs but within ponds different females are using different algae. Some algae cultured from cloacal swabs and spermatophores overlapped with the algae in eggs, suggesting that the spermatophores may be the source of the algae. Further investigations are needed to understand the establishment and ecological consequences of this symbiosis.

Identifying students' misconceptions about genetic drift and using them to improve instruction

Rebecca Price, *Tessa Andrews*

2A_402-SSE Education Symposium: Assessing Undergraduate Student Understanding of Evolutionary Biology
Sunday, June 22, 2014 8:45 AM-9:15 AM
Understanding genetic drift is crucial for a comprehensive understanding of biology, yet it is difficult for students to learn because it combines the conceptual challenges of both evolution and randomness. In this interactive presentation, we will begin by discussing the consensus that we have found among experts about the key concepts that undergraduate students should learn about genetic drift, focusing especially on which of these key concepts are most challenging. We will also discuss common misconceptions that students hold about genetic drift, including those you have observed among your students. We will present a recently developed tool called the Genetic Drift Inventory (GeDI) that instructors can use to identify (1) the aspects of genetic drift their particular population of students find most challenging, (2) misconceptions prevalent among students, and (3) the concepts that students understand well. Even as students develop accurate knowledge of genetic drift, they may also retain inaccurate ideas. The GeDI allows instructors to see this complexity. We will discuss how instructors can use results from the GeDI to frame instruction, for example by generating open-ended questions that help students reconstruct their ideas. We also propose a framework of how student thinking about genetic drift—and evolution more broadly—changes with instruction. Initially, undergraduates do not distinguish among mechanisms of evolution, often seeing natural selection as the only evolutionary force. As they gain knowledge, undergraduates tend to confuse genetic drift with other evolutionary concepts, such as random mutation, changes in allele frequency, migration, and isolation. As student comprehension continues to advance, new misconceptions emerge about genetic drift that incorrectly limit when genetic occurs. For example, students may think that genetic drift only occurs in small populations. We will facilitate a discussion about how instruction can inadvertently contribute to students' inaccurate ideas about genetic drift, as well as how instruction can help students develop scientifically accurate ones. We will close with information about how instructors can use the GeDI in their courses.

Student misconceptions about evolutionary developmental biology and using the EvoDevo Concept Inventory to document student learning

Kathryn Perez, *Anna Hiatt*

2A_402-SSE Education Symposium: Assessing Undergraduate Student Understanding of Evolutionary Biology
Sunday, June 22, 2014 9:15 AM-9:45 AM
Evo-devo concepts substantially expand our understanding of evolutionary processes. Recognition of the importance of evo-devo, as well as the pedagogical gains that can be made by discussing both evo-devo and microevolution has fueled recent efforts to incorporate evo-devo into evolutionary biology curricula. However, evo-devo content presents students with new conceptual challenges and potential difficulties in attempting to understand evolution. For example, while several evo-devo concepts rely on the supporting concept of conserved gene networks that operate in a variety of developmental contexts, many students hold that each trait of an observed phenotype is the result of the expression of a single gene. Pervasive conceptual difficulties such as these are also the most difficult kinds of misconceptions to address with targeted teaching interventions.

In this presentation we will discuss we will discuss a consensus of what evo-devo experts think are the most critical evo-devo concepts for undergraduates to know, and data on how many undergraduates interpret—and misinterpret—those critical concepts. We will also briefly discuss some of the foundational knowledge from evolution and development that is required for students to understand evo-devo. We also review some of the common conceptual difficulties students have with the subject. These data all contributed to the development of the EvoDevoCI; a rigorously validated assessment of evo-devo concepts suitable for lower and upper level undergraduate students. Finally, we will briefly describing two studies showing data on how the EvoDevoCI has been used to document improved student learning of evo-devo in undergraduate biology and across a biology curriculum.

Questions that we have for symposium attendees are: At what point do students learn evo-devo content in your departmental curriculum? Are evo-devo concepts part of any required courses? We will facilitate a discussion of these questions, considering their implications for how biologists and students understand these important evolutionary ideas.

Testing the molecular clock using simulated trees, fossils and sequences

Rachel Warnock, *Philip Donoghue*

2A_BalC-SSE Symposium: Reuniting fossil and extant approaches to macroevolution
Sunday, June 22, 2014 8:15 AM-8:30 AM
The molecular clock provides the most powerful means of establishing an evolutionary timescale. Approaches to calibrating the molecular substitution rate vary in their assumptions and complexity, differ in their use of geological evidence, and invariably yield different divergence estimates. Surprisingly, competing approaches to calibration have never been tested because, in reality the true evolutionary timescale is never known. Consequently, it has not been possible to assess the accuracy and precision with which divergence times can ever be known. The solution is to use simulated data, where the relationship between times of divergence, molecular rate variation and fossil evidence is known. We develop simulations that combine realistic models of speciation, molecular evolution and fossil preservation. We first test the accuracy and precision of four quantitative and probabilistic methods of deriving temporal constraints from the fossil record. Next, we implement these as bespoke calibration priors in Bayesian molecular clock analyses, and assess the accuracy and precision of posterior divergence estimates. The results demonstrate that paleontological constraints can be accurate but will typically be imprecise. Accurate molecular divergence estimates require both accurate and precise fossil-

based constraints. However, the accuracy of posterior estimates is not determined by the accuracy of the specified fossil-based calibrations. Instead, the accuracy is determined by the way in which the calibrations are effectively implemented by contemporary Bayesian models of divergence time estimation. This has material consequences for any scientific test that relies on an accurate and precise evolutionary timescale.

Using fossil data to cover for phylogenetic model assumptions

Emma Goldberg

2A_BalC-SSE Symposium: Reuniting fossil and extant approaches to macroevolution
Sunday, June 22, 2014 8:30 AM-8:45 AM

The interaction of trait evolution with speciation and extinction is of great macroevolutionary interest, including for questions about adaptive radiation and species selection. These processes were initially studied using the fossil record, and they are now widely inferred from extant species using statistical phylogenetic methods. These latter methods are based on explicit dynamic models of the underlying processes. This is a strength, in that it can provide much power to detect modes of character change and diversification. But it is also a weakness, in that violations of the model assumptions can have unknown consequences for our conclusions. Exposing and repairing model incompleteness that most affects biologically important conclusions is an essential avenue forward. One might hope, however, that many conclusions are robust to model simplifications, especially when working with large datasets. Here, we investigate to extent to which directly incorporating extinct lineages and past trait values can improve the reliability of phylogenetic inferences of character evolution and diversification, even when the models used are incomplete. We first consider the loss of self-incompatibility in Solanaceae, quantifying how increasing knowledge of its shared history affects conclusions about the irreversibility of its loss. We then consider, via simulation, patterns of geographic range evolution informed by paleontological data but un-modeled by phylogenetic comparative methods. We investigate how fossil-based data influences conclusions of how geographic range size affects lineage diversification.

The Sad Case of the Has-Been: Can We Detect Diversity Replacement within Extant Clades?

Peter Wagner, Andy Simpson

2A_BalC-SSE Symposium: Reuniting fossil and extant approaches to macroevolution
Sunday, June 22, 2014 8:45 AM-9:00 AM

Both paleontologists and neontologists recognize many cases where it appears that certain subclades within larger clades have had greater long-term success than the remainder of the clade. Neontologists typically model this as the elevated net diversification of the “winning” subclade. However, paleontologists often stress the decreased diversification of the “losing” group(s), i.e., subclades or paraphyletic grades with high diversity early in clade history, but greatly reduced diversity late in clade history. Here we explore how one model favored by some paleontologists, coupled logistic diversification, affects phylogenetic patterns among contemporaneous taxa (e.g., extant taxa). Under coupled logistic models, diversification within the whole clade is richness-dependent, so that net-diversification decreases as richness approaches some maximum. Replacement can occur when some subclade diversifies at the expense of other members of the clade, resulting in: 1) temporary increases in the net-diversification of the subclade and 2) reduced diversity of the remainder of the clade over time. Simulations show that if the “losing” members of the clade are still present, then standard methods of reconstructing diversity from phylogenies of “extant” taxa incorrectly suggest prolonged lags in overall clade diversification, with the successful subclade experiencing a strong increase in net diversification. It might be possible to recognize that simple exponential diversification with two separate net diversification rates did not happen: the distribution of branch lengths under coupled logistic diversification is more heterogeneous than it is under exponential models producing similar differences in final diversity. However, very large sample sizes would be needed to justify the greater number of parameters required by coupled logistic models than by exponential models. Where the coupled logistic and elevated net-diversification models make very different predictions is in the relative diversities of different portions of the clades at some points in their histories: and that can be tested only using fossil taxa. Fortunately, some very simple tests can demonstrate that sampled richness ratios significantly better matches one model or the other. For example, the fossil record of Old World primates indicates that the diversity of early apes relative to that of early monkeys is much greater than predicted by exponential models, but within ranges predicted by coupled logistic models. However, although extant taxa can hint at lost diversity, fossil data are necessary to appreciate the past success of evolutionary has-beens.

Do fossils and extant phylogenies agree upon patterns of mammalian diversification?

Samantha Price, Samantha Hopkins

2A_BalC-SSE Symposium: Reuniting fossil and extant approaches to macroevolution
Sunday, June 22, 2014 9:00 AM-9:15 AM

Most modern mammalian orders have their origins in the Cretaceous, however the timing and tempo of their crown-group radiations is regularly disputed, with molecular and fossil data often providing conflicting estimates. The persistent difficulty in reconciling fossil and modern data begs the question: are paleontological and comparative phylogenetic studies of diversification actually comparable? Using mammalian clades with comprehensive extant phylogenies and well-studied fossil records (Carnivora and Primates) we explore the inferences made from fossil occurrences and phylogenies at both the species and genus-level and calculate the rates of speciation, extinction and net diversification. Although it is well established that extinction rate is poorly estimated from extant-only phylogenies, we compare parameter estimates from different models of evolution (e.g. constant and variable rates) and the strength of their fit to the fossil record. Understanding how and why different patterns and processes are inferred from fossil and extant data is the first step towards a unified approach to macroevolution.

Ecological opportunity and ecomorphological evolution in North American canids

Graham Slater

2A_BalC-SSE Symposium: Reuniting fossil and extant approaches to macroevolution
Sunday, June 22, 2014 9:15 AM-9:30 AM

A long-standing hypothesis in adaptive radiation theory is that ecological opportunity constrains the rate at which clades diversify, but empirical support for a pattern of declining rates is rare in comparative data. A limitation of most studies of adaptive radiation is that they are based on extrapolation of past rates and diversity from molecular phylogenies of extant taxa. A more conclusive test of the ecological opportunity hypothesis would be based on a diverse clade with a rich fossil record and a well-resolved phylogeny. Here, I assess the fit of a series of macroevolutionary models, including models that allow phenotypic rates to vary as a function of time and past lineage diversity, to a novel phylogenetic comparative dataset of 95 living and extinct North American canids, spanning a period of 40 million years. Models implying time and diversity dependent rates of evolution are strongly rejected for body size and relative grinding area of the lower molars. Instead, Ornstein-Uhlenbeck processes implying rapid rates of adaptation to distinct adaptive peaks for three dietary categories are preferred for both traits. I suggest that diversity dependent evolutionary rates are probably uncommon in clades such as canids that exhibit a so-called pattern of ``replicated adaptive radiation". Instead, these clades might best be thought of as deterministic radiations in constrained Simpsonian sub-zones of a major adaptive zone. Support for adaptive peak models over early burst-like processes may be diagnostic of subzone radiations. Distinguishing where these processes start and end will require large-scale integration of paleontological and phylogenetic data and methods.

Nocturnality in Synapsids Predates the Origin of Mammals by Over 100 Million Years

Lars Schmitz, *Kenneth Angielczyk*

2A_BalC-SSE Symposium: Reuniting fossil and extant approaches to macroevolution
Sunday, June 22, 2014 9:30 AM-9:45 AM

The majority of extant mammals are nocturnal, and it has been hypothesized that this is the ancestral behavioral pattern for mammals. The predominance of nocturnality among mammals, and characters of the mammalian nervous and sensory systems suggest that early mammals passed through a “nocturnal bottleneck,” perhaps to avoid competition with and predation by dinosaurs. However, focusing on mammalian diel activity patterns ignores the fact that mammals are nested within a larger clade, Synapsida, and that nocturnality might have evolved in these mammalian ancestors well before the origin of mammals. Using scleral ring and orbit dimensions we demonstrate that 24 Carboniferous to Jurassic nonmammalian synapsids featured eye morphologies consistent with all major diel activity patterns, with examples of nocturnality as old as the Late Carboniferous (ca. 300 Ma). The presence of night-active nonmammalian synapsids calls for a reevaluation of the hypothesized link between the characters of early mammals and a shift to nocturnality. Earlier invasions of the nocturnal niche did not result in the morphological reorganization seen in early mammals, so either there is no causal link between nocturnality and the early mammal trait complex or early mammals adapted to this lifestyle in unprecedented ways.

Flash signal evolution in North American Photinus fireflies

Kathrin Stanger-Hall, *James Lloyd*

2B_201-Evolution of Signaling
Sunday, June 22, 2014 10:15 AM-10:30 AM

The study of communication systems is a complex topic in evolutionary biology. Communication systems consist of senders, signals and receivers, and the evolution of signals can be shaped by receivers and habitats. In this comprehensive study on the evolution of a visual communication system, a phylogenetic approach was used to study the flash communication signals of North American fireflies. With more than 30 described species, simple ON-OFF visual signals, variation in light signal traits, along with field data on habitat types, sympatric congeners and predators, the North American firefly genus Photinus offers an ideal study system to test hypotheses on the evolution of male and female visual signal traits.

Courtship Pheromone Evolution in Dusky Salamanders

Michael Steffen, *Ronald Bonett*

2B_201-Evolution of Signaling
Sunday, June 22, 2014 10:30 AM-10:45 AM

The biological world is rich with sounds, smells, and movements that serve as communication signals, and demonstrate the evolution of life. Conspecific mate recognition signals can delimit species boundaries and structure communities. However, signals and mate choice are evolutionarily labile, and few studies have examined the impact of signal discordance on lineage diversification in adaptive radiations. Salamanders produce a cocktail of proteinaceous courtship pheromones which are highly variable. Since these signals are encoded in the genome, their inheritance and patterns of divergence, convergence, and introgression can be readily analyzed in a phylogenetic and molecular evolution context. Dusky salamanders of the genus Desmognathus are endemic to eastern North America, and display dramatic disparity in ecology, body size and life history. However, some distantly related species are highly convergent in these traits, and behavioral studies have shown varying degrees of prezygotic isolation among divergent, yet ecologically similar species. In this study, we analyze the transcripts of pheromone genes in Desmognathus, and test patterns of molecular evolution and selection.

Ecological and genetic underpinnings of wing pattern diversity and evolution in butterflies

Krushnamegh Kunte, Deepa Agashe

2B_201-Evolution of Signaling
Sunday, June 22, 2014 10:45 AM-11:00 AM

The hallmark of life on earth is morphological diversity, which is represented in the spectacular sexually dimorphic and polymorphic wing patterns of butterflies. Biologists have long tried to find general ecological explanations for the evolution of morphological diversity, especially at intraspecific levels. We address this problem by investigating the remarkable diversity of mimetic wing patterns in butterflies, manifested in numerous sex-limited or otherwise polymorphic forms within species. Historically, the major hypotheses to explain these polymorphic forms have centered around the concepts of sexual selection, physiological tradeoffs, and shifting balance. While there is interesting evidence to support components of each of these ideas, a broad-ranging ecological explanation for this type of polymorphic wing patterns is still missing. Towards this end, we present a simple mathematical model that may explain the full gamut of polymorphic diversity exhibited by mimetic butterflies. Our model is based on frequency dependent natural selection (predation) and sex-specific advantages of mimicry, both of which are empirically established. Our model predicts that in ecological communities composed of toxic models and undefended mimics, different threshold mimic frequencies favor transitions between monomorphic, female-limited and polymoprhic mimicry. Data on 57 mimetic butterfly species showed that monomorphic mimicry was prevalent at low mimic frequencies whereas female-limited and polymorphic mimicry was prevalent at high mimic frequency, as predicted by the model. We further show with controlled experiments on the Papilio polytes butterfly that female-limited mimetic polymorphism in this species could not be explained by sexual selection, physiological tradeoffs or other hypotheses. However, the presence and density of models appeared to determine the presence and frequency of mimetic forms in a given locality. Thus, frequency-dependent natural selection in the form of predation appears to be the predominant force driving wing pattern polymorphism in Batesian mimetic butterflies. We further elucidate the genetic mechanism underlying this polymorphism in Papilio polytes. We show that doublesex, a transcription factor that controls sexual differentiation in insects, also controls sex-limited mimetic polymorphism via sex- and tissue-specific alternative RNA isoforms and differential expression. Polymorphic wing patterns in other species have also been shown to be controlled by master gene regulators that have different functions in other insects. In all these cases, the master regulators have been co-opted from the original function to produce polymorphic wings in butterflies. Our results suggest that the genetics of highly complex and diverse phenotypes may be relatively simple, and may involve frequent exaptations.

Warning signal polymorphism under positive frequency-dependent selection

Mathieu Chouteau, Monica Arias, Annabel Whibley, Melanie McClure, Mathieu Joron

2B_201-Evolution of Signaling
Sunday, June 22, 2014 11:00 AM-11:15 AM

Aposematism, whereby prey display conspicuous warning signals to advertise their unpalability to potential predators, is thought to be the only example of traits under positive frequency dependant selection. However, empirical evidence supporting this pattern of selection in natural systems is still lacking. This is in great part due to the difficulty in distinguishing whether the purifying selection observed in natural systems is the results of a linear positive frequency dependant selection or the result of a bi-modal selection, where one aposematic signal is recognized and avoided (advantaged) by predators and all other signals are quickly counter-selected at a similar rate independently of frequency. To differentiate between these patterns of selection, we took advantage of the mimicry polymorphism displayed in every locality by the butterfly Heliconius numata. Using malleable prey models and population genetic tools we demonstrate that within a community of educated predators, the fraction of predators having learned to avoid a given aposematic signal increases with the increasing frequency of the signal up to a given threshold whereby the highest possible fraction of predators is educated. Moreover, we show that this positive frequency dependent selection, which accelerates the loss of diversity and leads to monomorphism within populations, is nevertheless responsible for the maintenance of an outstanding diversity of aposematic signals across geography. We will present data on the maintenance of local polymorphism through positive frequency-dependent selection and discuss how antagonistic selective forces can maintain diversity in warning signals.

Responses to song playback vary with the vocal performance of both signal senders and receivers

Dana Moseley, David C. Lahti, Jeffrey Podos

2B_201-Evolution of Signaling
Sunday, June 22, 2014 11:15 AM-11:30 AM

Mating signals of many animal species are difficult to produce and thus should indicate signaler quality. Growing evidence suggests that receivers modulate their behavior in response to signals with varying performance levels, although little is known about if and how responses are affected by receiver attributes. To explore this topic we conducted two experiments with swamp sparrows, Melospiza georgiana, in which we challenged territorial males with playback of songs with trill rates that were natural, digitally reduced, or digitally elevated (control, low, and high performance, respectively). In our first experiment, we found that males responded more aggressively to control songs than to low-performance stimuli, that low-performance stimuli with the most severe trill-rate reductions elicited the weakest aggressive responses, and that the subjects' own trill rates predicted aggressive responses. In our second experiment, we found that male responses to high-performance stimuli varied significantly, in ways predicted by two factors: the degree to which we had elevated stimulus performance levels of high-performance stimuli, and subjects' own vocal performance levels. Specifically, males were less aggressive towards stimuli for which we had elevated performance levels to higher degrees, and subject males with higher vocal performances themselves responded more aggressively. These findings together offer a novel illustration of how responses to aggressive signals may rely not just on signal attributes, but also on attributes of responding animals themselves.

Patterns of genetic variation among Blackcaps (Sylvia atricapilla) with diverse migratory behaviors in Europe

Raeann Mettler

2B_206-Migratory Behavior
Sunday, June 22, 2014 10:15 AM-10:30 AM

Migratory divides are thought to facilitate behavioral, ecological, and genetic divergence among populations with different migratory routes. However, it is currently contentious how much genetic divergence is needed to maintain distinct migratory behavior across migratory divides. We investigate patterns of neutral genetic differentiation among Blackcap (Sylvia atricapilla) populations with different migratory strategies across Europe. We compare the level of neutral genetic divergence of populations migrating to southwestern (SW) or southeastern (SE) wintering areas with birds wintering in the British Isles following a recently established northwesterly (NW) migration route. The migratory divide between SW and SE wintering areas can be interpreted as a result of a re-colonization process after the last glaciation. Thus we predicted greater levels of genetic differentiation among the SW/SE populations. However, a lack of genetic differentiation was found between SW and SE populations, suggesting that interbreeding likely occurs among Blackcaps with different migratory orientations across a large area; therefore the SW/SE migratory divide can be seen as diffuse, broad band and is, at best, a weak isolating barrier. Conversely, weak, albeit significant genetic differentiation was evident between NW and SW migrants breeding sympatrically in southern Germany, suggesting a stronger isolating mechanism may be acting in this population. Populations located within/near the SW/SE contact zone were the least genetically divergent from NW migrants, confirming NW migrants likely originated from within the contact zone. Significant isolation-by-distance was found among eastern Blackcap populations (i.e. SE migrants), but not among western populations (i.e. NW and SW migrants), revealing different patterns of genetic divergence among Blackcap populations in Europe.

We additionally investigated a candidate locus associated with migratory behavior (ADCYAP1). The relationships between genetic variation at this locus, wing morphology and spring migratory phenology were explored among several wild Blackcap populations and within a single, large population in Freiburg, Germany. Additionally, sex-effects were investigated at these traits in association with migratory behavior. Overall, birds heterozygous at this locus had earlier spring phenologies across Europe. Males with longer allele sizes were found to have earlier spring phenologies, both among populations and within the single Freiburg population. A significant female-specific effect indicates an interaction between and ADCYAP1 allele size and wing shape, suggesting different genotype/phenotype combinations may similarly contribute to early spring phenology and thus arrival to breeding grounds, both across Europe and also within a single population.

Stepwise evolution of a complex behavioral trait: migration in Tyrant Flycatchers

Valentina Gomez, Roberto Márquez, Alex Jahn, Oscar Laverde, Daniel Cadena

2B_206-Migratory Behavior
Sunday, June 22, 2014 10:30 AM-10:45 AM

Migratory behavior is thought to evolve in response to ecological pressures, allowing animals to benefit from resource abundance in different geographic regions. Migration has convergently evolved in many lineages of birds involving a variety of strategies. For instance, some lineages are partially migratory, meaning that some individuals migrate and others stay as permanent residents. Among partially migratory species, all individuals may reproduce in the same place or migrants may reproduce elsewhere. Although many lineages of birds have been characterized as partially migratory, little is known about the evolution of this migratory strategy, which has been hypothesized to be an intermediate step towards the evolution of strict migration. We adopted a multi-scale approach to understand the evolution of partial migration under a phylogenetic framework. First, we tested discrete models of character evolution in the Tyrant Flycatchers (Aves: Tyrannidae) to determine the likelihood of partial migration representing an intermediate step in the evolution of strict migration. We also studied the relationship between the evolution of migratory behavior and phylogeographic and demographic history in the partially migratory Fork-tailed Flycatcher (Tyrannus savana). Our results provide support for the model of gradual evolution of migration (i.e. with partial migration being an intermediate step). In contrast to previous studies, we find that migration in flycatchers has evolved from resident ancestors and vice versa. Our microevolutionary analysis provides insights into the evolution of a complex behavioral trait that may potentially confer reproductive isolation between populations. This is a fundamental step towards understanding the role of behavioral shifts as drivers of diversification.

Cavity-nesting makes flycatchers fecund and fly farther: evolutionary links between cavity nesting, clutch size and migration in the Muscicapidae.

Sahas Barve, Nicholas Mason

2B_206-Migratory Behavior
Sunday, June 22, 2014 10:45 AM-11:00 AM

The ecology of cavity nesting in passerine birds has been studied extensively. Yet there are no phylogenetic comparative studies that quantify differences in life history traits between cavity and open-nesting birds in a passerine family. Here we test existing hypotheses regarding the evolutionary significance of cavity nesting in the Old World flycatchers (Family: Muscicapidae). We inferred a multi-locus phylogeny of 246 species, which we subsequently used to reconstruct the evolutionary history of cavity nesting and quantify correlations between nest types and specific life history traits. Within a phylogenetic generalized linear model framework, we found that maximum clutch size is larger in cavity-nesting lineages. Moreover, cavity nesting species are larger than open nesting species in high latitudes. Finally, we found that gains and losses of migratory behavior occur far more often in cavity-nesting lineages than open-nesting taxa, suggesting that cavity nesting may have played a crucial role in the evolution of migratory behavior. Together, these findings suggest that there are important macroevolutionary links between the evolution of cavity nesting, clutch size, interspecific competition and migratory behavior in a large clade of songbirds, the Old World flycatchers.

Genes, mice and Vikings

Jeremy Searle

2B_206-Migratory Behavior
Sunday, June 22, 2014 11:00 AM-11:15 AM

The species Mus musculus has a natural distribution in the northern part of the Indian subcontinent and the Near East. However, it also found throughout the rest of the world courtesy of humans. The English vernacular name for the species is 'house mouse' and it is because the species is able to utilise the food of humans and their livestock, and live in man-made dwellings, that they are able to live in all parts of the world. But it is of course their ability to get onto boats as stowaways that has transported house mice everywhere. This transport of mice has been going on for the past 12,000 years. By comparing the DNA sequences of house mice from different parts of the species distribution, it is possible to infer the history of transportation of the house mice. Mice from the source area of a particular colonisation will have similar DNA sequences to mice from the colonised location. Judging by these DNA comparisons many of the house mouse colonisations are just as would be predicted from our knowledge of the human history. I will illustrate this by describing inferred mouse colonisations that match well-described Viking spheres of influence in the North Atlantic region. Mice also provide evidence for some undocumented Viking movements, suggesting that they may be a valuable proxy for human history. Studies up to now have been largely based on mitochondrial D-loop sequences, but there is considerable potential for studies with genomic data – which are in progress.

CHALLENGING THE PARADIGM OF MONARCH MIGRATIONS: BEHAVIORAL COMPLEXITY AND ISOTOPIC VARIATION OF THE EASTERN NORTH AMERICAN POPULATION

Carol Chaffee

2B_206-Migratory Behavior
Sunday, June 22, 2014 11:15 AM-11:30 AM

Movement is one of the key factors that influences evolution. This project used the unique migration behavior of the monarch butterfly (Danaus plexippus) to investigate the effects of migratory behavior on population structure. Although monarchs are not yet endangered as a species, their migration is facing a variety of threats. Migration may be key to the stability of the species, for example by preserving or redistributing genetic variation. Understanding how movement influences the distribution of genetic variation across an organism's range is particularly important in conservation genetics. I used an approach that integrated genetic and stable isotope analyses to answer three research questions: 1) To what degree is the resident population in South Florida connected with the main migratory population? 2) Has the summer breeding range expanded northward? 3) Do monarchs from different origins mix in the Mexican overwintering colonies? I found that migrants from throughout the summer range enter the resident South Florida population, but that the degree of connectivity is different for males and females. Males immigrating to South Florida also are larger than resident males. My results indicate that monarchs are breeding well north of the published breeding limit, and that monarchs originating north of the putative breeding limit are successfully migrating to the overwintering colonies in Mexico. Finally, genetic variation is homogeneously distributed across the overwintering colonies in Mexico, but there are subtle differences between the overwintering colonies in origins of the butterflies at each colony. Thus, overwintering colonies are not equivalent. Overall, we show that monarch movement produces patterns with greater fine-scale complexity than had previously been described. Because of the conservation implications this complexity, future work investigating the processes that produce these patterns is warranted.

Resolving relationships in Cecropieae (Urticaceae): Implications for the evolution of an ant-plant mutualism

Erin Treiber, André Gaglioti, Sergio Romaniuc, Santiago Madrinan, George Weiblen

2B_301A-Coevolution
Sunday, June 22, 2014 10:15 AM-10:30 AM

Ant-plant mutualisms are abundant in the tropics and are an ideal model system for studying mutualisms. Despite many ecological studies of ant-plant mutualisms, in some systems, understanding the evolution of mutualism has been hindered by the lack of a solid of taxonomic framework. A common ant-plant mutualism in the Neotropics involves the genus Cecropia, fast growing pioneer trees important in forest regeneration. Relationships between genera in the tribe Cecropieae (Urticaceae) which includes Cecropia, Coussapoa, Musanga, Myrianthus, and Pourouma, are unknown and are necessary to investigate the evolutionary history of the Cecropia-ant mutualism. A phylogeny based on the NADH dehydrogenase (ndhF) chloroplast gene and 26S ribosomal DNA supports ant-less African Musanga embedded within Cecropia. Neotropical Pourouma and Coussapoa are highly supported sister groups. Myrianthus appears to be sister to the rest of the tribe, but with low support. The position of Musanga, embedded within Cecropia, suggests that the ant mutualism arose in the Neotropics and was lost during the colonization of Africa.

The population genetics of evolving games

Alexander Stewart

2B_301A-Coevolution
Sunday, June 22, 2014 10:30 AM-10:45 AM

Evolutionary game theory provides a quantitative framework for analyzing the behavior of rational agents, by encoding behavior in terms of strategies, and the results of interactions between players in terms of payoffs. However, the population genetics of even the simplest iterated games can be hard to analyze, owing to the complex and often counter intuitive relationship between the payoffs players receive, and the strategies present in a population. Here we present results on the evolution of iterated games in finite populations. We identify all subsets of memory-1 strategies that are globally stable against being selectively invaded by any other strategy, in arbitrary two player games. We show that such strategies dominate evolutionary dynamics when evolution occurs on the full set of memory-1 strategies, and we predict the relative abundancies of different strategy types at equilibrium. Finally, we employ these results to explore the evolution of cooperation when payoffs (in the form of costs and benefits) and strategies are allowed to co-evolve. We find that co-evolution between payoffs and strategies can often precipitate a dramatic collapse of cooperation, in which populations evolve towards payoff schemes that promote low levels of cooperation, and low average payoffs for all players.

Differential gene expression in freshwater snails infected and uninfected with a coevolving trematode parasite

Laura Bankers, Kyle McElroy, John Logsdon, Jeffrey Boore, Maurine Neiman

2B_301A-Coevolution
Sunday, June 22, 2014 10:45 AM-11:00 AM

Why sexual reproduction is so common ranks among the most important unanswered questions in evolutionary biology. One possibility is that sex increases the efficacy of adaptive molecular evolution by allowing mutations to be selected independently of genetic background. Potamopyrgus antipodarum, a freshwater snail native to New Zealand, is ideally suited to evaluate this hypothesis because closely related and phenotypically similar sexual and asexual individuals often coexist and compete within natural populations. These features of the P. antipodarum system enable us to make direct and powerful comparisons of patterns of molecular evolution between sexual and asexual conspecifics. Here, we take advantage of the fact that Potamopyrgus antipodarum is frequently infected by a coevolving, locally adapted, and virulent trematode parasite (Microphallus sp.) to compare patterns of adaptive evolution in genes that are involved in host immune response to parasite pressure. These genes have been shown to experience strong selection and coevolutionary interactions associated with adaptive evolution in a wide diversity of organisms, making them excellent candidates for testing hypotheses regarding the efficacy of adaptive molecular evolution across reproductive modes. We took initial steps toward evaluating a connection between sex and adaptive evolution by using RNA-seq to make gene expression comparisons in field-collected P. antipodarum differing in Microphallus infection status (infected vs. uninfected), and then used these comparisons to identify loci likely involved in host response to parasite infection. We included snails collected from three different lake populations to identify loci that might be generally involved in immune response as well as loci that might mediate local adaptation to parasite pressure. In our ongoing analyses, we have identified 370 differentially expressed transcripts between uninfected vs. infected snails, many with putative roles in immune/defense response and/or function. We will compare a subset of these loci across a wide range of sexual vs. asexual P. antipodarum lineages to evaluate the extent to which sexual reproduction facilitates adaptive molecular evolution. Identification of loci involved in immune response to parasites in natural populations of P. antipodarum will also be of broad interest to many biologists that study the molecular genetic mechanisms that drive coevolution and local adaptation.

Symbiotic partnership in brood protection: use of mycelial cover in a fungus-farming ant

Katherine Holmes, William Wcislo, Hermogenes Fernandez

2B_301A-Coevolution
Sunday, June 22, 2014 11:00 AM-11:15 AM

Ants of the tribe Attini have closely coevolved with their fungal symbiont for over 50 million years. The fungus serves not only as food, but as a protective nursery where brood are stored and covered with a thin layer of fungal mycelia, hypothesized to protect against microbial attack. Differences between mycelial cover on different brood types (eggs, larvae, and pupae) have been observed in colonies excavated from the field, and different agricultural groups display contrasting patterns. Older brood are more heavily covered in the most basal and derived attine groups, while brood of transitional taxa show the opposite pattern. However, these patterns are unaddressed in the literature, and it is unknown whether they reflect preferential treatment of certain brood types by workers, or environmental conditions such as predation. To test worker deposition of fungal mycelia, colonies of a phylogenetically “transitional” attine ant, Trachymyrmex cornetzi, were excavated in the field and brought into the lab. T. cornetzi has been used previously to study traits that diverge along phylogenetic lines, and here represents the unusual pattern of greater coverage on younger brood. Samples were created where a handful of workers were given one larva, one pupa, and a small amount of their fungus garden to reconstruct. Pupae had less cover than larvae both before and after a three-day trial, matching the pattern previously observed in the field. However, rate of deposition was not significantly different. This may suggest that deposition rates are highest in very young larvae, and decline as brood age towards the pupal stage. Our results suggest that field data showing contradictory patterns in mycelial cover across taxonomic groups accurately reflect strong differences in brood care practices across the phylogeny. If mycelial cover serves as a method of disease control, as hypothesized, this pattern is counterintuitive: sympatric species might be expected to have similar patterns of brood protection, and differ only by degree. Thus, the opposing practices of different taxonomic groups that our data indicates demands further investigation.

Co-evolution in the mountains: Phylogeographic comparison of a wood-feeding insect and its bacterial endosymbiont

Ryan Garrick, Zakee Sabree, Jeff Oliver

2B_301A-Coevolution
Sunday, June 22, 2014 11:15 AM-11:30 AM

Phylogeographic comparisons of a tightly co-associated taxon pair - a saproxylic cockroach (Cryptocercus punctulatus) and its obligate bacterial endosymbiont (Blattabacterium sp.) - are performed using coalescent-based and gene tree-based analytical approaches.

Selection on phenotypic traits in an experimentally introduced population of Brassica rapa in a novel environment

Michael Sekor, Steve Franks

2B_301B-Adaptation
Sunday, June 22, 2014 10:15 AM-10:30 AM
Examining the strength of selection on phenotypic traits over time can provide information on the targets and consistency of selective pressure. Due to the global mobility of humans, and therefore propagules, the selective pressures on, and evolutionary responses of, colonizing organisms are of particular concern. Much of the work on the selection and evolution of introduced species has been conducted after the introductions have occurred, leaving many factors uncontrolled or unobserved. This study examines the selection on phenotypic traits in a population of experimentally introduced plants in the first three seasons following introduction to a novel environment. My goals are to determine the phenotypic targets of selection and if the strength of selection changes during the first three generations following introduction. The experimental introduction occurred in May 2011, when Brassica rapa (field mustard) seeds from a population in the Mediterranean climate of Southern California were introduced to the temperate climate of New York. A variety of morphological and phenological traits were measured twice a week throughout the growing seasons. During the first two seasons of growth (2011 and 2012), there was significant direct linear selection for increased size (greater basal stem diameter [betaavg=0.487] and number of leaves [betaavg=0.579]). During the third growing season (2013), when weather patterns were more severe, there was no significant direct selection for increased size, but rather significant direct linear selection for longer duration of flowering [beta=0.386]. This suggests that during a period of severe weather, there was direct selection for plants that were able to flower longer to maximize seed set, rather than direct selection on increased overall size during the moderate growing seasons of the previous two years. A common garden experiment using the resurrection approach to compare the growth stored ancestors from the source population and descendants from the introduced population will be a test of evolution and local adaptation since introduction.

The relative importance of primary and secondary resources in adaptive radiation

Jeremy Heath, Patrick Abbot, John Stireman

2B_301B-Adaptation
Sunday, June 22, 2014 10:30 AM-10:45 AM
The most thoroughly studied adaptive radiations, including Darwin's finches and the cichlid fishes of the African rift lakes, have revealed adaptation to primary resources as a major driving force; both the finches and the fishes have mainly diversified with respect to feeding apparatus. Few studies of adaptive radiations have investigated diversification with respect to secondary resources such as enemy-free space. Here we study gall morphology in an incipient radiation of gall-making midges, nominally referred to as Asteromyia carbonifera (Diptera: Cecidomyiidae). These galls are attacked by up to 7 different parasitoids that apply significant selection pressure on gall thickness and diameter. Gall morphology has responded to this pressure, which has resulted in the maintenance of several sympatric and even syntopic gall morphotypes. We test the relative importance of plant genotype and enemies in driving diversification in this system through the production of adaptive landscape surfaces and calculation of selection gradients.

Transient Overdominance Can Constrain Evolvability During Rapid Evolution

Jeremy Draghi, Michael Whitlock

2B_301B-Adaptation
Sunday, June 22, 2014 10:45 AM-11:00 AM
Many recent studies have shown how initial adaptive substitutions constrain subsequent evolution through epistasis, but most work has focused on haploid systems. Here we show that overdominant alleles arising in a diploid model can reduce the rate of adaptation. We show how the strength and duration of this constraint depend strongly on the underlying genetic architecture of the trait, as well as the shape of the relationship between the trait and fitness. These results demonstrate how evolvability in diploids may be shaped by factors that cannot be predicted from haploid models.

Short-term density exposure affects male reproductive success in threespine stickleback (Gasterosteus aculeatus)

Emily Weigel, Jenny Boughman

2B_301B-Adaptation
Sunday, June 22, 2014 11:00 AM-11:15 AM
Seasonal changes often occur which can shift population demography and which traits may be optimal in a given environment. So what might occur when demographic changes affect multiple male traits to different degrees? Using the freshwater fish, threespine stickleback (Gasterosteus aculeatus), whose density is known to change across the breeding season, we experimentally manipulated male density (high or low, to simulate early- and late-season conditions) for two weeks and then randomly assigned individuals to single-male nesting tanks. We then exposed the males to females daily and recorded nesting and courtship behavior, as well as male throat coloration and nest perimeter, area, and weight. We found that males at low density were more likely to nest, nested faster, and initiated courtship quicker than males at high density. Furthermore, although nest weights did not differ between treatments, nor did they predict success with females, male nest area and nest compactness (as measured by perimeter) were larger at low density, perhaps increasing their conspicuousness. This work demonstrates that even short-term shifts in demography can have multiple consequences for the males that experience them.

Genotyping by sequencing and latitudinal divergence in wild sunflower

Ed McAssey, John Burke

2B_301B-Adaptation
Sunday, June 22, 2014 11:15 AM-11:30 AM
Understanding the genetic basis of local adaptation is a primary goal of evolutionary biology. Population genetic differentiation is a popular metric for quantifying allele frequency differentiation among populations and by quantifying FST from loci throughout

the genome it is possible to identify regions of the genome that are exceptionally differentiated and thus likely to play a role in adaptation. Wild sunflower, Helianthus annuus, is the progenitor of cultivated sunflower and is found throughout North America. Studying local adaptation in crop progenitors has the potential to inform breeding efforts with respect to global climate change and furthermore, the study of latitudinal gradients is important to aid in our understanding of how genetic diversity is partitioned in geographically widespread species. Previously we have utilized a single nucleotide polymorphism (SNP) chip to describe differentiation across the genome among wild populations ranging from Texas to Canada. To build on this work we sought to increase our marker density from 205 polymorphic loci generated from the SNP chip. To that end, we have leveraged a GBS protocol for generating thousands of markers throughout the genome. Here we show that this protocol is capable of generating over 8,000 150 base pair tags that were both found in at least 6 of the 8 individuals sequenced and map uniquely to the cultivated sunflower genome. Although only about 3,000 markers map uniquely to the current 17 chromosome assemblies, GBS markers have increased the average marker number per chromosome from 12.06 to 173.56. Using a random subset of polymorphic GBS markers we were able to identify latitudinal differentiation, which is consistent with previous research on these populations. These markers will greatly aid future studies of the molecular basis of local adaptation in a widespread crop progenitor species.

Population genetics and phylogeography of wild maize along environmental gradients.

Luis Enrique Eguiarte, Jonas Aguirre, Valeria Souza

2B_302A-Plant Evolution
Sunday, June 22, 2014 10:15 AM-10:30 AM

Wild maize or teosinte, Zea mays ssp. parviglumis and Zea mays ssp. mexicana are found in Mexico from altitudes ranging from 300 meters above sea level to almost 2600 m, growing in a wide range of climates, soils and surrounding vegetation. We describe here the first results of an analysis of 41 wild populations, including data form chloroplast, mitochondria and nuclear genes (ISSRs, microsatellites and 33000 SNPs), along with detailed climatic and ecological analyses. Our results show that the overall genetic diversity in teosinte is high within most populations for nuclear markers, but some populations have only one chloroplast or mitochondrial haplotype. The analysis indicate very strong genetic structure for maternal markers (both chloroplast and mitochondria); in contrast, we found moderate differentiation with the nuclear genes, but clear patterns of local adaptation and a large number of candidate genes. The results suggest that local adaptation -- in addition to geographic distance -- are important drivers of differentiation among populations. The genetic structure found in our studied wild maize population in Mexico does not adjust to the standard classification of two subspecies, including several well defined geographical clades. It also throws some intriguing light on the areas and dates of the origin and domestication of maize that does not adjust to published models and literature. These results show the importance of using climatic and ecological analyses in addition to a large set genetic nuclear data, along with chloroplast and mitochondria information from big set of populations and individuals to understand the patterns of differentiation and the origin of new genetic groups.

The root of the flowering plants, re-re-revisited.

Isabel Marques, Don Les, Terry Macfarlane, John G. Conran, Paula Rudall, Maria Logacheva, Dmitry D. Sokoloff, Margarita V. Remizowa, Sean W. Graham

2B_302A-Plant Evolution
Sunday, June 22, 2014 10:30 AM-10:45 AM

Most molecular evidence points to a root of flowering-plant phylogeny that divides the angiosperm crown group into Amborella vs. all remaining species. However, a subset of analyses have persistently recovered alternative arrangements, typically connecting the root node between Amborella plus water lilies, vs. all other angiosperms. These results may be a result of low taxon density in angiosperms or outgroups, but concern seems warranted about this issue given the large phylogenetic distance that separates angiosperms from the other extant seed plants, a possible source of strong systematic error. Some recent publications have focused on using whole plastid genome samplings to investigate this problem (for analysis of the subset of protein-coding plastid gene regions, the plastid gene set). However, the number of relevant lineages that have had their plastid genomes sequenced is still relatively sparse. Here we revisit this question with an expanded sampling of plastomes from multiple lineages around the root node of angiosperm phylogeny. We are aiming for a complete genus-level sampling from the ANITA grade of angiosperms, and currently have 12 of the ~15 genera represented, which we generated using genome-survey sequencing and de novo assembly. Our sampling includes multiple outgroups and other angiosperms, in addition to multiple representatives of the aquatic family Hydatellaceae (Nymphaeales). We also sequenced full plastid circles for a representative subset of taxa to investigate genome structural evolution among these lineages, which define the earliest splits in angiosperm phylogeny.

Introgression of the allele for red fruit color from cultivated to wild papaya through feral intermediates

Richard Moore, Meng Wu, Jamicia Lewis

2B_302A-Plant Evolution
Sunday, June 22, 2014 10:45 AM-11:00 AM

Red fruit color in cultivated papaya is the result of a 2bp loss-of-function insertion in the coding region of the beta-lycopene cyclase gene that normally regulates the conversion of lycopene (red) to beta-carotene (yellow). In order to address the origin of this allele, we sample genetic diversity at the beta-lycopene cyclase locus in a survey of red-fruited and yellow-fruited cultivars, wild papaya populations in Costa Rica, and feral individuals within the same region. We found a strong signature of positive selection in red cultivars the form of a selective sweep spanning over 100kb, consistent with selection for this allele in red cultivars during papaya domestication. Furthermore, we found that while the red allele exists at

The mechanisms of frequency-dependent selection in gynodioecious Lobelia siphilitica

L. Ruth Rivkin, Andrea Case, Christina Caruso

2B_302A-Plant Evolution
Sunday, June 22, 2014 11:00 AM-11:15 AM

Frequency-dependent selection occurs when the fitness of an individual depends on its phenotype and on the frequency of that phenotype within the population. Negative frequency-dependent selection is thought to be common in gynodioecious plants, where individuals are either female or hermaphroditic plants; if the fitness of female plants is limited by the availability of pollen to fertilize their ovules, then females should have higher fitness when they are rare relative to hermaphrodites. Although negative frequency-dependent selection is often invoked to explain how females persist in gynodioecious species, it is rarely experimentally tested. To test whether females have higher fitness when rare, we manipulated the frequency of female and hermaphrodite plants within artificial populations of the gynodioecious wildflower, Lobelia siphilitica. We also hand-pollinated half of the female plants in each population to test whether the mechanism of frequency-dependent selection is variation in pollen availability. Females set 44% more fruits in populations where they were rare relative to hermaphrodites, as expected if frequency-dependent selection contributes to the persistence of females in gynodioecious species. However, the relationship between fruit set and female frequency was the same for hand- and open-pollinated plants, indicating that variation in pollen availability was not the mechanism of frequency-dependent selection. Instead, both hand- and open-pollinated females produced 33% more flowers in populations where they were rare, suggesting that changes in flower production can also be a mechanism of frequency-dependent selection. This mechanism could explain how females persist in gynodioecious species even when reproduction is not limited by pollen availability.

Optimal sampling of plant populations for ex-situ conservation of genetic biodiversity, considering realistic population structure

Sean Hoban, Scott Schlarbaum

2B_302A-Plant Evolution
Sunday, June 22, 2014 11:15 AM-11:30 AM

Ex situ conservation collections (e.g. seed banks or botanic gardens) require high diversity to enable future reintroduced populations to adapt, but are limited in size due to financial constraints. Keeping in mind the goal of maximizing diversity while minimizing collection size, collectors must decide how many samples to collect, and from which populations. Population genetic structure (i.e. subdivision), which is common in plants, may be an important consideration for such collections because it results in locally restricted alleles or traits, which have high conservation value. Population structure also means that other alleles are redundant, i.e. present in more than one population, increasing their chance of being sampled. It has been previously suggested, in general terms, that when a species is subdivided and/or has a large range, samples should be taken from across the range, but the relative advantage of such spatially distributed sampling has not been quantified in any study. To fill this knowledge gap, we utilized computer simulations to evaluate the expected performance of an array of sample sizes and several spatial distributions of sampled populations under different levels of realistic hierarchical population structure. Specifically, we quantified how population structure affects the expected probability of capturing different categories of alleles (especially rare alleles). Our findings suggest that when range-wide population structure exists, the spatial distribution of sampled populations is crucial: sampling one population per region captured up to 175% more alleles than sampling all populations in one region, and sometimes nearly as much as sampling all existing populations. The spatial effect is strongest for poorly connected (low gene flow) species, and for particular allelic categories. Under realistic population structure, moderate sampling (25-30) from few but widely-spaced populations performs well, which differs from previous recommended sampling sizes that do not consider structure. Results are consistent for biallelic (SNP) and hypervariable (microsatellite) markers, and for simulated medium and large geographic ranges. Our results demonstrate that spatial considerations are crucial aspect when establishing an ex situ collection, especially in poorly connected plant species. Our simulation approach can be extended to particular species and other spatial patterns such as clines. We use the widely distributed tree butternut (Juglans cinerea L) as a case study for planning a sampling strategy.

What ion channel gene duplications can tell us about the origin(s) of the nervous system

Benjamin Liebeskind, David Hillis, Harold Zakon

2B_302B-Trait Evolution
Sunday, June 22, 2014 10:15 AM-10:30 AM

Animals are the only multicellular lineage to have nervous systems, suggesting that the evolution of complex electrical signaling was an extremely unlikely event. However, recent phylogenetic data supports the idea that the nervous system, or at least complex nervous systems, may have evolved several times in the animal lineage. To what extent are the nervous systems of extant animals convergent?

The profusion of genomic data allows us to compare the genetic complements of extant animals and infer what genes were present in ancestral lineages. We have previously shown that the genes which cause action potentials in nerve and muscle, the voltage-gated sodium channels, have an ancient origin, and that key molecular and biophysical changes occurred convergently in multiple animal phyla which suggest multiple origins of complex nervous systems (Liebeskind et al. 2011). But extant nervous systems rely on many different ion channel types for their complexity.

Here, we use a gene tree/species tree reconciliation approach to illustrate the evolutionary history of the main ion channel gene families that power the nervous system. We find broad support for the idea that complex nervous systems arose independently in multiple animal lineages. Interestingly, however, the gene families with the largest independent radiations tend to be those that shape, rather than create action potentials. This suggests that the common ancestor of extant animals was capable of simple electrical impulses, and that the retention of a core set of ion channel genes set the stage for the convergent evolution of complexity. Thus we favor a more gradual scenario of parallel evolution rather than a model of convergent evolution of nervous systems de novo. This gradualist model best explains the patterns we see today and helps clarify one of the most remarkable achievements of the evolutionary process.

Search for the evolutionary origin of the brain

Hiroshi Shimizu

2B_302B-Trait Evolution
Sunday, June 22, 2014 10:30 AM-10:45 AM

How the brain appeared during metazoan evolution is a challenging problem. A widely accepted scenario is that nervous system started as diffuse nerve net in primitive invertebrates like Hydra and that nervous system became cephalized later in advanced invertebrates like Planaria. By using Hydra, we started a project to search for the nervous system that shows functions of the brain in a primitive form. The primitive functions of the brain are (1) perception of external stress, (2) processing of the stress information, (3) behavioral response to the external stress. We obtained evidence that the nervous system in the peduncle of Hydra shows the functions above listed. We interpret the evidence to demonstrate that the peduncle nervous system of Hydra constitutes brain of a primitive form. We are currently analyzing the anatomy of the peduncle nervous system and investigating possible mechanism of information processing by the diffuse nerve net.

Impacts of anthropogenic disturbance to phenotypic traits under selection in incipient speciation

Justin Yeager, Ralph Saporito, Kevin McGraw, Cori Richards-Zawacki

2B_302B-Trait Evolution
Sunday, June 22, 2014 10:45 AM-11:00 AM

An active dynamic exists between phenotypes and local habitats whereby over time selection works to shape species such that their fitness is often increased by adaptiving to local conditions. Local habitats not only serve as the setting by which phenotypic signals are perceived, but can can also the source of traits that can influence them. Disturbance due to anthropogenic land use may change not only the signaling environment, but also the fitness landscape of a species. The Panamanian poison frog Dendrobates pumilio displays an impressive variety of rapidly diverged color patterns throughout a relatively small geographic range. (Aposematic) coloration is thought to be central to reproductive isolation between populations where phenotypic divergence is thought to be generated and maintained by the product of prezygotic isolation via female mate choice and postzygotic isolation via predatory avoidance to honest aposematic signaling. Here we show the effects local microhabitats have on the availability of exogenous resources such as defensive alkloids, and fitness and color-influencing carotenoids. We put these differences into context using visual modeling techniques to infer how disturbance effects divergent traits under selection.

Estimating phenotypic selection in an age-structured moose Alces alces population by removing transient fluctuations

Thomas Kvalnes, Steinar Engen, Bernt-Erik Saether, Erling J. Solberg

2B_302B-Trait Evolution
Sunday, June 22, 2014 11:00 AM-11:15 AM

We provide an extension for the selection differential in the Robertson-Price equation for the mean phenotype in an age-structured population. We demonstrate that temporal changes in the mean pheno-type caused by transient fluctuations in the age-distribution and variation in mean phenotype among age classes, which can mistakenly be interpreted as selection, will disappear if reproductive value weighting is applied. We use this to show that the change in any weighted mean phenotype in an age-structured population may be decomposed into between- and within-age class components. Using reproductive value weighting the between-age class component becomes pure noise, generated by previous genetic drift or fluctuating selection. This component, which we call transient quasi-selection, can therefore be omitted when estimating age-specific selection on fecundity or viability within age classes. This approach provides a general approach to analyse selection on the mean phenotype in fluctuating age-structured populations.

We apply this approach to estimate selection on birth time and calf body mass in a population of individually marked moose Alces alces from northern Norway. In this area mean spring temperatures has increased by 1 degree Celcius over the last half a century, and the same trend is present during the study period, though only significant in April. Contrary to our expectations we find that birth dates has increased over the years, and there is no support for negative or positive selection of birth time. On the contrary, we detect negative selection of calf body mass across years which is strongest in the first age class, though there has been no temporal change mean calf body mass.

The Unbearable Lifespan of Beings: A Revision to the Evolutionary Theory of Ageing

Adam Chippindale, Christopher Kimber

2B_302B-Trait Evolution
Sunday, June 22, 2014 11:15 AM-11:30 AM

Drosophila repeatedly reared on a short lifecycle for three decades show no detectable decline in lifespan, contrary to the predictions of the evolutionary theory of ageing. Genetic variation conforming to extant theory (antagonistic pleiotropy, mutation accumulation) may be lacking, but this is not supported by multiple experimental analyses. Using experimental mutation accumulation in early life, we show that selection against harmful mutations has life-extending effects approximately eight times beyond the age of reproduction enforced in lab culture. These data suggest severe constraint on the evolution of longevity imposed by positive pleiotropy. The Evolutionary Theory of Ageing has not given much weight to the importance of positive pleiotropy, limiting its ability to explain the lifespan of organisms.

Multimodal signaling in the North American barn swallow: influences of intra- and intersexual selection on signal evolution

Matthew Wilkins, Maxwell Joseph, Joanna Hubbard, Rebecca Safran

2B_302C-Sexual Selection
Sunday, June 22, 2014 10:15 AM-10:30 AM

Complex signals, involving multiple components within and across modalities (e.g. visual or acoustic), are ubiquitous in animal communication. Numerous studies show benefits of complex signals in reducing search costs and maximizing signal efficacy. However, the interactions between multiple components of complex signals across modalities have not often been considered. Additionally, studies of complex signaling have typically focused on the role of female preferences in driving complexity, ignoring the contribution of intrasexual competition. Here, we utilize the North American barn swallow (Hirundo rustica erythrogaster) to demonstrate a novel approach for understanding the evolution of complex communication systems, in the context of male and female receivers. We integrate model testing with correlation-based phenotype networks to infer the contributions of intra- and intersexual selection on the evolution of the barn swallow communication system. We find that different signaling traits likely evolved via female choice versus male-male competition, with little signal overlap across contexts. We suggest that applying our approach broadly across taxa and sender-receiver contexts will afford researchers new insight into the selective pressures and constraints affecting the evolution of communication.

Intrasexual competition between females leads to aggression toward sexually receptive intruders in convict cichlids (Amatitlania siquia)

Ashley Robart, Barry Sinervo

2B_302C-Sexual Selection
Sunday, June 22, 2014 10:30 AM-10:45 AM

While the role of intrasexual aggression between males in shaping mating dynamics has long been recognized, the role of female intrasexual aggression in the competition for mating opportunities is less well understood. Rather than competing for quantity of mates, females may instead compete for access to the benefits, such as parental care, that males provide. Unmated females may compete for access to already mated males and if this causes a reduction in the reproductive success of the primary female then selection should favor females that behave aggressively toward rival females. Increased aggression toward rival females can effectively maintain monogamy in simultaneous polygynous species and this same behavior may prevent male desertion in predominantly monogamous species. Convict cichlids (Amatitlania siquia) form monogamous pairs and provide up to six weeks of biparental care to their offspring. Sexually receptive females have distinctive coloration of black pigmentation with iridescent flecks of blue, orange, and yellow. These unpaired females actively court paired males guarding offspring, and parental males have been observed to desert their current brood in order to mate with the new female. To examine the role of aggression by parental females in maintaining their mating status, we conducted an experiment to investigate whether parental females respond differently to a confined intruder depending on the intruder's reproductive status. Parental females responded more aggressively to sexually receptive females compared to non-reproductive females. Sexual receptivity of the confined intruder did not affect aggression levels toward other nearby fish, indicating that parental females did not increase their overall level of aggression when presented with a sexual rival but directed their attacks only toward the perceived threat. By increasing their behavioral response toward sexual rivals, parental females may be able to mitigate threats to their breeding status. The number of offspring reaching independence decreases under female-only care, and thus females have a strong incentive to maintain the pair-bond as long as possible. Increased aggression toward sexual rivals may play an important role in the maintenance of monogamy, which will aid in females maximizing their reproductive success for the breeding event.

The eunuch phenomenon: adaptive evolution of genital emasculation in sexually dimorphic spiders

Matjaz Kuntner, Ingi Agnarsson, Daiqin Li

2B_302C-Sexual Selection
Sunday, June 22, 2014 10:45 AM-11:00 AM

Under natural and sexual selection traits often evolve that secure paternity or maternity through self-sacrifice to predators, rivals, offspring, or partners. Emasculation—males removing their genitals—is an unusual example of such behaviours. Known only in insects and spiders, the phenomenon's adaptiveness is difficult to explain, yet its repeated origins and association with sexual size dimorphism (SSD) and sexual cannibalism suggest an adaptive significance. In spiders, emasculation of paired male sperm-transferring organs (palps), results in 'eunuchs'. This behaviour has been hypothesized to be adaptive because (i) males plug female genitals with their severed palps (plugging hypothesis), (ii) males remove their palps to become better fighters in male–male contests (better-fighter hypothesis), perhaps reaching higher agility due to reduced total body mass (gloves-off hypothesis), and (iii) males achieve prolonged sperm transfer through severed genitals (remote-copulation hypothesis). Prior research has provided evidence in support of these hypotheses in some orb-weaving spiders but these explanations are far from general. Seeking broad macroevolutionary patterns of spider emasculation, we review the known occurrences, weigh the evidence in support of the hypotheses in each known case, and redefine more precisely the particular cases of emasculation depending on its timing in relation to maturation and mating: 'pre-maturation', 'mating', and 'post-mating'. We use a genus-level spider phylogeny to explore emasculation evolution and to investigate potential evolutionary linkage between emasculation, SSD, lesser genital damage, and sexual cannibalism. We find a complex pattern of spider emasculation evolution, all cases confined to Araneoidea: emasculation evolved at least five and up to eleven times, was lost at least four times, and became further modified at least once. We also find emasculation, as well as lesser genital damage and sexual cannibalism, to be significantly associated with SSD. These behavioural and morphological traits thus likely co-evolve in spiders. Emasculation can be seen as an extreme form of genital mutilation, or even a terminal investment strategy linked to the evolution of monogyny. However, as different emasculation cases in araneoid spiders are neither homologous nor biologically identical, and may or may not serve as paternity protection, the direct link to monogyny is not clear cut.

Are female mating decisions adaptive when environments vary? A test using natural resource variation

Jennifer Hamel, Christine Miller

2B_302C-Sexual Selection
Sunday, June 22, 2014 11:00 AM-11:15 AM

Female mate choice can vary according to environmental context. Few studies have examined whether context-dependent mate choice is adaptive, and, if adaptive, whether fitness benefits are direct or indirect. Leaf-footed cactus bugs (Narnia femorata) provided an opportunity to test if context-dependent female mate choice results in direct or indirect fitness benefits. In this species, males defend high- or low-quality cactus territories were offspring develop – territories with or without cactus fruit, a high-quality nutritional resource. Females discriminate against males when males are reared without fruit, but only when they encounter those males in territories with fruit. We examined the direct and indirect fitness consequences of female mate choice across contexts. We found that mating context (high- or low-quality cactus territory) and male diet (reared with or without fruit) influenced both female fecundity and female reproductive success. In contrast, we found that offspring diet, but not sire diet, influenced offspring adult body size. Our findings suggest that for female N. femorata, context-dependent mate choice is adaptive, and results in direct, but not indirect fitness benefits.

Runaway and good genes processes are not ends of a continuum

Geoffrey Hill

2B_302C-Sexual Selection
Sunday, June 22, 2014 11:15 AM-11:30 AM

Biologists have long debated the evolution of animal ornamentation via female choice. Early in this discussion, a dichotomy in explanations emerged in which mate choice was proposed to be either adaptive, leading to the evolution of condition-dependent signals of quality, or arbitrary, leading to the evolution of aesthetic traits. In recent reviews, the evolutionary processes leading to adaptive or arbitrary mate choice have been recast as ends of a continuum. I propose that ornamental traits that signal condition are distinct from arbitrary signals of attractiveness in degree of elaboration, in the information that they convey, and in the evolutionary processes through which they evolve. Condition-dependent traits evolve as signals of respiratory efficiency and especially signals of mitonuclear compatibility. In contrast, aesthetic traits evolve as signals of species identity allowing females to choose mates with shared mitochondrial types. Once they are fixed in a population, arbitrary signals of species identity can be elaborated through a runaway sexual selection process into the gaudy traits displayed by some species. The outcome of these processes is two distinctly different types of ornaments that evolve to serve distinctly different signal function. Display traits can be fully understood only by embracing this dual nature of animal ornamentation.

Chromosomal inversions and avian speciation

Daniel Hooper, Trevor Price

2B_303-Macroevolution
Sunday, June 22, 2014 10:15 AM-10:30 AM

Birds have long been used as models of speciation and are the best-studied group with respect to how behavior and ecology contribute to population divergence but an integrated evaluation requires an assessment of factors that drive post-mating isolation as well. Despite strong evidence that chromosome rearrangements contribute to adaptation and speciation in other groups, the degree to which they do so in birds remains to be examined. Indeed, chromosome rearrangements have been dismissed as unimportant in avian evolution despite the paucity of study and some evidence to the contrary. The Old-World finch family Estrildidae (order Passeriformes) provides an ideal system for studying variation in rates of chromosome evolution and the underlying factors responsible. The Estrildids comprise over 100 morphologically and karyotypically diverse species broadly distributed across Africa, Asia, Australasia, and Melanesia. A phylogenetic approach to investigating the drivers of inversion evolution in Estrildids based on a combination of cytological, demographic, and geographic data shows that the rate of inversion evolution varies almost 4-fold between equivalently aged continental and island radiations. The fixation rate of inversions differs greatly between groups of Estrildids; inversions accumulate four times faster on average in continental groups. Rates of rearrangement are strongly correlated with range overlap of species and marginally with population size. My results support an adaptive model of karyotype evolution whereby gene flow between diverging populations establishes the selective advantage for chromosomal rearrangement.

Macro- and microevolutionary perspectives on the evolution of terrestrial egg-laying in frogs

Justin Touchon

2B_303-Macroevolution
Sunday, June 22, 2014 10:30 AM-10:45 AM

The ability to reproduce away from water has evolved repeatedly in animals but the way that organisms shift from one state (reproducing in water) to an alternative state (reproducing out of water) is not well understood. Amphibians are ideal organisms for studying this transition as non-aquatic forms of reproduction have evolved more than 50 times independently. Using a group of South and Central American treefrogs in the genus Dendropsophus that span from aquatic to terrestrial egg-laying, I have been studying variation in adult behavior and embryo development. Aquatic egg-laying is ancestral and fixed terrestrial reproduction has evolved several times in the genus, with flexible reproduction being found in multiple species as the most probable intermediate stage. Furthermore, it appears that terrestrial oviposition behavior evolves before embryo adaptations for developing in air that preclude development in water. Although selection from aquatic predators pushes frogs to lay eggs out of water, comparing populations of the species Dendropsophus ebraccatus demonstrates that obligate terrestrial egg-laying can only evolve in environments which are wet enough to prevent egg desiccation on land. This has implications for our understanding of the evolution of terrestriality and, more generally, the role of plasticity in evolution.

The Diversification of LINE Transposable Elements in Vertebrate Genomes: Patterns and Processes

Akash Sookdeo, Stephane Boissinot

2B_303-Macroevolution
Sunday, June 22, 2014 10:45 AM-11:00 AM
The Diversification of LINE Transposable Elements in Vertebrate Genomes: Patterns and Processes

Akash Sookdeo and Stephane Boissinot

LINEs (Long Interspersed Nuclear Elements) constitute the dominant category of autonomously replicating retroelements in vertebrate genomes. They have been a significant source of evolutionary novelties and have considerably affected the size and structure of vertebrate genomes. In fact, with the exception of autopolyploidy, LINE abundance is the major determinant of genome size differences among vertebrates. The impact LINEs have on the evolution of their host depends on their abundance and diversity which result from the interactions between the rate of transposition, the intensity of selection against new inserts and the demographic history of populations. To decipher between these different processes we performed a comprehensive evolutionary analysis of the LINEs in the genome of 12 vertebrate species representative of all major vertebrate lineages (mammals, reptiles, amphibians, fish). Two general patterns emerged. First, there is a clear difference between mammals and non-mammalian vertebrates: LINEs in mammalian genomes have a very low diversity but are represented by extremely large copies number whereas non-mammalian vertebrates have a large diversity of LINEs, each represented by small copy numbers. This suggests a fundamental difference in the way mammalian and non-mammalian genomes interact with their intra-genomic parasites. Second, we determined that, in all vertebrates, the diversification of LINEs is driven by the acquisition of novel promoter sequences, suggesting that novel LINE lineages emerge and amplify only when they do not compete with other lineages for host-encoded transcription factors. We hypothesize that the emergence and replicative success of LINE lineages depends on their ability to colonize a novel transcriptional niche in the genome of their host.

Sample sequencing of 40 squamate reptile genomes reveals extensive evolutionary dynamics of genomic repeat element landscapes

Richard Adams, Daren Card, Drew Schield, Todd Castoe, Jacobo Reyes Velasco

2B_303-Macroevolution
Sunday, June 22, 2014 11:00 AM-11:15 AM
More than 450 million years of vertebrate evolution has resulted in surprisingly low variation in gene number, despite tremendous variation in overall genome size. The genomic repeat landscape, however, exhibits a complex evolutionary history that is highly correlated with fluctuations in genome size and structure. Furthermore, these non-coding repeat elements are now known to play import roles in diverse genomic processes, including recombination, regulation of gene expression, and regional chromatin state. Recent sequencing of 32 Squamate genomes has revealed extensive variation in the genomic repeat element content of Squamate reptiles. This remarkable variation contradicts the accepted view that the greatest variation in genomic repeat content exists between major amniote clades (e.g., between mammals and birds), and not within any one lineage. In this study, we expanded taxonomic sampling and gathered preliminary data on the genomic repeat landscape of Squamate reptiles. Our results indicate unprecedented divergence in repetitive content, structure, and abundance within a major amniote lineage, with certain Squamate species exhibiting a repeat content of ~50% (similar to mammals), while other species having a proportion of repeats less than 30% (more similar to birds). Our results indicate that both transposable elements and simple sequence repeats (microsatellites) contribute significantly to repeat landscape variation among species, and further demonstrate that certain transposable elements previously identified to be associated with microsatellite expansion and venom gene duplication appear to be greatly expanded in venomous lineages of snakes.

Tick-tock goes the croc: Three genome drafts indicate slow molecular evolution in crocodilians and provide insight into archosaur evolution

David Ray, Richard Green, Benedict Paten, Travis Glenn, Edward Braun, Brant Faircloth, Federico Hoffmann, Toni Gabaldon, Fiona McCarthy, Carl Schmidt, Matthew Fujita, Juan Opazo, Arian Smit

2B_303-Macroevolution
Sunday, June 22, 2014 11:15 AM-11:30 AM
We present genome drafts of three crocodilians, Alligator mississippiensis (the American alligator), Crocodylus porosus (the saltwater crocodile), and Gavialis gangeticus (the Indian gharial), each representing one of the three extant families of the Order Crocodylia. The larger clade that includes turtles, crocodilians, and birds is noteworthy in the exceptionally slow karyotype evolution in all three groups and slow morphological evolution of turtles and crocodilians. We find that this slow rate of evolution is recapitulated at all levels within crocodilian genomes including nucleotide substitutions, insertions and deletions, transposable element content and movement, and chromosomal synteny. Furthermore, analysis of heterozygosity indicates that each of the three crocodilians suffered a reduction in population size through the Pleistocene. Finally, using these crocodilian genomes, multiple avian genomes, and multiple outgroups, we inferred the genome of the archosaurian common ancestor, providing a tool to investigate the genetic starting material of crocodilians, birds, and dinosaurs.

Exploring pattern and process in the evolutionary history of the mycorrhizal symbiosis

Hafiz Maherali, Brad Oberle

2B_304-Microbial Evolution
Sunday, June 22, 2014 10:15 AM-10:30 AM
The vast majority of plants form symbioses with soil fungi, which provide plants with nutrient uptake services in return for sugars from photosynthesis. Even though the symbiosis is widespread, several plant lineages have evolved the ability to exclude fungi from their roots, suggesting that the symbiosis is not always favoured by natural selection. To understand the causes of variation in the symbiosis, we used a ~3000 taxon database and a fossil calibrated molecular phylogeny to reconstruct of the evolutionary history of the symbiosis. We also explored evolutionary associations between ecological climate niches and the Arbuscular Mycorrhizal (AM), Ecto Mycorrhizal (EM) and Non Mycorrhizal (NM) character states. Estimates of transition rates away from the ancestral AM state suggested that losses of the symbiosis (the NM state) are more frequent than transitions to the EM state. Nevertheless, transition rates back to the AM symbiosis from the NM state were an order of magnitude more frequent than losses, suggesting that natural selection tends to favour the evolution of this symbiosis. We found that transitions from the AM to the NM state and from the AM to the EM state were accompanied by a shift to colder climate niches. This pattern is consistent with previous reports of greater cold sensitivity in fungal lineages that form AM associations relative to fungal lineages that form EM associations. Cold climates may therefore restrict the evolution of the AM symbiosis, but not the EM symbiosis. These findings will assist future tests of causal hypotheses about the origin, maintenance and consequences of the mycorrhizal symbiosis.

Individual variation in the gut microbiome of wild mushroom-feeding Drosophila

Vince Martinson, John Jaenike

2B_304-Microbial Evolution
Sunday, June 22, 2014 10:30 AM-10:45 AM
As in all animals, the insect body is teeming with complex communities of microorganims that affect many aspects of host biology. The species composition of the gut microbiota is thought to be environmentally acquired in most insects and influenced by diet, geography, age, and sex. Endosymbiotic mutualists can provide nutrients, detoxify diets, or provide protection from pathogens; conversely, pathogens can manipulate reproduction, alter behavior, or sterilize their host. However, the interaction between these infections and the gut microbiota is unknown. Drosophila is a genus that includes an abundance of ecologically varied species, in Upstate New York there are several specialist species that can subsist on toxic mushrooms. These flies are susceptible to the same nematode parasite (Howardula aoronymphium) and are differentially infected by endosymbionts. Here we survey the bacterial microbiota of individual wild-caught flies from the mushroom-feeding species, D. putrida, D. falleni, and D. neotestacea. Geographic and temporal collections allow us to identify individual microbiota variation and host-restricted bacteria. By sampling individuals that differ in infection status of either endosymbionts (i.e. Wolbachia and Spiroplasma) or parasites (i.e. nematode and trypanosomatid) we assess their effect on the microbiome.

Gut microbiome diversity across cichlid fish in Lake Tanganika

Karen Sullam, Peter McIntyre, Catherine Wagner, Susan Kilham, Jacob Russell

2B_304-Microbial Evolution
Sunday, June 22, 2014 11:00 AM-11:15 AM
Intestinal microbes play an essential role in their hosts' digestion, development, immune system and overall fitness. Though gut bacterial communities are known to vary widely among vertebrates, the relative influences of evolutionary lineage, surrounding environment, and diet of the host are poorly understood. In this study, we examine these factors in shaping the gut bacteria across cichlid fishes from Lake Tanganyika, East Africa using Illumina amplicon sequencing of 16S rRNA. First, we surveyed the gut bacteria of 26 cichlid species and 6 non-cichlid species representing diverse trophic ecologies (algivory, piscivory, invertivory, omnivory, zooplanktivory, scale-ripping) collected from a single site. Preliminary results suggest that both phylogeny and diet play a role in shaping gut bacterial communities. In the second part of our study, we analyzed two algivorous cichlids that differ in feeding strategy and trophic morphology, including one grazer-scraper, Petrochromis sp. "kazumbe", and one browser, Tropheus brichardi, collected from eight discrete sites. Gut microbial communities differed somewhat consistently between these species, but there were also strong differences within species according to geographic location. In particular, the gut bacterial community of Petrochromis sp. "kazumbe" appears to show distinct geographic structure relative to a large embayment separating groups of sites. Overall, our analyses indicate that gut bacterial communities in Tanganyikan fish are shaped by the trophic ecology of their hosts as well as phylogenetic and biogeographic influences. This study provides new insights into understanding the mode and tempo of gut microbiota shifts across ecologic, phylogenetic and geographic distances.

The evolution and ecology of ant gut microbiomes

Corrie Moreau, Jacob Russell

2B_304-Microbial Evolution
Sunday, June 22, 2014 11:15 AM-11:30 AM
Molecular methods are revealing how endosymbiotic bacteria have facilitated the origins and maintenance of herbivory across the ants. Using next-generation sequencing to uncover ant microbial community diversity we are testing the association of gut bacteria with host phylogeny and host trophic ecology using stable isotopes to determine whether the stability and composition of gut communities can be explained by shared evolutionary history or trophic level. These findings demonstrate that herbivorous ants have a stable and diverse gut microbiome which likely facilitated their shift to a herbivorous diet.

An evolutionarily conserved epigenetic element converts wild fungi from metabolic specialists to generalists

Alex Lancaster, Daniel F. Jarosz, Jessica Brown, Susan Lindquist

2B_305A-Molecular Evolution
Sunday, June 22, 2014 10:15 AM-10:30 AM

[GAR+] is a protein-based element of inheritance that allows yeast (Saccharomyces cerevisiae) to circumvent a normal hallmark of their biology: extreme metabolic specialization for glucose fermentation. When glucose is present, even in trace quantities, yeast will not use other carbon sources. [GAR+] allows cells to circumvent this "glucose repression". When [GAR+] appears spontaneously, it allows a small fraction of a yeast population to "hedge it's bets" by evading glucose repression. We find these de novo rates correlate with the yeast's ecological niche. Evolutionarily distant fungi also possess similar epigenetic elements, and many of the proteins involved in the [GAR+] phenotype show significant homology across these evolutionary distances. Furthermore, population genetic modeling based on these experimental data support an inference that the bet-hedging characteristics of [GAR+] may be under selection, suggesting that it may be a broadly conserved adaptive strategy.

Resource abundance influences genome-wide DNA methylation levels in wild baboons (Papio cynocephalus)

Amanda Lea, Jeanne Altmann, Sayan Mukherjee, Susan Alberts, Jenny Tung

2B_305A-Molecular Evolution
Sunday, June 22, 2014 10:30 AM-10:45 AM

Ecological variation, experienced in both early life and adulthood, can have strong, stable, and persistent effects on adaptively relevant traits in mammals. For example, resource limitation in early life predicts reduced adult fertility in preindustrial human populations, faster reproductive senescence in wild red deer, and reduced lifetime fitness in wild baboons. However, the molecular mechanisms that mediate these relationships remain unclear. Recent evidence suggests that changes in DNA methylation, which can affect gene expression and, via these changes, downstream organismal phenotypes, may contribute to the persistence of early life effects. However, we still know little about the degree to which ecological variation mediates epigenetic patterning in natural populations, or about the plasticity of these effects when the environment changes. To address these questions, we measured genome-wide DNA methylation in wild male baboons (N=66) that experienced lifelong differences in resource abundance: either a calorie-rich diet obtained by foraging near a human settlement, or a lower calorie diet obtained from natural foraging in a savannah environment. We used multiplexed reduced representation bisulfite sequencing (mRRBS) to measure CpG methylation levels at over 300,000 sites, representing over 60% of genes and CpG islands in the baboon genome. We found evidence for a relationship between diet and DNA methylation at 2-fold more sites than expected by chance. Intriguingly, some of the most dramatic changes occurred near PFKP, an insulin-responsive gene involved in the glyocolytic pathway, and KCNIP4, which has been linked to obesity in humans. To investigate plasticity in the diet-DNA methylation relationship, we further investigated DNA methylation levels in males that switched between feeding regimes in early adulthood (N=8). Both clustering and machine learning classification approaches indicated that switching males more closely resembled low calorie, wild-feeding males, regardless of whether they originated from wild-feeding social groups or switched into them as adults. However, site-by-site analyses suggested a mosaic pattern containing molecular signatures of both early life and adult environments. Our findings suggest that some genes are stably affected by early life diet, while other genes remain plastic in response to prevailing resource abundance.

Preliminary Evidence for DNA Methylation as a Mechanism of Adaptive Transgenerational Plasticity in the Annual Plant Polygonum persicaria

Jacob Herman, Sonia Sultan

2B_305A-Molecular Evolution
Sunday, June 22, 2014 10:45 AM-11:00 AM

Transgenerational plasticity has garnered much research interest in recent years, but several key questions remain: how often do these environmentally induced effects influence fitness; for how many generations do they persist; and how are these effects inherited? Recent studies of the annual plant Polygonum persicaria showed that drought stress induces functionally appropriate changes in offspring root growth that persist for at least two generations and lead to increased survival under severe drought stress of seedlings whose grandparents and parents grew in dry soil. I will present preliminary evidence that inheritance of drought-induced DNA methylation changes may be a mechanism for transmitting these adaptive effects. The results of methylation-sensitive AFLP (MSAP) analysis of ~200 anonymous marker loci suggest that drought causes changes in DNA methylation that are transmitted to offspring grown in a common, moist-soil greenhouse environment. I will also present tests for drought-induced changes in DNA methylation patterns within a generation, including tests for correlations between specific drought-induced DNA methylation epialleles and adaptive, drought-induced phenotypes. The use of multiple, highly inbred Polygonum genetic lines in these studies allows for assessments of genetic diversity in the induction and inheritance of phenotypes and DNA methylation patterns.

The role of MEE57 and global 5mC methylation on natural variation in flowering time in Arabidopsis thaliana

Joshua Banta, Christina Richards

2B_305A-Molecular Evolution
Sunday, June 22, 2014 11:00 AM-11:15 AM

Heritable phenotypic variation may be influenced by epigenetic changes, adding another layer of complexity to evolutionary processes. But specific examples linking genetic variation, epigenetic variation, and phenotypic variation are rare. Genome-wide methylation of DNA strongly influences flowering phenology in Arabidopsis thaliana laboratory strains, and natural A. thaliana strains vary in their genome-wide methylation levels. Genes of the METHYLTRANSFERASE gene family are important regulators of genomewide DNA methylation patterns in A. thaliana. We found that one of these genes, MATERNAL EFFECT EMBRYO ARREST 57

(MEE57) harbors high-frequency, naturally segregating, non-synonymous alleles that are associated with variation in flowering phenologies among wild strains. This suggests that MEE57 provides a mechanism by which genomewide methylation patterns vary among naturally occurring individuals of A. thaliana, thereby influencing flowering time in the wild.

Molecular evolution of the RH2-opsin complex in Neotropical cichlid fish: are they different or just slower than African cichlids?

Julián Torres Dowdall, Michele Pierotti, Frederico Henning, Kathryn R Elmer, Axel Meyer

2B_305A-Molecular Evolution
Sunday, June 22, 2014 11:15 AM-11:30 AM

Cichlid fishes are very colorful – they are called Buntbarsche, colored perches in German - and they possess one of the most diverse visual systems among vertebrates. This made them an important system for the study of how visual sensitivity evolves in response to natural and sexual selection. The adaptive molecular evolution of opsin proteins in cichlids from the African Great Lakes is strongly correlated to their recent adaptive radiation and their pronounced sexual dimorphism in coloration. Much less is known about the visual system of Neotropical cichlids, the sister lineage of African cichlids. Work on the Trinidadian pike cichlid suggests that Neotropical cichlids might have a reduce set of opsins, particularly in the green sensitive RH2-complex where only one paralog of the three found in African cichlids appears to be functional. This, coupled with the fact that the radiation of Neotropical cichlids is ancient and sexual dimorphism in coloration is not the norm in this lineage, suggests that the rate of adaptive molecular evolution might be lower in Neotropical than in African cichlids. To test this hypothesis, we compared the molecular evolution of the RH2 opsins between Neotropical and African cichlids. We characterized the diversity of RH2 opsin genes in the Neotropical lineage by taking advantage of the ongoing Amphilophus citrinellus species-complex genome project. Then, we sequenced these opsins in Neotropical lake cichlids and combined it with published sequences from African lake cichlids to look for evidence of selection. We found functional copies of three paralogs of RH2 (RH2B and two RH2A) in Neotropical lake cichlids, which parallels those found in African cichlids. This might imply a date for the RH2A duplication event before the divergence of the African and Neotropical lineages. However, we cannot completely discard the hypothesis that there have been independent duplication events. Furthermore, we found evidence for positive selection in green-sensitive opsins of Neotropical cichlids, as previously found for rhodopsin. However, the signatures of selection were consistently weaker in Neotropical cichlids when compared to those seen in the opsin genes of African cichlids. This is potentially due to the rarity of sexual dimorphism in coloration in the Neotropical lineage, which might tend to reduce reinforcement on the molecular evolution of opsins due to sexual selection. Comparisons between the opsin proteins of Neotropical and African cichlids has the potential to further our understanding of the adaptive evolution of visual systems in response to natural and sexual selection.

Gene expression dynamics in a hibernating primate

Sheena Faherty, José Luis Villanueva-Cañas, M.Mar Albà, Anne Yoder

2B_305B-Gene Expression
Sunday, June 22, 2014 10:15 AM-10:30 AM

Extant mammals display a vast array of morphological characteristics, behavioral responses, and physiological traits. These apparent differences between taxa offer fascinating tools for investigations into the evolutionary dynamics that give rise to the panoply of mammalian species seen today. Contemporary comparative evolutionary analyses provide considerable potential to answer questions regarding the evolutionary forces shaping complex phenotypic adaptations, such as hibernation.

In recent years we have witnessed how the study of the molecular processes involved in mammalian hibernation has shifted from investigating a few carefully selected candidate genes to performing large-scale differential gene expression analysis. Currently, the use of next-generation high-throughput transcriptome sequencing (RNA-Seq) provides a global, unbiased view of how genes function in concert to regulate hibernation behavior.

To date, much work has been accomplished to illuminate the means by which differential gene expression is involved in the switch from a summer active phenotype to a winter hibernation phenotype in some of the most well studied hibernating species including ground squirrels (Spermophilus spp.), American black bears (Ursus americanus), and little brown bats (Myotis lucifugus); however, there is a significant knowledge gap concerning the underlying genetic mechanisms that govern hibernation in the only primates known to naturally exhibit hibernation behavior, the dwarf lemurs (Genus Cheirogaleus) endemic to Madagascar.

This study aims to elucidate differential gene expression dynamics in white adipose tissue from four captive C. medius housed at the Duke Lemur Center. To that end, we used next-generation transcriptome sequencing from samples collected at three time points throughout the year, which resulted in over 300 million reads. Our downstream analyses uncovers over 300 genes that show differential expression between the active and hibernation state in dwarf lemurs. In addition, we find that pathways involved in oxidation of fatty acids were enriched during hibernation when compared with the active state. By applying next-generation sequencing approaches to a non-traditional primate model system, we have the capability to investigate intriguing evolutionary questions that were previously intractable.

RNA-seq Reveals Regional Differences in Transcriptome Response to Heat Stress in the Marine Snail Chlorostoma funebralis

Lani Gleason, Ron Burton

2B_305B-Gene Expression
Sunday, June 22, 2014 10:30 AM-10:45 AM

To investigate the role of gene regulation in adaptation of marine ectotherms to different climates, we used a transcriptomic approach to examine thermal stress response in heat sensitive and heat tolerant populations of the intertidal marine snail Chlorostoma (formerly Tegula) funebralis. In this study, snails from two southern (heat tolerant) and two northern (heat sensitive) populations were acclimated to a common lab environment, exposed to a heat stress representative of natural low tide conditions, and then analyzed using RNA-Seq to characterize changes in gene expression associated with stress and differences in expression across geographic regions. Changes in expression following stress were dominated by genes involved in apoptosis, response to mis and unfolded proteins, and ubiquitination of proteins. Heat shock proteins (Hsps) were up-regulated in both northern and southern populations, but the magnitude of the response was significantly greater in northern populations for the majority of Hsp70s, while the southern populations showed greater up-regulation for roughly half of the Hsp40s, which are co-chaperones for Hsp70s. Differential expression analysis of the control versus treatment genes in the northern and southern populations respectively revealed that 55 genes (31.1% of all genes differentially expressed (DE) between control and treatment conditions in northern populations), responded to heat stress only in the northern populations. Moreover, several of the molecular chaperones and antioxidant genes that were not DE in the southern populations instead showed higher constitutive expression under control conditions compared to the northern populations. The expression levels of some of these genes such as an Hsp40 homolog were also found to positively correlate with survival following heat stress. This suggests that expression of these genes has evolved a degree of “frontloading” that may contribute to the higher thermal tolerance of southern populations. These results indicate both up-regulation and frontloading of genes may be employed in evolutionary adaptation to thermal environments; moreover, the data also suggest populations differ with regard to which mechanisms have evolved for specific sets of genes.

The role of gene expression variation on climatic adaptation in Drosophila melanogaster

Vinayak Mathur, Paul Schmidt

2B_305B-Gene Expression
Sunday, June 22, 2014 10:45 AM-11:00 AM

Background and relevance:

Studying genetic responses and identifying mechanisms of adaptation to variable environments is essential in developing a comprehensive understanding of evolutionary dynamics in natural populations. Adaptive mechanisms in response to climatic factors help us understand the evolutionary dynamics of populations. The interplay of temperature and photoperiod cues is vital for several biological processes in nature. Additionally, these factors serve as predictable proxies for climatic variation over various spatial and temporal scales. We are interested in understanding the role transcriptome expression variation plays in the potential for adaptation to these climatic variables. In addition to adaptation, we want to understand whether certain gene expression patterns are associated with increased performance and fitness in particular environments or under specific environmental conditions.

Experimental design: We performed a whole genome expression screen for two natural populations of Drosophila melanogaster derived from high and low latitude sources in eastern North America. Both populations were placed for five days under four fully factorial variables: hot (29 °C) and cold (14 °C) temperatures and long (15 hrs Light: 9 hrs Dark) and short day photoperiod (9 L: 15 D) conditions. RNA was then extracted and sequenced from each of the four treatment combinations. The flies were also assayed to test their phenotypic stress response under heat shock, chill coma and starvation resistance after being placed in both field and lab conditions for a period of five days.

Results: Phenotypic stress response results show that northern and southern populations of flies respond differentially to environmental cues. The data demonstrates that southern populations are generally more starvation tolerant, whereas northern populations are more resistant to heat shock. These phenotypic data are placed in the context of the molecular data from the whole genome expression screen. Using this transcriptomic data we are identifying candidate genes that show significant and differential genotype by environment interactions, and thus represent candidates in the adaptive response to climatic variation. The expression of these candidate genes will then be manipulated and direct effects on phenotype and fitness will be examined.

Conclusion: This work combines phenotypic and genotypic data to answer questions of fitness and adaptation. Specifically, we are investigating 1) how the geographical origin of the population affects response to environmental cues and 2) how the variation in response is associated with variation in genotype. These investigations allow us to use genotypes to understand the potential adaptive basis of phenotypic responses.

In what types of environments is inbreeding depression strongest?

Aneil Agrawal, Li Yun

2B_305B-Gene Expression
Sunday, June 22, 2014 11:00 AM-11:15 AM

Selection against inbred genotypes (i.e, inbreeding depression, ID) is stronger in some environments than others. In what types of environments should we expect to find strong ID? Previous studies indicate that ID is positively correlated with the stressfulness of the environment in which it is measured. However, it remains unclear why stress, per se, should increase ID. To our knowledge, only 'competitive stress' has a logical connection to the strength of ID. Using D. melangaster, we estimated ID for viability in 22 different environments. These environments were simultaneously characterized for (i) stressfulness (the reduction in absolute viability) and (ii) density-dependence, as a measure of the sensitivity of fitness of individuals to those around it. Though stress and density dependence are moderately correlated with each other, ID is much more strongly correlated with density dependence.

Some (do not) Like It Hot: The Role of Tumor Necrosis Factor Receptor in Heat Stressed Corals

Nikki Traylor-Knowles, Francois Seneca, Stephen Palumbi

2B_305B-Gene Expression
Sunday, June 22, 2014 11:15 AM-11:30 AM

Corals are complex, beautiful animals that harbor symbiotic algae. Sometimes called, "the rainforests of the ocean," they provide shelter and food for other ocean organisms. They are however, in danger due climate change, and little is known about how they can adapt and deal with these changes. The tumor necrosis factor receptor (TNFR) may act as a molecular switch and help determine how corals react to environmental stress, including heat stress. The “front-loading” of TNFR expression in corals that have historically been exposed to stressful environmental conditions could be indicative of resilience in corals. TNFR has the potential to be a “coral health biomarker.” There is a subset of genes with expression values that are correlated with the expression of TNFR in corals. We hypothesize that the function of these genes with TNFRs in corals is involved in many important cellular processes; including immunity, apoptosis and combating environmental stress. I am currently testing the role of different TNFR genes in response to heat stress in the coral Acropora hyacinthus from American Samoa in order to understand how the gene expression of TNFR reacts to changes in the environment. The novel role of TNFR as a heat-induced switch could broaden our understanding of the evolutionary role of this gene.

Combined morphological and multigene analysis allows comprehensive taxon sampling of the subfamily of pitvipers (Serpentes: Crotalinae)

Allyson Fenwick, Christopher Parkinson

2B_306A-Phylogenies and Phylogenetics
Sunday, June 22, 2014 10:15 AM-10:30 AM

Pitvipers are a useful model organism for many evolutionary questions, including biogeography and comparative biology. The group can be of even better use with a phylogeny including a maximal number of species. Although several studies have thoroughly sampled species relationships of genera or related groups of genera, the most comprehensive study to date included 126 of 224 currently-described species. Pitvipers share a challenge with a number of other vertebrate groups in that specimens are commonly preserved with formaldehyde, making tissues unavailable for DNA analysis but preserving thousands of specimens for morphological examination.

This study combines morphological data for over 90% of species with multigene mitochondrial data for over 75% and a nuclear locus for over 40%. It is the first study to include morphology in a large-scale phylogenetic context for Asian pitvipers. We evaluate the placement of limited-data morphology-only taxa (approximately 98% incomplete in a matrix of over 4500 characters) and the effect of combining these independent datasets. We investigate pitviper intergeneric relationships, which have been historically difficult to resolve due to short internal branches. We discuss species- and genus-level relationships which have not been reported or have been controversial in prior work.

Using full-genome sequencing to infer the species tree in Neodiprion sawflies (Hymenoptera: Diprionidae)

Matthew Niemiller, Kim Duong, Catherine Linnen

2B_306A-Phylogenies and Phylogenetics
Sunday, June 22, 2014 10:30 AM-10:45 AM

North American pine sawflies in the genus Neodiprion offer an excellent opportunity to study how host use, behavior and development influence adaptation and speciation, as extensive variation exists in a wide range of ecologically-relevant traits among taxa in the genus. However, estimating an accurate species tree for comparative studies has proven difficult in this group. Specifically, recent divergence (i.e., incomplete lineage sorting) and interspecific gene flow have complicated previous efforts of species-tree inference that utilized a handful of loci. Next-generation sequencing now allows the generation multilocus data sets consisting of hundreds to thousands of unlinked loci for phylogenetic inference, which have the potential to provide further resolution to the processes underlying speciation. Here, we generated phylogenomic data from 22 taxa in the N. lecontei species group and related outgroups and used a recently developed reference genome for N. lecontei to guide genome assembly and annotation. We will compare estimates of the species tree using several recently developed approaches for genome-scale species tree inference, including *BEAST (with subsampling of loci), MP-EST, BFD* and PHYLDOG, as well as a previous estimate of the species tree based on three nuclear genes. We will then propose phylogenetic hypotheses for the N. lecontei species group based on these analyses. An accurate specie tree and the genomic resources generated will provide the foundation for future comparative studies examining genetic convergence of candidate genes underlying phenotypic traits that are the target of adaptive evolution in Neodiprion.

Phylogenomics and biogeography of a rapid radiation of crocidurine shrews across the Philippines

Thomas Giarla, Jacob Esselstyn

2B_306A-Phylogenies and Phylogenetics
Sunday, June 22, 2014 10:45 AM-11:00 AM

The Philippine archipelago is a global biodiversity hotspot and a commonly used island biogeographic model, but the mammalian fauna remains poorly understood. New mammal species are still regularly described, including within the diverse Old World shrew genus Crocidura (>175 species). Previous attempts to resolve the evolutionary relationships among Philippine Crocidura species (10 currently described) have been based on a limited number of loci, yielding poorly supported phylogenetic trees. To resolve these relationships, we sequenced thousands of ultraconserved elements

(UCEs) and whole mitochondrial genomes (WMGs) across multiple individuals from nearly all Philippine Crocidura species using a sequence capture approach. We inferred phylogenetic trees for both UCEs and WMGs by applying species-tree methodologies and locus-concatenation approaches. Our results suggest that the radiation of shrews across the Philippines was rapid. The concatenated gene tree and the species tree feature short internodes, highlighting the importance of using phylogenomic datasets to resolve rapid radiations.

Anchored phylogenomics and transcriptomics: comparisons between two next-gen data sets used for estimating deep-level relationships in Lepidoptera

Jesse Breinholt, Alan Lemmon, Emily Lemmon, Akito Kawahara

2B_306A-Phylogenies and Phylogenetics
Sunday, June 22, 2014 11:00 AM-11:15 AM

Butterflies and moths are some of the most charismatic and well-known insects. Relationships between major butterfly and moth superfamilies, especially those among the megadiverse clade Ditrysia, remain largely uncertain. Our recent application of transcriptomic data (938 genes) to lepidopteran phylogenetics resulted in strong support for challenging inter-familial relationships, such as those within the superfamily Bombycoidea. In the present study, for transcriptomes analysis we present a new Lepidoptera-specific core ortholog set for use in the program Hamstr built from 6,568 putative single copy orthologs and an anchored phylogenomics probe set of 855 genes that successfully captures targets across the diversity of lepidopteran superfamilies. We sampled taxa from 19 superfamilies across the Lepidoptera and generated transcriptomes and anchored hybrid enrichment data to estimate higher relationships of this diverse insect order. We compare the resulting topologies and node support from several different data sets and discuss the benefits and shortcoming of the two methods. One striking result was the strong support for the placement of butterflies within the lower microlepidopteran grade of superfamilies in nearly all of our analyses. Furthermore, our results indicate that nucleotide saturation, especially at the third codon position, affect both types of data and must be accounted for when estimating deep-level lepidopteran relationships

---

Rapid phylogeny construction from next-gen sequencing data

Rachel Schwartz, Reed Cartwright

2B_306A-Phylogenies and Phylogenetics
Sunday, June 22, 2014 11:15 AM-11:30 AM

Whole genome sequence data provides exciting opportunities to estimate phylogenies accurately. We have developed software, which we call SISRS (pronounced “scissors”) that rapidly extracts an alignment of variable, homologous sites from next-gen data, regardless of synteny, using a composite assembly and custom filters. We demonstrate the effectiveness and speed of this approach using simulated and empirical data from genome and transcriptome sequencing. For each empirical dataset, we identified hundreds of thousands of variable sites, resulting in a fully supported, bifurcating tree.

Determining orthology using identity thresholds reduces the comparability of genomic datasets

Michael Harvey, Robb Brumfield

2B_306B-Methodology
Sunday, June 22, 2014 10:15 AM-10:30 AM

Comparing patterns of genetic diversity across species permits insight into the shared processes responsible for organismal diversity. As massively parallel sequencing approaches are used to examine more species, there is understandable interest in using genomic datasets to compare diversity across datasets. Comparisons are hampered, however, by differences resulting from the way genomic datasets are processed.

Unlike in the days of conserved primers and standardized markers, assessing the orthology of massively parallel sequencing reads is not straightforward. Sequence identity thresholds are typically established in an attempt to assemble orthologous data while separating or removing paralogous data. Due to differences across the genome in the amount of variation, however, thresholds are expected to imperfectly distinguish between paralogous and orthologous data. As a result, a substantial number of more divergent orthologous regions may be removed inadvertently from many datasets.

We examined the influence of the loss of orthologous regions due the use of identity thresholds on estimates of genetic diversity. We used simulations to examine the effect of thresholds on simulated datasets with shallower versus older divergences as well as small versus large population sizes. We used the filtered datasets to estimate commonly used indices of diversity including theta and divergence time with a coalescent-based approach. We found that applying the same thresholds separately on each dataset resulted in differences in the number of orthologous loci removed, and also in a commensurate downward bias in estimates of divergence time and theta. Consistent with the simulation results, we observed a decrease in parameter estimates with lower identity thresholds in real next-generation sequencing data from populations of a Neotropical bird.

Our results suggest that the use of identity thresholds may bias inferences from massively parallel sequencing datasets particularly when comparing across species, populations, or genomic regions with different levels of variation. We suggest that the limited comparability of massively parallel sequencing datasets could be alleviated by using prior information to inform thresholds, removing paralogs using heterozygosity rather than identity thresholds, correcting inferences using truncated probability distributions, or using loci that are sufficiently conserved that assembly is straightforward and thresholds are unecessary. We expect that genomic datasets, combined with approaches to account for or avoid truncation in the distribution of locus variation, will improve comparability across datasets and permit new insights into patterns of diversity across species.

Temporal scaling of spontaneous mutation rates: implications for the neutral theory of molecular evolution

Philip Gingerich

2B_306B-Methodology
Sunday, June 22, 2014 10:30 AM-10:45 AM

Temporal scaling is to rates and their corresponding time denominators as fractal scaling is to sizes and their corresponding measurement-unit denominators. Spontaneous mutation rates (mutations/nucleotide/generation) are known for substantial samples of (1) ssRNA+, (2) ssRNA−, (3) dsRNA, (4) ssDNA, (5) dsDNA, (6) bacterial DNA, (7) unicellular eukaryote DNA, (8) multicellular eukaryote DNA, (9) multicellular eukaryote mtDNA, and (10) human pedigree mtDNA. Temporal scaling of rates for each group yields log-rate versus log-interval (LRI) temporal scaling slopes that are consistently negative, with slope values ranging from −0.31 to −0.66. Negative slopes mean that rates averaged over multiple generations substantially underestimate the base rate of interest: the rate per generation on a time scale of one generation. Stochastic change typically has a negative temporal scaling slope, but the expectation for random mutation is a slope on the order of only about −0.05. In four (and probably seven) of the ten RNA, DNA, and mtDNA groups studied, observed temporal scaling slopes are significantly more negative than expected by chance. Slopes more negative than expected indicate that molecular evolution is systematically constrained rather than neutral. This constraint is a signature of stabilizing natural selection. Finally, negative temporal scaling slopes dictate the mathematical form of clock-like behavior for molecular evolution driven by spontaneous mutation.

Teams of Transcription Factors are rewired in the evolution of Ascomycota fungi

Adriana Munoz

2B_306B-Methodology
Sunday, June 22, 2014 10:45 AM-11:00 AM

The upstream regulator of a group of functionally linked and co-regulated genes, a group known as a regulon, sometimes changes in related species. Nonetheless function and expression of the orthologous gene group across those Species is conserved. Specific cases of such transcriptional network rewiring have been characterized, but there are likely to be many more instances than have been reported so far. For example, it has been reported that Rap1 in Saccharomyces cerevisiae substituted Tbf1/Cbf1 in Candida albicans for ribosomal RP genes. A systematic computational approach to detect transcriptional network rewiring is needed to gain insight into evolutionary mechanisms as well as to interpret experimental results in related model organisms. We develop a novel computational technique to detect rewiring of transcriptional networks where the Transcription Factor (TF) regulating a set of genes is replaced by another TF during evolution. Our method is applied to evolutionarily conserved co-expressed gene groups across 23 yeast species for 126 TFs. Our dataset of Species includes Saccharomyces cerevisiae, Candida albicans and Ashbya gossypii. The last one is economically important pathogen of cotton. Our method successfully detects TF substitution for the ribosomal RP regulon consisting of ribosomal RP genes. It is intriguing that sometimes a group of TFs appears to be switched with a second group of TFs for a group of genes. Then, we use our technique to answer a question: Can a group or "team" of Transcription Factors (TFs) switch with another team of TFs for a collection of related genes in related Species through evolution? For a group of 30 RP genes, our method finds a team of six TFs that collectively switch with another team of six other TFs for 10 most recently evolutionary diverged Species after the Whole Genome Duplication (WGD) event. In another example, for a "Regulation of Growth" gene, we find a team of three TFs that collectively switch with another team of five other TFs for the same 10 Species including Saccharomyces cerevisiae. We can estimate the time of the switch to be 100 million of years ago, the estimated time when the WGD occurred.

Detecting concerted demographic history using hierarchical approximate Bayesian computation

Yvonne Chan, Michael Hickerson

2B_306B-Methodology
Sunday, June 22, 2014 11:00 AM-11:15 AM

Methods that integrate population-level sampling from multiple taxa into a single community-level analysis are an essential addition to the comparative phylogeographic toolkit. Here we present a statistical framework for such an analysis based on hierarchical approximate Bayesian computation (hABC) with the goal of detecting concerted demographic histories across an ecological assemblage. Detecting how species within communities have demographically tracked each other in space and time is important with regards to understanding the effects of future climate and landscape changes and the resulting acceleration of extinctions, biological invasions and potential surges in adaptive evolution. Furthermore, whether species responded individualistically or in concert is at the center of related questions about the abiotic and biotic determinants of community assembly. Our method combines population genetic datasets from multiple taxa into a single analysis to estimate: 1) the proportion of a community sample that demographically expanded in a temporally clustered pulse; and 2) when the pulse occurred. The method is appropriate for population-level DNA barcode data broadly sampled across a wide breadth of taxa and can accommodate dataset heterogeneity such as variability in effective population size, mutation rates, and sample sizes across species and exploits the statistical strength from the simultaneous analysis of multiple species. This hABC framework used in a multi-taxa demographic context can increase our understanding of the impact of historical climate change by determining what proportion of the community responded in concert or independently, and can be used with a wide variety of comparative phylogeographic datasets as biota-wide DNA barcoding data sets accumulate

---

A general nonparametric method for correcting the allele frequency spectrum for misidentified ancestral states

Chris Nasrallah, Alexander Griffing, Jeffrey Thorne

2B_306B-Methodology
Sunday, June 22, 2014 11:15 AM-11:30 AM

The allele frequency spectrum is an effective tool for the detection of positive selection. But the power of the frequency spectrum depends on being able to correctly determine which alleles are derived and which are ancestral. Misidentification of the derived state mimics the effect of positive selection, leading to frequent false positives. The problem is compounded when the variants are indels, because misidentification leads to classifying an insertion as a deletion (and vice versa). The ancestral allele is often determined by estimating the allele carried by the common ancestor of the lineage of interest and an outgroup species, and using this as a proxy for the true ancestral allele. This is problematic, even when a probabilistic model is used to do so, due to multiple mutations on the lineage of interest. Requiring consistency with additional outgroup species does not fully resolve the misidentification and results in much of the data being discarded. Here we present a straightforward nonparametric method for correcting the observed allele frequency spectrum for misidentified ancestral states. The method uses the frequency of polymorphic and fixed site patterns to estimate the ancestral state probabilities and treats the observed allele frequency spectrum as a mixture of correctly identified and misidentified sites. The method makes no assumptions about the presence or absence of natural selection, the model of evolution, or the exact phylogenetic tree relating the species. Additionally the method can be used for both SNPs and indels and can be used with any group of species.

Diversification of seepage salamanders across a complex geologic landscape

David Beamer, Sean Graham

2B_306C-Phylogenetic Systematics
Sunday, June 22, 2014 10:15 AM-10:30 AM

The seepage salamander, Desmognathus aeneus, occupies many distinct physiographic regions and several independent river drainage basins. Within this range, seepage salamander populations tend to be localized and most are apparently disjunct. The disjunct nature of these populations coupled with the complex geological and ecological history of the region occupied by these salamanders provides conditions which are conducive to lineage diversification. During the course of a range wide survey of seepage salamander, we visited nearly every historical site from which this species has been reported; in addition we discovered many previously unknown populations. Here we report the first phylogeographic survey of these minute salamanders. A Bayesian phylogenetic reconstruction of both mitochondrial DNA and nuclear genes reveals the presence of several well supported, distinct evolutionary lineages. The presence of multiple lineages within seepage salamanders has important conservation implications.

Evolution of a troglobitic salamander, Eurycea spelaea

John Phillips, Sarah Emel, Dante Fenolio, Ronald Bonett

2B_306C-Phylogenetic Systematics
Sunday, June 22, 2014 10:30 AM-10:45 AM

The biology of many cave-dwelling organisms (troglobites) is poorly known due to their cryptic lifestyles and inaccessible habitat. Low dispersal and high habitat fragmentation has led to significant phylogeographic structure in several widespread subterranean organisms. However, an insufficient amount of phylogeographic studies of troglobites exist. This is of particular importance given the potential for unrecognized cryptic species within troglobitic taxa. The Grotto Salamander (Eurycea spelaea), endemic to the Ozark Plateau, is confined to life in caves during its adult life. Currently there is only one recognized species of Grotto Salamander, but recent work has revealed high levels of genetic diversity and indications of cryptic speciation. In this study, we further investigate the fine scale genetic diversity and geographic structure within E. spelaea. Mitochondrial DNA shows evidence of three highly divergent lineages across the Ozarks. We employed next-generation sequencing techniques to compare nuclear genes to mitochondrial divergence and test if these patterns are correlated with geologic and hydrologic features of the Ozark Plateau. In order to better understand the pressures directing the evolution of cave-dwelling vertebrates, we compared the phylogeographic structure in E. spelaea with other troglobitic salamanders.

Phylogeographic analysis of the polytypic Red-crowned Ant Tanager Habia rubica (Cardinalidae) at a continental scale

Pablo Lavinia, Natalia Garcia, Patricia Escalante, Natalia Trujillo-Arias, Kazuya Naoki, Cristina Miyaki, Fabricio Santos, Pablo Tubaro, Dario Lijtmaer

2B_306C-Phylogenetic Systematics
Sunday, June 22, 2014 10:45 AM-11:00 AM

The Neotropics harbor the highest avian diversity of the world, but the study of the processes leading to this accumulation of bird species has gained more attention just during the last two decades. Phylogeographic studies of Neotropical species have been concentrated mainly in the Amazon basin, the Andes mountain range and more recently the Atlantic Forest, but analyses at a continental scale are comparatively rare. In this study we explore the intraspecific diversity of the Red-crowned Ant Tanager (Habia rubica), a lowland forest dweller with a fragmented distribution with four major areas: Central America and southeastern Mexico; Pacific coast of southern Mexico; the Atlantic Forest in eastern South America; and the Yungas-Amazonia complex in western South America. This species is one of the most polytypic passerines in the region, with 17 subspecies, but several of these are poorly differentiated and hard to recognize. Here we include nearly 120 tissue samples from 9 countries throughout the species distribution and we perform genetic analyses based in two mitochondrial markers (cytochrome c oxidase subunit I and cytochrome b) and two nuclear loci, one Z-linked (intron 9 of the low density lipoprotein receptor gene) and one autosomal (intron 5 of the β-fibrinogen gene). We have generated unrooted median-joining and statistical parsimony networks, and inferred phylogenies using both Bayesian and maximum parsimony methodologies. The analyses of the mitochondrial markers have shown the existence of four main lineages with deep divergence that match the fragmented areas of the species distribution.The deepest split is between the populations of Central America and Mexico from those of South America, despite the existence of a high genetic divergence (6-7% in mitochondrial DNA) both between the two northern clades (Central America-southeastern Mexico and Pacific coast of Mexico) and the two South American clades (Atlantic Forest and Yungas-Amazonia complex). Preliminary analysis of nuclear markers show less resolution but congruent results .Additionally, we are carrying out complementary studies of behavioral characters (vocalizations), and our preliminary results show the existence of significant differences in both temporal and frequency variables of the song that are consistent with the lineages found in the genetic analyses. We believe that the high divergence found among clades and the presence of differences in vocalizations suggest that a taxonomic revision of this species is needed. The analyses of the obtained patterns could also provide new insights into the history of some of the most overlooked forest habitats of the region.

RAD-Seq-based phylogenetics of New World oaks (Quercus L.)

John McVay, Andrew Hipp, Paul Manos

2B_306C-Phylogenetic Systematics
Sunday, June 22, 2014 11:00 AM-11:15 AM

The genus Quercus (oaks) of North and Central America comprise the majority of oak global diversity, however relationships within and among the taxonomic sections and series remain poorly understood. Here we utilize genomic-scale DNA sequence data (RAD-Seq) to infer the relationships among the New World oaks, leveraging the most species- and nucleotide-rich dataset to date. Sequence data was collected for 287 individuals; homologous loci across individuals were identified via clustering algorithm, and maximum likelihood estimates of phylogenies were produced. When concatenated (3252671 sites; 174373 parsimony informative sites), these data provide a robust estimate of the deep splits among the major clades of North American oaks, largely validating previous treatments, but also revealing some novel relationships. Clustering at differing percentage similarity thresholds within loci produced largely concordant trees, with differences within each estimate due to anomalous placement of poorly sequenced individuals. The phylogeny reveals a pattern of early-branching northern clades, with parallel dispersals into Latin America for the two major clades: red (section Lobatae) and white oaks (section Quercus). We also find evidence for two distinct Holarctic radiations in the white oaks. With a framework of the phylogeny established, these data are being used to explore genomic signatures of hybridization in regional subclades by subsampling both taxa and loci, and employing methods that incorporate population-level processes, such as lineage sorting and introgression, into models of sequence evolution.

Cryptic and not-so-cryptic species complexes in sea cucumbers reveal rapid rates of secondary sympatry

Francois Michonneau, Gustav Paulay

2B_306C-Phylogenetic Systematics
Sunday, June 22, 2014 11:15 AM-11:30 AM

Having a clear understanding of species limits and their geographical distributions are critical to formulate hypotheses about speciation, and the relative contributions of ecological and historical factors explaining their ranges. In the sea, where geographical barriers to gene flow are rare, the potential for long-ranging dispersal is high, and the taxonomy of most groups chaotic, basic information about the identity of species and their geographical distribution is lacking. Large-scale biodiversity surveys combined with barcode sequencing speed up the documentation of this basic information and allows for the identification of species complexes. Here, we illustrate how by studying in detail two species complexes of sea cucumbers identified with this approach, we gain insights into the dynamics of their diversification. Holothuria impatiens first described from the Red Sea, was thought to occur across the Indo-Pacific, the Caribbean and the Mediterranean Seas. We combined nuclear and mitochondrial markers, using phylogenetic methods and the multispecies coalescent to show that "H. impatiens" is actually a complex of at least 13 reciprocally monophyletic species. Some are restricted to an oceanic bassin, while others are wide ranging. None but one species can be told apart based on the morphological character typically used in sea cucumber taxonomy (shape of microscopic calcareous skeletal elements). Most can however be distinguished based on their live appearance/coloration. We used a similar approach to demonstrate that the three species in the Holothuria edulis complex easily distinguishable morphologically but not with mitochondrial data, are most likely reproductively isolated. In both complexes, we found that species that diverged less than 100,000 years ago are co-occuring. This pattern contrasts with what has been found in other marine invertebrates where it typically takes over 5 millions years for sister species to co-occur. The biological mechanisms that allow for such rapid rates of secondary sympatry need to be investigated, in order to understand the variety of processes that have generated the high diversity characterizing the Indo-Pacific biota.

Assessing students' mental models of evolutionary change across the tree of life using the ACORNS instrument

Ross Nehm

2B_402-SSE Education Symposium: Assessing Undergraduate Student Understanding of Evolutionary Biology
Sunday, June 22, 2014 10:15 AM-10:45 AM

Empirical studies have revealed several limitations with multiple-choice (MC) assessments designed to measure students' knowledge of and naïve ideas about natural selection. First, while clinical oral interviews and constructed response assessments indicate that many students' mental models of natural selection and evolutionary change are comprised of heterogeneous mixtures of naïve and scientific ideas (Nehm & Schonfeld, 2008), many MC tests assume that students harbor homogeneous mental models and consequently only allow students to choose a "right" (scientifically normative) or a "wrong" (non-normative) answer option. Tests constructed in this format tend to produce faulty inferences about students' mental models of evolution. Second, although students' evolutionary reasoning has been shown to be strongly influenced by the taxa (e.g., plant vs. animal), traits (e.g., functional vs. non-functional), polarities (e.g., trait gain vs. loss), familiarities (e.g., penguin vs. prosimian), and scales (within vs. between species) of the item features contained in the assessment items (Nehm & Ha 2011; Opfer et al. 2012), many evolution assessments continue to ignore the effects of item features on biological reasoning, or only examine reasoning in one context (e.g., familiar animals). Tests constructed in this format tend to produce non-generalizable inferences about students' evolutionary understanding.

The ACORNS (Assessment of COntextual Reasoning about Natural Selection; Nehm et al. 2012) is an open-ended (written) diagnostic test designed to address the limitations of prior test designs. The ACORNS was developed to reflect the cognitive processes that students use to think about evolution, and validly assess the diverse ways in which students explain evolutionary change. Specifically, the instrument reveals students' cognitive models (e.g., pure scientific models, mixed models, and pure naïve models) as well as differences in reasoning (the mixtures of ideas they use) across item features (e.g., trait gain vs. loss in animals and plants). Several peer-reviewed studies have documented the psychometric properties of the ACORNS, including facets of construct validity (e.g., substantive validity, external convergent validity) and reliability (e.g., internal consistency) at several educational levels (high school, undergraduate, expert biologists) in multiple countries (USA, Korea, Germany, China). Studies testing for gender bias also indicate that the test does not discriminate between male and female test takers. Symposium attendees will be introduced to the ACORNS assessment, provided access to assessment items, introduced to an online portal that can be used to score open-ended responses to ACORNS items (www.evograder.org), and provided with examples of how the test has been used to measure learning.

Knowledge about and positive attitudes toward evolutionary theory: Curricular effectiveness as measured by the Evolutionary Attitudes and Literacy Survey (EALS)

Patricia Hawley

2B_402-SSE Education Symposium: Assessing Undergraduate Student Understanding of Evolutionary Biology
Sunday, June 22, 2014 10:45 AM-11:15 AM
The present work examined changes in students' (from the University of KS) attitudes toward and knowledge of evolution measured by the Evolutionary Attitudes and Literacy Survey (EALS) in response to curricular content. Student responses on the survey were compared across an evolutionary psychology course, an introductory biology course with significant evolutionary content, and a political science course with no evolutionary content. A multiple group repeated measures confirmatory factor analysis (CFA) was conducted to examine latent mean differences in self-reported Evolution Knowledge/Relevance, Creationist Reasoning, Evolutionary Misconceptions, and Exposure to Evolution. A significant and notable increase in Knowledge/Relevance, as well as decreases in Creationist Reasoning and Evolutionary Misconceptions were observed for the evolutionary psychology course, whereas the biology course demonstrated no change in Knowledge/Relevance and a significant increase in Evolutionary Misconceptions. The implications of these findings for the measurement of knowledge and attitudes, as well as evolution education are discussed.

An expanded survey of evolutionary mode in fossil lineages

Gene Hunt, Melanie Hopkins, Scott Lidgard

2B_BalC-SSE Symposium: Reuniting fossil and extant approaches to macroevolution
Sunday, June 22, 2014 10:15 AM-10:30 AM
Previous analyses of evolutionary patterns, or modes, in fossil lineages have overwhelming focused on three simple models: stasis, random walks, and directional evolution. Here we use likelihood methods to fit an expanded set of evolutionary models to a large compilation of evolutionary changes in ancestor-descendant series of populations from the fossil record. In addition to the standard three models, this set includes more complex models with punctuations and shifts from one evolutionary mode to another. As in previous studies, we find that stasis is common in the fossil record, as is a strict version of stasis that entails no real evolutionary changes. Incidence of directional evolution is relatively low (13%), but somewhat higher than in previous studies because our analytical approach can more sensitively detect noisy trends. Complex evolutionary models are often favored, overwhelmingly so for sequences comprising many samples. This finding is consistent with evolutionary dynamics that are, in reality, more complex than any of the models we consider. Finally, we use our empirical collection of evolutionary sequences and a long and highly resolved proxy for global climate to inform simulations in which traits adaptively track temperature changes over time. When realistically calibrated, we find that this simple model can reproduce important aspects of our paleontological results. We conclude that observed paleontological patterns, including the prevalence of stasis, need not be inconsistent with simple adaptive dynamics, even in the face of unstable physical environments.

An expanded survey of mosaic evolution in fossil lineages

Melanie Hopkins, Gene Hunt, Scott Lidgard

2B_BalC-SSE Symposium: Reuniting fossil and extant approaches to macroevolution
Sunday, June 22, 2014 10:30 AM-10:45 AM
Most analyses of evolutionary mode in fossil lineages focus on individual traits. Previous work has shown that individual traits measured from the same series of ancestor-descendent fossil populations may show different modes of evolution, implying that mosaic evolution is common across a wide range of organisms throughout Earth history. This previous work focused on modeling trait evolution using three simple models of uniform evolutionary dynamics (random walk, directional change, and stasis). Here we use likelihood methods to fit an expanded set of evolutionary models, including more complex models with punctuations as well as shifts from one evolutionary mode to another, to a larger compilation of fossil sequences. We find that within species lineages where more than one trait was measured, mode of evolution almost always varied among the traits, confirming previous findings. However, traits often shared the same type of evolutionary mode (either simple or complex). The timing of shifts in evolutionary dynamics among traits best fit by complex models of evolution was coordinated as frequently as not. In fact, within this dataset, we see examples where trait evolution is tightly correlated, examples where traits vary in the timing of shifts despite showing the same mode of evolution, and examples where there is no correspondence between mode of evolution or timing

of shifts among the measured traits. Finally, single traits may show variation in evolutionary mode even in situations where the overall morphological evolution of the lineages is dominated by one type of mode.

The 5% solution: is it sufficient?

Sandra Carlson, Holly Schreiber, David Bapst

2B_BalC-SSE Symposium: Reuniting fossil and extant approaches to macroevolution
Sunday, June 22, 2014 10:45 AM-11:15 AM

Brachiopoda is a clade of marine invertebrates in which approximately 95% of the named species are extinct. Reuniting paleobiological and biological approaches to the macroevolutionary study of the Brachiopoda offers some unique challenges – how representative are patterns among the extant 5% for the entire clade? How many of the extinct 95% lie outside of the crown clade? Locating the crown clade is essential to generalizing patterns of character evolution beyond the 5%, requiring detailed comparison of molecular and morphological phylogenetic hypotheses for both extant and extinct species. Furthermore, limitations of the fossil record require comparison to traditional Linnean classifications, as macroevolutionary processes among the Brachiopoda are often still inferred from patterns among supraspecific taxa, whose phylogenetic validity remain untested.

In our studies of the relationships among the '5%' extant articulated brachiopods, we have often uncovered disagreements between traditional classifications based on morphology, morphological phylogenies and molecular phylogenies of the same taxa. The differences between supraspecific groupings and inferred phylogenies are complex, implying a mosaic of agreement and disagreement at different taxonomic levels between these three sources of data. Brachiopoda as a phylum and a clade is supported by molecular and morphological data; so is the same set of extant orders and suborders, and they agree on their patterns of relationship. As we descend the taxonomic hierarchy and consider older and more basal clades, however, discordance increases. Superfamilies of Terebratellidina have some agreement to groups found by phylogenetic analyses, while superfamilies of Terebratulidina have less concordance with inferred phylogenies. Superfamilies of Rhynchonellida are in relatively poor agreement. Overall, most families are in poor agreement. This is problematic for macroevolutionary studies based on these non-monophyletic supraspecific taxa.

Molecular systematic analyses using the extant '5%' of brachiopods support the general hypothesis that body size has increased over the Phanerozoic for many animal groups. However, testing the hypothesis with the addition of extinct taxa from the fossil record and with known relationships to the crown clade allow for additional tests of this macroevolutionary hypothesis. Comparative analyses using phylogenies inferred from detailed molecular and morphological data can reveal macroevolutionary patterns and processes that cannot be detected in the absence of either the fossil record or comprehensive phylogenetic hypotheses.

Multilevel evolutionary processes in time and space

David Jablonski

2B_BalC-SSE Symposium: Reuniting fossil and extant approaches to macroevolution
Sunday, June 22, 2014 11:15 AM-11:45 AM

Integrating fossil and extant data can provide novel insights. Fossil data include direct morphological, spatial, and environmental information on a certain subset of extant and extinct taxa; extant data include an independent phylogenetic framework, and a richer set of phenotypic, biogeographic, and ecological variables, across a much broader range of taxa, than can be retrieved from the fossil record. In macroevolutionary analyses, multilevel processes sometimes operate in concert, and sometimes in opposing directions that can allow hitchhiking and other indirect effects. A new approach to comparative analysis of diversifications in time-stratified data re-affirms that diversifications can follow a variety of trajectories: Type 1, where morphological or functional diversity outstrips taxonomic diversity (this is more than an "early burst," but a discordance between taxonomic and phenotypic diversification that signifies an especially marked array of diverged phenotypes relative to the number of genealogical units that arise); Type 2, where morphological and taxonomic diversity are concordant, once the exponential expectation for early taxonomic diversification is incorporated; and Type 3, where morphological diversity lags taxonomic diversity. These dynamics are hierarchical: diversification by more inclusive clades can show Type 1 patterns while individual subclades show Type 2s or 3s (e.g. Blastozoa vs Blastoidea, Mollusca vs Bivalvia, ecological carnivores vs Carnivoramorpha), supporting the classic view that open ecospace is a crucial promoter of evolutionary bursts, although it may not be sufficient: present-day archipelagos and rift-valley lakes do not appear to be good analogs to the major diversifications of the geologic past when analyzed in this way. Geographic range size is often viewed as an emergent property of species, and as a bridge between local organismal adaptation and the extinction risk or speciation rate of clades, but its role can be complex in a multilevel system, and range-size distributions can evolve over time. In global analyses of extant marine bivalves, widespread species often tend to track widespread oceanic temperatures, rather than adapting to a wide variety of temperatures. This tolerance-range relationship evidently is an effective path to extinction-resistance for much of evolutionary time, indicating that most extinction is driven by local or regional perturbations, but during the end-Cretaceous mass extinction species-level geographic range was an ineffective buffer, and widespread clades survived preferentially, regardless of the geographic ranges (and presumed physiological tolerances) of their constituent species. This hierarchical shift in extinction selectivity evidently drove the loss of many aspects of organismic traits by macroevolutionary hitchhiking effects.

WHOLE GENOME RESEQUENCING OF EXPERIMENTAL LINEAGES OF DROSOPHILA MELANOGASTER EXPOSED TO CHRONIC LARVAL MALNUTRITION FOR OVER 150 GENERATIONS

R. Craig Stillwell, Tadeusz Kawecki

2C_201-Experimental Evolution

Sunday, June 22, 2014 1:30 PM-1:45 PM
Experimental evolution studies that are combined with whole genome sequencing offer great promise into providing insights about the mechanisms that drive evolution. Here we present a genome-wide analysis of six replicate lineages of Drosophila melanogaster that have been exposed to chronic larval malnutrition for >150 generations of selection. Compared to six replicate control populations, these populations now survive much better and develop/grow markedly faster on the poor food. The selected populations also have considerably longer development times and are smaller when raised on standard food. We pool sequenced 400 flies of each of the selected and control lineages after selection was relaxed and the lines were raised on standard food for two generations. Using next generation sequencing technology, we hope to unravel the genomic basis of evolutionary change driven by this malnutrition and identify candidate genes and pathways that are involved in the response to selection. We also hope this will generate new hypotheses about the molecular and physiological basis of improved malnutrition tolerance.

Male-limited evolution shapes sexual dimorphism in longevity

Hwei-yen Chen, *Alexei Maklakov*

2C_201-Experimental Evolution
Sunday, June 22, 2014 1:45 PM-2:00 PM
Sexes age at different rates and have different life expectancies across the animal kingdom but what causes the longevity “gender gaps” remains one of the most fiercely debated puzzles among biologists and demographers. Historically, “gender gaps” were claimed to stem from asymmetric inheritance of sex chromosomes or mitochondrial genomes leading to increased mutation load and reduced longevity in males. Alternatively, sex-limited selection in either sex can result in the evolution of sexual dimorphism if there is substantial sex-limited genetic variation in longevity. Here we use experimental evolution in roundworms, where males live longer than females, to show that both existence and magnitude of sex differences in longevity can depend exclusively on male-limited evolution. By increasing male extrinsic mortality rate, we experimentally demonstrated evolution of sexual monomorphism in longevity in a sexually dimorphic animal. Remarkably, when extrinsic mortality was increased in a condition-dependent manner, males evolved increased longevities thereby widening the “gender gap”. These results challenge the key role of asymmetric inheritance theories for longevity “gender gaps” and firmly advance sex-specific extrinsic mortalities as a primary evolutionary cause of intrinsic sex differences in longevity.

Conflict increases cooperation between microbial species

William Harcombe

2C_201-Experimental Evolution
Sunday, June 22, 2014 2:00 PM-2:15 PM
How does community context shape the selection for inter-specific cooperation? We investigate this question with a novel mutualism between Escherichia coli and a mutant Salmonella enterica. In lactose media E. coli excretes carbon byproducts required by S. enterica, and the S. enterica mutant excretes a costly amino acid that the E. coli can no longer produce. We competed mutualistic S. enterica against the non-cooperative wildtype in the presence of E. coli and found that the mutualist settled to 45% of the Salmonella population. The mutualism was then made more complex by changing the environment such that a third species, Methylobacterium extorquens, was required to provide nitrogen. Increasing community complexity dropped the frequency of cooperators maintained in the S. enterica population to 10%. Interestingly, if M. extorquens is switched from a mutualist to a competitor with S. enterica (i.e. nitrogen is made freely available), the ratio of cooperators increases to 60%, the highest observed frequency. Genome-scale metabolic modeling qualitatively recapitulates our results and suggests that a competitor increases inter-specific cooperation by reducing the benefit of cheaters. This work indicates that to understand the prevalence of mutualists it will be important to consider not only with whom each species is interacting, but also how they are interacting.

Evolution of ecological dominance of yeast species in high-sugar environments

Kathryn Williams, *Justin Fay*

2C_201-Experimental Evolution
Sunday, June 22, 2014 2:15 PM-2:30 PM
Evolutionary innovation that causes dramatic changes in lifestyle may permit the ecological dominance of descendent lineages. However, lineage dominance may lag behind innovation because dominance depends on certain environments or evolution of other traits. Identifying when dominance occurred in relation to innovation will help elucidate the role of innovation and subsequent evolved traits in the ecological success of some species. In this study, we explored fermentation in the presence of oxygen, an innovation in the yeast lineage, and dominance of Saccharomyces cerevisiae in high-sugar environments. Fermentation in the presence of oxygen evolved around whole genome duplication (WGD) in the yeast lineage and is suspected to confer dominance in high-sugar environments like grape juice. However, the relative fitness of most post-WGD species remains unknown and other traits besides fermentation in the presence of oxygen have been implicated in S. cerevisiae’s dominance. To determine when dominance in high-sugar environments evolved in the yeast lineage, we quantified the relative abundance of multiple pre- and post-WGD species following growth in co-culture with S. cerevisiae in two high-sugar environments: high-sugar rich medium and grape juice. S. cerevisiae was able to dominate nearly all other pre- and post-WGD species in both high-sugar environments except for its sibling species, S. paradoxus, indicating dominance evolved recently in the lineage that gave rise to S. cerevisiae and S. paradoxus. To test whether inherent growth differences could explain the dominance of S. cerevisiae, we measured the intrinsic growth rate of each species grown in monoculture in both high-sugar environments. During monoculture, all species grew as well as S. cerevisiae in high-sugar rich medium, while the majority of species grew slower than S. cerevisiae in grape juice. These results indicate that multiple mechanisms contribute to the dominance of S. cerevisiae in high-sugar environments. To further examine the phenotypic basis of S. cerevisiae’s growth advantage, we measured the intrinsic growth rate of each species in response to ethanol,

low-pH, and nutrient supplements. S. cerevisiae grew significantly better than multiple other species in response to ethanol and low-pH, and generally, S. cerevisiae did not benefit from additional nutrient supplements while the growth of many other species was enhanced. Overall, our results indicate that S. cerevisiae's dominance in high-sugar environments is not associated with evolution of fermentation in the presence of oxygen around WGD and that multiple recently evolved traits contribute to the ecological success of S. cerevisiae.

Experimental removal of parental care leads to the evolution of reduced offspring dependence in the burying beetle, Nicrophorus vespilloides

Matthew Schrader, Benjamin Jarrett, Rebecca Kilner

2C_201-Experimental Evolution
Sunday, June 22, 2014 2:30 PM-2:45 PM

Parents of many species provision their young after hatching or birth. Such provisioning is an important component of parental care that simultaneously influences the phenotype of offspring and the selective environment they experience. While there is considerable direct evidence that parents infleunce offspring phenotype, the evidence that offspring adapt to varaition in the level or form of parental care is less direct. We used experimental evolution to examine how populaitons of the burying beetle, Nicrophorus vespilloides, adapt to the complete removal of post-hatching parental care. We found that adaptation to the removal of post-hathcing parental care involved rapid changes in larval survival in the absence of care. Other measures of larval performence, such as the ability of larvae to consume a breeding carcass and larval mass at dispersal did not differ consistently between lines that had evolved with or without care.

Gymnosperm plastomes reveal rampant rearrangements and the retention of ndh pseudogenes in the Pinaceae

Stacey Thompson

2C_206-Phylogenetics and Phylogeography
Sunday, June 22, 2014 1:30 PM-1:45 PM

Chloroplast genomes are haploid uniparentally-inherited molecules, useful for estimating divergence and tracking gene flow. Although chloroplast genome structure is highly stable across the majority of angiosperms, gymnosperm plastomes are labile, with extensive gene losses and rearrangements, typically associated with a reduction of the inverted repeat. This poses small challenges for assemblies, with experimental validation typically required for contig ordering, gap filling, and isoform confirmation. To assess plastome structure within a broad phylogenetic framework, chloroplast genomes were sequenced, assembled and validated from Abies sibirica, Gnetum gnemon, Juniperus communis, Picea abies, Picea glauca, Picea obovata, Pinus sylvestris, and Taxus baccata. All ndh genes were fully retained in J. communis and T. baccata, completely excised in G. gnemon, and progressively pseudogenized in P. sylvestris and A. sibirica, suggesting convergent losses in the Pinaceae and Gnetales. Similarly, the inverted repeat appears to be independently reduced in Pinaceae and Cupressophyte clades. While there was high structural conservation between the plastomes of A. sibirica, P. sylvestris, and G. gnemon with their closest relatives, rampant rearrangements were detected within Picea and the Cupressophytes. Two major inversions and two translocations were detected between Juniperus and relatives, including a major 36 kbp Juniperus-specific inversion, flanked by two copies of trnQ and AT-rich breakpoints. At least four inversions have occurred after the divergence of Taxus baccata and Cephalotaxus wilsoniana, the largest being 20 kbp. A deep phylogenetic split was detected within Picea abies, and polyphyly of the group confirmed with sequence data that spans the mitochondrial genome. We will highlight applications of chloroplast genomes to our understanding of divergence and gene flow within conifers.

Tracing the dispersal of the baobab Adansonia digitata (Malvaceae: Bombacoideae) from Africa to the Indian Ocean region: An interdisciplinary approach

Karen Bell

2C_206-Phylogenetics and Phylogeography
Sunday, June 22, 2014 1:45 PM-2:00 PM

The baobab, Adansonia digitata, is indigenous to the African continent, but also found across the Indian Ocean region. Previous work has assumed that Medieval Arab traders dispersed the species from Africa to this region. In collaboration with researchers from in social science disciplines, I investigated the Arab trader dispersal hypothesis by analysing genetic structure and phylogenetic patterns of A. digitata in conjunction with historical references. Ten microsatellite loci in baobabs from Africa and across the Indian Ocean were used to examine genetic diversity and test for recent bottlenecks. A Bayesian classification scheme assigned individuals to genetic clusters, and phylogenetic analysis determined relationships between clusters. This data was combined with historical records of A. digitata introductions, and archaeological evidence of ancient trade routes, to examine various introduction scenarios. In this presentation, I will demonstrate how interdisciplinary data can be used to determine source populations for introduced species and infer dispersal pathways, supporting or refuting hypotheses posed by botanists and historians. I will provide evidence that the genetic history of baobab dispersal in the Indian Ocean region is more complex than the medieval Arab trader hypothesis.

Exon capture phylogenomics of Australian skinks

Jason Bragg, Sally Potter, Craig Moritz

2C_206-Phylogenetics and Phylogeography
Sunday, June 22, 2014 2:00 PM-2:15 PM

The Eugongylus group of skinks arose approximately 31 Ma. and became highly diverse in Australia, with ~140 extant species in 16 genera. We are using the Eugongylus group as a model taxon for understanding diversification on the Australian landmass, from macroevolutionary to phylogeographic scales. We have been pursuing this research using the approach of exon capture, and will present data illustrating the effectiveness of the method for generating data for thousands of loci with a broad spectrum of evolutionary rates. Finally, an advantage of using protein coding exons as markers is that a range of molecular evolutionary analyses can be performed -- we will highlight some inferences that can be drawn from these analyses.

Using genome-wide RAD markers to resolve character evolution and species history in Nymphalid butterflies

Emily Ebel, Sean Mullen

2C_206-Phylogenetics and Phylogeography
Sunday, June 22, 2014 2:15 PM-2:30 PM

Restriction-site associated DNA (RAD) methods can inexpensively generate large numbers of genome-wide markers for essentially any species. However, for phylogenetic studies of diverse, rapidly evolving taxa, mutations in restriction sites over time can lead to significant data loss for deep nodes. Here, we use double digest RAD to generate both SNP and marker presence/absence data for 57 species of mimetic Adelpha and Limenitis butterflies. The resulting phylogenies robustly indicate a rapid species radiation of tropical butterflies, in which labile wing pattern elements independently evolved multiple times. Selective pressure for mimicry, in synergy with the ability to exploit new food sources, appears to have driven rapid speciation in the lowland tropics. We demonstrate that RAD markers are a flexible tool for studying character evolution and species relationships, particularly when biologically relevant missing data is a component of evolutionary inference.

Pyrosequencing of surface waters in the English Channel reveals novel early-diverging fungal diversity

Kathryn Picard, Rowena Stern

2C_206-Phylogenetics and Phylogeography
Sunday, June 22, 2014 2:30 PM-2:45 PM

Although zoosporic fungi comprise the earliest-branching lineages within the fungal tree of life, they are also the most poorly characterized phylogenetically. Limited sampling of these fungi, especially from marine and estuarine habitats, and the combination of short backbone internodes with long diverging branches during the early evolution of the Fungi, account for much of this uncertainty. The primary hindrance to uncovering the full extent of zoosporic fungal diversity is the historical reliance on culture-dependent methods, resulting in the description of only the most abundant taxa, or those most amenable to isolation in the laboratory. The recent use of culture-independent molecular methods to characterize fungal diversity and community composition in terrestrial, freshwater, and extreme environments has revealed novel, early-diverging fungal phylotypes. Additionally, these studies have found that zoosporic fungal lineages are often the dominant fungal component of their respective ecosystems.

Since the recent description of the Cryptomycota from environmental cloning studies, increased efforts have been made to characterize and catalog early-diverging fungi, yet marine habitats – and surface waters, in particular – remain largely unexplored. For this study, the newly developed autonomous Water and Microplankton Sampler (WaMS) was used to capture microplankton (

It all adds up: The genetics of thermal reaction norm variation for antibiotic resistance

Jennifer Knies, Angus Angermeyer, Daniel Weinreich

2C_301A-Disease and Resistance
Sunday, June 22, 2014 1:30 PM-1:45 PM

The thermal reaction norm, a trait's response to temperature, is most naturally viewed as a continuous response to temperature and for fitness associated traits, generally shows a slow increase with rising temperature until peaking at the optimal temperature, and then it rapidly decreases. The genetic variation for the thermal reaction norm determines the temperature range of a species and ultimately a species' survival in the face of changing temperatures such as global climate change. Here, we investigate the effect of point mutations on the organismal thermal reaction norms for antibiotic resistance in the bacterium Escherichia coli and after controlling for the cell response, for 32 alleles of the beta-lactamase antibiotic resistance gene. Antibiotic resistance was measured for all combinations of five mutations in the beta-lactamase antibiotic resistance gene at six temperatures spanning 21ºC. The organismal thermal reaction norms have their highest resistance at the lowest temperature (20ºC) and decline in resistance with increasing temperature. The thermal reaction norms for the 32 beta-lactamase alleles, after controlling for the cell alone response, rise with increasing temperature, peak around 35ºC, and then decrease. Additive mutational affects explain the 16-fold difference in maximum resistance between alleles, but are less effective at explaining the 10ºC span in optimal temperature. At each temperature, we quantified the variance in resistance explained by each mutation and by interactions among mutations and between mutation and temperature. Holding temperature constant, additive mutational effects explain nearly all of the variance in resistance, though pairwise interactions become more significant at higher temperatures. Lastly, we present a principled model of enzyme kinetics and stability that explains the general phenomena of increased resistance variance with temperature and changes in the optimal temperature in this system.

Immune memory drives the evolution of virulence in an emergent wildlife pathogen

Paul Williams

2C_301A-Disease and Resistance
Sunday, June 22, 2014 1:45 PM-2:00 PM

Accumulating experimental evidence from various host-pathogen systems indicates that imperfect host immunity, by altering life history trade-off structures between transmission duration and efficacy, plays an important role in shaping the evolution of pathogen virulence. However, examples from natural systems, and the theoretical foundations for understanding this outcome, are lacking. Here we report on experimental and modeling work of imperfect immune memory in the North American house finch to explain increases in the virulence of its bacterial pathogen, Mycoplasma gallisepticum, that have occurred following the pathogen's emergence. Our experimental work shows that host immune memory, induced by prior infection, introduces plasticity to trade-offs, while modeling results confirm that the nature of these plastic changes can induce the evolution of higher optimal pathogen virulence. More generally, our findings can be used to better understand the mechanisms by which imperfect vaccination in humans may select for more virulent pathogens. In light of these potentially pathological outcomes, our findings further suggest a cautious approach to the design and utilization of imperfect vaccines against human pathogens.

Rate of resistance evolution in long- and short-lived hosts

Emily Bruns, Michael Hood, Janis Antonovics

2C_301A-Disease and Resistance
Sunday, June 22, 2014 2:00 PM-2:15 PM

Conventional wisdom suggests that adaptive evolution should occur more slowly in long-lived organisms with long generation times than in short-lived organisms. However, the opposite may be true for the evolution of disease-resistance traits where the strength of the selection for resistance increases with longevity. We model evolution of resistance to a sterilizing disease and show that longer-lived hosts evolve resistance over a greater range of conditions and do so more rapidly than short-lived hosts. Our results may explain the low disease infection rates that have been observed in many long–lived host species.

Genomic Variations Associated with Gonococcal Antimicrobial Resistance

Jeanine Abrams McLean, Carroll Serena, Mike Frace, Steven Johnson, David Trees

2C_301A-Disease and Resistance
Sunday, June 22, 2014 2:15 PM-2:30 PM

Multidrug antibiotic resistance in Neisseria gonorrhoeae has become a significant global public health concern. The recent development of increased resistance to extended-spectrum cephalasporins has fueled the need to determine the molecular mechanisms associated with the evolution of gonococal antimicrobial resistance. Studies have shown that the presence of the mosaic penA allele is associated with increased cephalosporin resistance. Moreover, evidence suggests that mutations in other genes, in combination with the mosaic penA allele, may also contribute to elevated resistance. To identify these accessory mutations, we compared whole genome sequences of a gonococcal strain containing the mosaic penA allele to derived laboratory-selected mutants that exhibited significantly higher resistance. The comparison of mutants derived from the original strain allowed us to identify specific genomic variations on an isogenic background, which may contribute to higher levels of cephalosporin resistance in N. gonorrhoeae.

Elevational disease distribution in a natural plant pathogen system: Insights from genetic variation in resistance and morphology.

Jessie Abbate

2C_301A-Disease and Resistance
Sunday, June 22, 2014 2:30 PM-2:45 PM

Factors governing species distributions have become a central topic of discussion on the potential impacts of global climate change. The distribution of parasitic organisms is particularly important, as emerging and re-emerging infectious diseases are predicted to increasingly threaten public health, agriculture, and biodiversity. Experimental evidence for the ecological and evolutionary factors that may determine disease distributions in natural systems is sparse. In particular, the intimate association of species-specific parasites with their hosts, often having long and entwined evolutionary histories, is sometimes characterized by a co-evolutionary arms race which may also play an important role in shaping where disease is found. Here, we investigated evolutionary factors that may contribute to the restricted distribution of anther-smut disease caused by Microbotryum spp. in high-elevation populations of its widespread host species, Silene vulgaris, in the alpine region of eastern France. Controlled laboratory inoculations were conducted in host populations from along four replicate transects to test the hypothesis that the pathogen is excluded from lower elevations by physiological resistance in the host. We found that high-elevation hosts were actually more likely to have higher rates of avoidance resistance (i.e., lower rates of successful infection, classically used to test for "resistance" in this system), rates of recovery resistance (i.e., delay or clearance disease following infection) were higher in diseased plants originating from lower elevations. Consistent with previous studies, we also found little variation in infectivity of fungal strains across elevation. These results indicate that spatial structure in host recovery resistance may contribute to the restricted distribution of anther-smut disease in S. vulgaris, whereas the contrary pattern of avoidance resistance may instead result from - rather than cause - the selective pressure of the sterilizing fungus' current elevational range.

Context-dependent effects of sampling design and demographic history on genome scans for local adaptation

Katie Lotterhos, Michael Whitlock

2C_301B-Adaptation
Sunday, June 22, 2014 1:30 PM-1:45 PM

Genome scans based on landscape SNP data are a popular way to uncover the genetic basis of adaptive variation to heterogeneous environments. In this study, we compare various types of genetic-environment associations (GEAs) with Fst outlier tests in four demographic histories: island model, isolation by distance, range expansion from one refugium, and range expansion from two refugia. In addition, we explore how sampling design on the landscape (random, paired samples, or transects) affects the relative power of each statistic. Our results clearly show that GEAs are more powerful that Fst for the island model, and that Fst is more powerful than GEAs for isolation by distance. Both types of tests had moderate power for the range expansion scenarios. We also found subtle differences in power among statistics that depended on how many individuals were sampled from the landscape. In most cases, paired samples had the highest power to detect loci that were locally adapted. Our results were based on empirical p-values, because we found that p-values from the programs were not reliable. We advocate for using a set of putatively neutral loci to create empirical p-values.

Constraints on speciation and local adaptation: On the role of variable selection acting among adaptive traits.

Aaron Comeault

2C_301B-Adaptation
Sunday, June 22, 2014 1:45 PM-2:00 PM

Selection varies widely among populations and traits, and different modes of selection have different evolutionary consequences. Divergent selection, for example, plays an important role in structuring variation among populations, driving the processes of adaptive divergence and speciation. Balancing selection, on the other hand, maintains variation within populations, thereby constraining divergence and, in some cases, speciation. Despite these contrasting effects, the evolutionary ramifications of selection that varies in its mode among traits remain largely underappreciated. In the stick insect Timema cristinae partial reproductive isolation has evolved between host plant ecotypes as a result of strong divergent selection acting on a dorsal pattern polymorphism that provides varying degrees of crypsis on alternate species of host plant. Here we describe how selection acts to maintain a second trait that is present within populations of T. cristinae and does not differ in frequency among host plant types: a green - melanic colour polymorphism. We show that this colour polymorphism is maintained by balancing selection that is the result of a combination of ecological factors including spatially variable selection among plant microhabitats, resistance to pathogens, adaptation to climate, and sexual selection. In stark contrast to the dorsal patterning polymorphism, balancing selection acting on the colour polymorphism maintains variation within populations and, in a system dominated by divergence with gene flow, provides a mechanism to explain incomplete adaption and speciation. To further explore how selection acting on these two polymorphisms might influence evolution we carried out genome-wide association mapping to determine the genetic architecture of both traits. We show that both colour and dorsal pattern are under simple Mendelian genetic control and that SNPs associated with phenotypic variation of both traits are genetically linked. This genetic linkage between traits provides a mechanism through which maladaptive alleles at the locus controlling dorsal patterning phenotypes can avoid selection when linked to the rare colour allele. Taken together, our results demonstrate how selection and genetic architecture can interact to constrain local adaptation and speciation.

Evidence for rapid adaptation to an environmental contaminant in a model songbird

Claire Ramos, John Swaddle, Daniel Cristol

2C_301B-Adaptation
Sunday, June 22, 2014 2:00 PM-2:15 PM

Human-induced rapid environmental change, including pollution, is the greatest threat to wildlife populations. Mounting evidence suggests that evolutionary responses to environmental change are becoming increasingly prevalent on a global scale. Evolutionary responses may be particularly important in the case of pollutants, which can have strong fitness effects. We performed a multigenerational dosing experiment examining the effects of methylmercury exposure on reproductive success in the zebra finch (Taeniopygia guttata). We found significant variation among full-sibling families in the effects of methylmercury on several reproductive parameters. We also found increased reproductive success in the second generation of birds exposed to the highest doses of methylmercury relative to birds in the first generation of exposure. This suggests strong response to selection for mercury tolerance at higher doses. These results have important implications for the evolution of tolerance as well as risk assessment and wildlife conservation efforts on sites with legacy contamination.

Functional analysis of adaptive evolution of ADH in Drosophila

Mohammad Siddiq, Lora Picton, Joe Thornton

2C_301B-Adaptation
Sunday, June 22, 2014 2:15 PM-2:30 PM

A goal in evolutionary genetics is to understand how changes at the sequence level produce changes in function and fitness. The Drosophila ADH protein provides a classic and tractable model for studying this issue: population genetic analysis of the Adh coding sequence indicated adaptive evolution, a hypothesis that is concordant with the expansion of D. melanogaster into alcohol-rich environments. However, functional assays are necessary to establish whether the molecular signature of selection on Adh is causally related or merely correlated to the increased fitness of D. melanogaster in fermenting environments. We have therefore traced the evolution of ADH function in flies of the D. melanogaster subgroup using ancestral reconstruction and biochemical assays. In spite of ADH's essentiality in ethanol catabolism, we find that the protein has not functionally changed. The discordance between sequence and functional evolution broadly raises questions about our ability to ascertain adaptation from sequence patterns and correlative evidence.

Climate change and the high fitness costs of seasonal camouflage mismatch in snowshoe hares

Marketa Zimova, L. Scott Mills, J. Josh Nowak

2C_301B-Adaptation
Sunday, June 22, 2014 2:30 PM-2:45 PM

Decreasing snow cover duration is one of the strongest signals of climate change across the temperate zone of the Northern hemisphere. The resulting later onset of snow in the fall and earlier loss of snow in the spring represents a new, potentially severe stressor for at least 11 color molting species and their respective communities. Snowshoe hares (Lepus americanus), an important prey species for many forest carnivores, molt from brown to white in winter to match their background and avoid detection from predators. The mistiming between ground snow cover presence and photoperiod-induced color molts results in camouflage mismatch during spring and fall. We previously found minimal plasticity in either seasonal color molt phenology to track seasonal snowpack or anti-predatory behaviors to minimize color mismatch, implying a 4-8 fold increase in mismatch by the end of the century. Here, we investigated the cost of color mismatch and the potential to adapt to the increasing mismatch through evolution.

We observed nearly 200 wild hares over three widely disparate snow years and two study sites in Montana, USA, and monitored their survival, coat color molt phenology and color mismatch weekly using radiotelemetry. First, we found high variation in phenology of coat color molts and consequently in color mismatch between individuals. Next, we detected high fitness costs of mismatch, with hares suffering 3- 7% lower weekly survival rates when color mismatched. Without adaptive changes in the molt phenology, these fitness costs coupled with decreasing duration of snow season were projected to decrease annual survival by 12% by mid-century and 24% by late-century. Such decreases in survival could be sufficient to cause hare populations to decline strongly towards extinction, with annual geometric growth rate decreasing by 11% (24%) by mid (late) century. However, because natural selection is operating against color mismatch and there is a substantial individual variation in coat color phenology, we conclude that there is a strong potential for evolution to rescue hares from the dire consequences of camouflage mismatch.

Direct and correlated responses to artificial selection for herbicide resistance in Ipomoea purpurea: Divergence in traits and the transcriptome

Regina Baucom, Trent Leslie

2C_302A-Plant Evolution
Sunday, June 22, 2014 1:30 PM-1:45 PM
Human-mediated selection can lead to rapid evolution in very short time scales, and the evolution of herbicide resistance in agricultural weeds is an excellent example of this phenomenon. An enduring question about this process is whether or not intense selection for increased resistance can lead to correlated changes in other traits that may have important consequences for organismal fitness. Here we assess this question at the level of the phenotype and the plant transcriptome in the agricultural weed Ipomoea purpurea using the tools of artificial selection and RNA-seq. We examined the evolutionary response to direct artificial selection for increased and decreased resistance to the herbicide glyphosate and the potential that plant size and growth traits respond via indirect selection. We then assessed gene expression at the level of the transcriptome to determine if selection on resistance leads to divergent responses in transcribed genes. We found rapid responses to artificial selection—lines selected for increased resistance over two generations exhibited less plant damage and a lower proportion of individuals that died post-spray compared to control and susceptible lines. We also found that resistant lines exhibited fewer leaves pre-herbicide than both control and susceptible lines, indicating a trade-off between plant size and resistance status. In addition to phenotypic divergence among selection lines, we also found differences in gene expression. Nineteen genes were differentially expressed between resistant and susceptible lines, one of which is a cytochrome P450 gene that belongs to a large plant family of genes involved in xenobiotic detoxification. Our work suggests that selection for divergence in herbicide resistance can lead to both the evolution of the phenotype and differential gene expression of the transcriptome, and that such divergence can lead to potential allocation costs.

The impact of inbreeding depression on the evolution of herbicide resistance in the agricultural crop weed, Ipomoea purpurea

Anneka Jankowiak, Regina Baucom

2C_302A-Plant Evolution
Sunday, June 22, 2014 1:45 PM-2:00 PM
How changes in mating system influence the evolution of herbicide resistance has yet to be considered in any weed species. It is unknown if, during the process of resistance evolution, a population may become more inbred and suffer fitness consequences due to inbreeding depression. A large scale field experiment was conducted using selectively bred glyphosate resistant and susceptible Ipomoea purpurea lines to address this question. Maternal lines from resistant and susceptible families were self-pollinated to produce inbred progeny, and outcrossed to three paternal lines within their resistance class to produce outcrossed half sibs for comparison. We also performed this same crossing scheme using a second generation of artificially selected resistant/susceptible lines. We observed inbreeding depression in all size and fitness characters. We further found that this inbreeding depression was present only in the resistant lines and was detected in both generations of artificial selection. We hypothesize that, in inbred resistant individuals, a pleiotropic interaction between the resistance locus and deleterious recessives leads to lower fitness of inbred, resistant plants compared to outcrossed, resistant plants.

Male-driven evolution of self-compatibility in diploid and polyploid Arabidopsis

Kentaro Shimizu, Chow Lih Yew, Takashi Tsuchimatsu, Timothy Paape, Rie Shimizu-Inatsugi

2C_302A-Plant Evolution
Sunday, June 22, 2014 2:00 PM-2:15 PM
Stebbins stated that evolution of self-compatibility is a most frequent evolutionary transition in plants, and moreover, polyploid species tends to be self-compatible (SC). However, he also suggested that polyploidy may retard adaptive evolution because additional duplicated copies could retain original function. Then, how could polyploid species become self-compatible despite of duplicated S-loci? We have studied the molecular basis of the self-compatibility of the allotetraploid Arabidopsis kamchatica, which was derived from diploid self-incompatible A. lyrata and A. halleri, as well as of the diploid A. thaliana. In the sporophytic self-incompatibility system of Brassicaceae including Arabidopsis, the S-locus harbors female specificity gene SRK, male specificity gene SCR/SP11 and Smi small RNA regulating the dominance of SCR. Using crossing experiments, we showed that the female components of SI (including SRK) are still functional in many accessions. Because SCR gene is too polymorphic to design conserved PCR primers, we obtained anther transcriptome data by using the Ion Torrent next generation sequencer. We found that both of the duplicated SCR were non-functional in A. kamchatica. Our compilation of empirical data demonstrated that the evolution of self-compatibility tends to be derived from mutations in the male component in wild species including A. thaliana, in contrast to cultivated species. We conducted forward simulation studies by

integrating molecular data such as mutational bias, and indeed found the pattern that male SC-conferring mutations were more likely to be fixed than were female SC-conferring mutations in a wide range of parameters.

Plant defenses in the genus Physalis are not constrained by trade-offs between constitutive and induced defenses

Deidra Jacobsen

2C_302A-Plant Evolution
Sunday, June 22, 2014 2:15 PM-2:30 PM

Plants have evolved a variety of defenses (such as trichomes, tough leaves, or production of toxic chemicals) to protect themselves from herbivores. These defenses are often costly for plants to produce and therefore it is hypothesized that trade-offs should exist between growth and defense or between potentially redundant defenses (such as constitutive and induced defenses). A trade-off between constitutive and induced defenses could explain variation between species in plant defenses; however, studies at different evolutionary scales and in different systems have failed to demonstrate a universal positive or negative association between constitutive and induced defenses. This work aims to determine whether other factors, such as life history or mating system, affect levels of constitutive and induced defenses. To address these questions, I examined the relationship between constitutive and induced defenses in species of the genus Physalis (Solanaceae) with different life histories/mating systems. Assays of Manduca sexta herbivore growth rates (a specialist on Solanaceous species) on undamaged and induced plants of each species were used to quantify overall levels of plant resistance. Examination of these species suggests no trade-off between constitutive and induced defenses. Although annual and perennial species are predicted to have different allocation to constitutive and induced defenses based on variation in temporal herbivore environment, annual and perennial species did not differ in levels of constitutive or induced resistance. This indicates that plant defenses within Physalis are not constrained by life history or by trade-offs between constitutive and induced defenses. Hence, these two types of defense are not redundant and the lack of a trade-off suggests that different mechanisms are maintaining variation in plant defensive strategies.

Allopolyploidy, diversification, and the Miocene grassland expansion

Michael McKain, Matt Estep, John Hodge, Trevor Hodkinson, Daniel Layton, Simon Malcomber, Remy Pasquet, Dilys Vela, Jinshun Zhong, Elizabeth Kellogg

2C_302A-Plant Evolution
Sunday, June 22, 2014 2:30 PM-2:45 PM

Polyploidy's role in the diversification of plant species has long been a subject of debate. The identification of ancient whole genome duplication events in the green plant phylogeny, especially those occurring prior to major species radiations or the origin of novel phenotypes, has suggested that polyploidy may be a driving force in diversification. Alternatively, studies of more recent polyploid events have demonstrated that polyploid lineages may actually have lower rates of speciation relative to closely related diploid lineages. Furthermore, lineage diversification rates relative to WGD events corroborate the WGD Radiation Lag-Time Model demonstrating that there is often an extensive period of time between a polyploid event and diversification, suggesting that polyploidy itself is not the driving force behind diversification. Here, we focus on the tribe Andropogoneae (subfamily Panicoideae, family Poaceae), a group of C4 grasses that include economically important species such as maize, sorghum, and sugarcane, as well as ecological dominants such as big bluestem (Andropogon gerardi), little bluestem (Schizachyrium scoparium), and yellow Indiangrass (Sorghastrum nutans). We reconstructed a phylogeny of approximately 10% of Andropogoneae species using four nuclear loci supported with a smaller sampling of full plastome sequences. We identified genetic allopolyploid events using nuclear gene trees that showed support from more than one locus. Our data suggest there were at least 28 independent tetraploid events encompassing 32% of sampled species. Parental genomes of most polyploid species diverged during the late Miocene coincident with the expansion of the major C4 grasslands that dominate the earth today. Despite the ubiquity of polyploidy in the clade, only three lineages have undergone any major diversification since polyploidy: the Zea-Tripsacum clade, the Bothriochloa-Capillipedium-Dicanthium clade, and the Miscanthus-Saccharum clade. We conclude that, within Andropogoneae, polyploids are produced frequently, but only occasionally lead to increased diversification.

Local adaptation in herbivore feeding preferences: a marine-terrestrial contrast

Erik Sotka

2C_302B-Trait Evolution
Sunday, June 22, 2014 1:30 PM-1:45 PM

Herbivorous insects tend to specialize on a subset of available host plants, and this specialization appears correlated with high rates of local adaptation and adaptive radiation. A focus on specialist insects, however, comes at the expense of a broader understanding of the evolutionary ecology of the many ecologically-important herbivores with more generalist diets. As an example, the dearth of studies on local adaptation in generalist herbivores suggests that generalists rarely locally adapt. We tested this hypothesis over the past decade with marine herbivores, most of whom have highly generalist diets. We find that crustacean and echinoderm herbivores routinely adapt to local seaweed diets, and in particular, to seaweed chemical defenses. The consistency by which marine generalists adapt to local seaweeds suggest that terrestrial generalist herbivores should locally adapt at higher frequently than is currently appreciated.

Asymmetric mismatch in secondary genital morphology increases harm to Drosophila females

J.P. Masly, Yoshitaka Kamimura

2C_302B-Trait Evolution
Sunday, June 22, 2014 1:45 PM-2:00 PM

Although several evolutionary forces have been proposed to contribute to genital morphological diversification, it is unclear which might act early during the evolution of novel structural traits. We test the hypothesis that mismatch between interacting male and female secondary sexual structures gives rise to increased harm to females, consistent with the outcome predicted from a history of sexual conflict. We mate Drosophila sechellia females to males from a collection of D. mauritiana-D. sechellia interspecific genetic introgression lines that possess quantitative morphological variation in the posterior lobe of the genital arch, an external genital structure that can cause wounds to the female abdomen during mating. We find that males with smaller posterior lobes, and those that possess lobes with similarities in shape to D. mauritiana, cause more severe wounding compared to either D. sechellia males with strain-specific morphologies or introgression males that possess larger lobes or lobes with more pronounced D. sechellia features. These results suggest a possible history of sexual conflict during the evolution of the posterior lobe in D. sechellia, but also suggest a potential contribution of divergence in sensory recognition mechanisms to posterior lobe evolution.

'Engine for speciation'? Experimental alteration of sexual conflict shows evidence of reproductive isolation in Drosophila Melanogaster.

Zeeshan Syed, Martik Chatterjee, N.G PRASAD

2C_302B-Trait Evolution
Sunday, June 22, 2014 2:00 PM-2:15 PM

Inter-sexual conflict (henceforth used interchangeably with sexual conflict) gives rise to rapid antagonistic coevolution in traits related to reproduction in both sexes(e.g. sex peptides are one of the fastestevolving proteins). Such high rate of evolution can potentially create divergence in genes responsible for these traits between populations with very low or no gene flow (allopatric populations). Hence, it has been hypothesized that sexual conflict can act as a potential mediator for reproductive isolation in sexually reproducing allopatric populations. Although mathematical models and comparative phylogenetic studies support this idea, such instances are very rare in experimental evolution studies.

Here, we tested whether sexually antagonistic coevolution can cause reproductive isolation in a set of populations of the fruit fly Drosophila melanogaster that are subjected to different levels of intersexual conflict for nearly a hundred generations. We show that allopatric populations having high level of sexual conflict indicate signs of incipient reproductive isolation, both behaviorally and in terms of competitive fitness, whereas allopatric populations with low level of sexual conflict do not show any such signs. Matings between allopatric individuals facing high levels of sexual conflict have lower copulation duration and sperm competitive ability compared to their sympatric counterparts but no such difference is present in the regime with lower level of sexual conflict. This is one of the rare experimental results to support the idea of sexual conflict as an 'engine for speciation'.

The Contribution of Rare and Common Variants to Standing Variation for Quantitative Traits in Capsella grandiflora

Young Wha Lee, Emily Josephs, John Stinchcombe, Stephen Wright

2C_302B-Trait Evolution
Sunday, June 22, 2014 2:15 PM-2:30 PM

What are the evolutionary mechanisms that maintain quantitative trait variation? This is a fundamental question with implications for the genetic architecture of traits and the relevance of standing variation in the process of adaptation. In particular, the contributions of balancing selection to the maintenance of quantitative trait variation is unclear. Our dataset comprises 189 Capsella grandiflora individuals from one deme (πsyn=0.012), sequenced with deep coverage (30-110X) and phenotyped for a number of ecologically relevant traits including nitrogen use efficiency, flowering time, and fertility. The population sample consists of largely unrelated outbred individuals, and is highly polymorphic with rapid decay of linkage disequilibrium between polymorphic sites. We conduct a Genome Wide Association Study to identify common alleles underlying quantitative trait variation, and ask whether patterns of variation in linked sites indicate the contributions of balancing selection or partial sweeps.

Genome Wide Association Mapping to examine genetic basis of quantitative traits in natural populations

Arild Husby

2C_302B-Trait Evolution
Sunday, June 22, 2014 2:30 PM-2:45 PM

An important goal in evolutionary biology is to understand how genetic variation is maintained in natural populations and for this we need to know the loci underlying fitness related traits and the selective forces operating on them. Advances in next generation sequencing has made it possible to carry out genome wide association mapping studies also on non-model organisms and here we report on such efforts using data on two long-term studies on birds. We used a 50k and a 10k custom made ‘SNP chip’ in the collared flycatcher and house sparrow respectively to map the genetic basis of fitness related traits. I will discuss our findings and their implications for the genetic architecture of traits and the potential such GWAS efforts hold for mapping traits in other non-model organisms.

Sexual selection impedes ecological specialization

Karin Pfennig, Cody Porter, David Pfennig

2C_302C-Sexual Selection
Sunday, June 22, 2014 1:30 PM-1:45 PM

Ecological specialization is the expression of phenotypes that are especially effective at utilizing a particular resource. When ecological specialization arises within a population, it can generate resource polymorphisms whereby individuals express alternative resource-use ecomorphs. Such within-population specialization is gaining increasing attention, because the evolution of alternative ecomorphs may ultimately contribute to sympatric divergence. Indeed, within-population ecological specialization is potentially a key component in the origin of novel traits, ecological speciation, and adaptive radiation. However, for sexually reproducing species, the evolution and maintenance of ecological specialization critically depends on how sexual selection impacts the evolution of alternative ecomorphs. Yet, the role of sexual selection – particularly condition-dependent mate choice – in the process of ecological specialization remains unclear. We experimentally evaluated the effects of sexual selection on ecological specialization in spadefoot toads. Spadefoot toad tadpoles experience resource competition, which favors alternative ecomorphs that specialize on different diets. We found that sexual selection reduced, but did not preclude, ecological specialization. We also found that sexual selection produced phenotypes with reduced fitness. Nevertheless, the effect of sexual selection on disruptive selection favoring alternative ecomorphs was lower than the effects of ecological opportunity or competitor density. Thus, sexual selection can impact ecological specialization, but its effects might be subtle. We discuss our results in light of ecological speciation and the origins of novel resource-use phenotypes.

Causes of Rapid Divergence of Female Genital Morphology in Bahamas Mosquitofish (Gambusia hubbsi)

Christopher Anderson, Justa Heinen-Kay, Brian Langerhans

2C_302C-Sexual Selection
Sunday, June 22, 2014 1:45 PM-2:00 PM

The rapid divergence of male genital morphologies represents one of the most established trends in evolutionary biology, though understanding of the rate and mechanisms of female genital evolution are comparatively obscure. Three major mechanisms could lead to rapid genital divergence in females and result in patterns of correlated evolution with male genital morphologies: (1) ecological variation that alters the context of sexual selection for both males and females, (2) sexually antagonistic selection based on sexual conflict between sexes, and (3) selection against inter-population mating (sometimes referred to as “lock-and-key.”). We conducted an empirical study investigating of the roles of these three non-mutually exclusive mechanisms of rapid female genital divergence using the model system of Bahamas mosquitofish (Gambusia hubbsi). Independent populations of these fish inhabit blue holes characterized by the presence or absence of a predator. We defined and measured 8 distinct female genital traits to assess variation in each across predation regime. We addressed male-female genital coevolution by assessing correlations between trait divergence and genetic relatedness amongst population pairs. Our results show strong divergence in female genital morphology between the two predation regimes, with evidence of male-female genital coevolution in one trait: the shape of female genital opening. We did not uncover any evidence in support of sexual conflict in driving patterns of correlated male-female genital evolution. However, we found support for the third hypothesis (lock-and-key) based on evidence that the most highly-related populations displayed the largest divergence in male and female genital traits. Altogether, this study reveals that both ecological variation and reinforcing selection favoring reproductive isolation underlies diversification patterns of female genitalia in Bahamas mosquitofish.

Comparative analyses of biomechanical reproductive traits in harvestmen support intersexual coevolution via simultaneous mechanisms

Mercedes Burns, Jeffrey Shultz

2C_302C-Sexual Selection
Sunday, June 22, 2014 2:00 PM-2:15 PM

Reproductive traits have a long history as taxonomic characters, but their precise functions and the combination of evolutionary processes underlying their diversification are not well understood. Most researchers attribute diversity in reproductive structures to either sexual selection by female choice, intersexual conflict or to some poorly-defined synthesis of the two. In order to assess the presence or absence of simultaneous effects of choice and conflict, we analyzed biomechanically-inspired variables from both sexes of 29 harvestman species using phylogeny-based comparative approaches. Our results corroborated the hypothesis that female choice and intersexual conflict can operate simultaneously at differing intensities to generate a continuous spectrum of forms. Canonical correlation analysis of male and female traits revealed a strong relationship consistent with sexual coevolution in precopulatory structures. Species with pregenital barriers specialized for intersexual conflict dominated one end of the spectrum, those lacking such specializations (including those with gift-bearing penile sacs) dominated the other, and there was a significant region of overlap. Similar results were obtained with principal components analysis. Furthermore, linear discriminant analysis could not reliably distinguish groups defined by the presence or absence of gift-bearing penile sacs or groups defined by the presence or absence of female pregenital barriers, results that are inconsistent with the hypothesis that female choice and intersexual conflict act in a mutually exclusive manner. Our results suggest that the relative intensities of female choice and intersexual conflict that have shaped the reproductive mechanisms of individual species can be quantified. This ability will allow statistical comparisons with quantifiable ecological, life-history or social variables and may ultimately reveal the arrangement of evolutionary factors that shape diversity in reproductive structures.

Battle of the sexes: may the best fly win in reproduction

Trinh Nguyen, Amanda Moehring

2C_302C-Sexual Selection
Sunday, June 22, 2014 2:15 PM-2:30 PM

Males and females often have differing reproductive strategies to increase their individual fitness, which can result in sexual conflict. Males usually increase their fitness by mating multiply, while repeated mating comes at a high cost to females. Polyandrous females can receive indirect benefits of multiple mating by increasing the fitness of their offspring through additive and non-additive genetic effects, such as good genes or compatible genes. These benefits are acquired through mechanisms of sexual selection which can act at many levels: behavioural through female mate choice, or postmating through sperm competition and cryptic female choice. To tease apart the antagonistic relationship between males and females in sexual reproduction, males from D. melanogaster isolines were ranked for their quality using a variety of fitness traits. The performance of high and low quality males were then tested for their fertilization success independently (cryptic female choice), in the presence of competition (sperm competition), and via female mate choice. These different aspects of sexual selection at both pre- and postmating levels were examined to determine how they contribute to overall male mating success, providing insight into how populations evolve in response to sexual selection.

Ecological divergence, adaptive radiation and the evolution of sexual signaling traits in a complex of Australian agamid lizards

Danielle Edwards, Jane Melville, Leo Joseph, Scott Keogh

2C_302C-Sexual Selection
Sunday, June 22, 2014 2:30 PM-2:45 PM

Diversification is often linked to either ecological diversification or sexual signal evolution. We explore the contribution of adaptive and sexual signal evolution in the radiation of the Ctenophorus maculatus species complex using species trees, multivariate niche comparisons and comparative phylogenetic analyses. In the C. maculatus complex, lineages have radiated in response to arid sand habitat development, with ecological and phenotypic diversification in ecomorphology, dorsal marking, chemical signaling, and visual signaling traits tracking habitat diversification through time. We suggest that the evolution of chemical signaling and dorsal marking traits is significantly impacted by ecological factors. Our results also suggest that visual signaling traits may function to reinforce the boundaries between ecologically distinct lineages in the C. maculatus complex. This study provides empirical support for an intricate relationship between ecological and signal evolution in speciation, one often ignored when these factors are studied in isolation.

How is geographic variation within species related to macroevolutionary patterns between species?

M. Caitlin Fisher-Reid, John Wiens

2C_303-Macroevolution
Sunday, June 22, 2014 1:30 PM-1:45 PM

The relationship between microevolution and macroevolution is a central topic in evolutionary biology. An aspect of this relationship that remains very poorly studied in modern evolutionary biology is the relationship between within-species geographic variation and among-species patterns of trait variation. We tested the relationship between climate and morphology among and within species in the salamander genus Plethodon. We focus on a discrete color polymorphism (presence and absence of a red dorsal stripe) that appears to be related to climatic distributions in a common, wide-ranging species (Plethodon cinereus). We find that this polymorphism has been maintained among and within species for >40 million years. Furthermore, we find a strong relationship between climatic variation and morph frequencies among species. These between-species patterns are similar (but not identical) to those in the broadly distributed Plethodon cinereus, although there is a lack of significant climate-morphology relationships within other polymorphic species. Overall, our study highlights the possibility that adaptive geographic variation may be important for large-scale macroevolutionary patterns, and explores one of many scenarios by which this may occur.

A Nearly Neutral Theory of Ecology and Macroevolution

James Rosindell, Rampal Etienne, Luke Harmon

2C_303-Macroevolution
Sunday, June 22, 2014 1:45 PM-2:00 PM

Ecological neutral theory has been controversial because it assumes all individuals are ecologically equivalent regardless of their species identity. Rather than taking this assumption literally, the theory is better regarded as a null model, an approximation or as a first step towards more realistic models. Perhaps one of the most exciting properties of ecological neutral theory is that it makes dynamic predictions about both ecology and macroevolution and so might provide an interesting approach to link these two fields. Unfortunately, there are problems with the predictions of neutral theory over evolutionary timescales; however, this presentation will reveal how small departures from neutrality are enough to resolve these. The addition of fitness differences to neutral theory does not prevent species coexistence as one might expect. Instead, when implemented with a progressive model of evolution analogous to the Red Queen Hypothesis, nearly neutral theory opens up a wide range of new possibilities for the modeling of ecology and macroevolution.

The vanishing refuge revisited

Roberta Damasceno, Maria Strangas, Ana Carolina Carnaval, Miguel T Rodrigues, Craig Moritz

2C_303-Macroevolution
Sunday, June 22, 2014 2:00 PM-2:15 PM

Tropical areas are extremely biodiverse both because of high species and functional/phenotypic diversity. A plethora of evolutionary processes have interacted with environmental change over space and time to shape this extraordinary diversity. Recent emphasis on ecological aspects of speciation draws attention to how selection can drive divergence and speciation. In this context, we are motivated to revisit one model of speciation, the vanishing refuge model (VRM) that encapsulates all these aspects.

The VRM reconciles ecogeographic speciation with a modification of the forest refuge model in an attempt to explain patterns of distribution where sister or closely related species inhabit contrasting habitat types. The model evokes vicariance and divergent selection, leading to genetic divergence and phenotypic disparity among populations, eventually leading to speciation caused by climate-driven fragmentation of forested areas that vanish and give place to drier and more open habitats. Thirty years after its publication, this model remains relevant for integrating both geographic and ecological mechanisms of divergence and speciation, and it can be straightforwardly transferred to species in other vanishing biomes.

We take advantage of the accumulating evidence on ecogeographic variation in the mega-diverse central corridor of the Brazilian Atlantic Forest and adjacent dry biome, one of the original motivating systems, spanning across a range of phylogenetic depths, to (1) make clear predictions on patterns of genetic structure, phylogenetic relationships, habitat and climate histories, and phenotypic disparity resulting from this model, and (2) consider alternative hypotheses on drivers of divergence and speciation that result in diversity patterns similar to those expected under the VRM. We identify several candidate systems and we test the predictions of VRM with one case, with data on habitat shifts, phylogeography and ecologically relevant phenotypes. We also explore how some taxa will be more likely than others to diversify in response to the shrinking and vanishing refugia. In this context, we predict that additionally to the presence of pre-adaptations to distinct environmental conditions, divergent selection is aided by high lability in tolerance traits, in such taxa. Our findings support the view that divergent selection acting in populations from geographic isolates in climatically dynamic areas can be a powerful force driving population divergence and, potentially, speciation and also highlight how populations in peripheral isolates show potential to adapt locally. We conclude by suggesting that studies on population divergence and speciation will benefit from more integrated analyses of molecular and phenotypic divergence.

Big groups, bad eggs and biogeography: regional and global patterns of brood parasitism's effect on cooperative breeding

Michael Wells, F. Keith Barker

2C_303-Macroevolution
Sunday, June 22, 2014 2:15 PM-2:30 PM

There has been great interest in how complex social behaviors, such as cooperative breeding, evolve and are maintained. However, it is still unclear what exactly sparks the transition to group living. Recent work in birds has suggested a number of candidates for this change including environmental uncertainty, construction of expensive and defensible nests, and brood parasitism. Brood parasites are argued to precipitate group formation by selecting for group-coordinated parasite defense. One recent study found a correlation between brood parasitism and cooperative breeding, but examined this relationship from a geographically restricted rather than global perspective. We investigated evolutionary correlations between brood parasitism and cooperative breeding at a global scale, including nearly all bird species and brood parasites. We found that at a global level, there is a strong positive correlation between cooperative breeding and brood parasitism, as found previously for specific continents. However, when we investigated our findings regionally we found that the global pattern is driven exclusively by relationships within Africa and Australia, suggesting a more complex causal relationship in the transition to cooperative breeding. We discuss possible explanations for contrasting global and regional results.

Connecting macroevolution to the genetics of adaptation: a case study using stomatal ratio

Christopher Muir, James Pease, Leonie Moyle

2C_303-Macroevolution
Sunday, June 22, 2014 2:30 PM-2:45 PM

Variation in quantitative traits is often characterized by a unimodal distribution; a few species reside in the tails of the distribution, but most are clustered about the mean. In contrast, some traits are multimodal, hinting at distinct peaks in the adaptive landscape. Here, we focus on a recently identified case of multimodality in stomatal ratio among terrestrial plants. Plants typically have all their stomata on the bottom of leaf (hypostomy) or roughly half their stomata on both leaf surfaces (amphistomy), with a dearth of intermediates between these states. We analyze a simple cost-benefit model of stomatal ratio which predicts that intermediates are rare because they are often universally unfit, falling in a valley between two peaks in an adaptive landscape. However, this raises the classic problem of how peak shifts can occur. One possibility is that mutations of large effect allow peaks shifts by passing over fitness valleys. Consistent with this hypothesis, we identify two large effect loci that account for most of the interspecific difference in stomatal ratio between hypo- and amphistomatous tomato species. Our work suggests that multimodality in stomatal ratio reflects distinct fitness peaks and that fitness valleys might not impose strong constraints over macroevolutionary time when large effect mutations are available.

Divergence in life-cycle associated with variation in circadian genes in the European corn borer

Genevieve Kozak, Rebecca Levy, Brad Coates, Erik Dopman

2C_304-Insect Evolution
Sunday, June 22, 2014 1:30 PM-1:45 PM

Many species in temperate climates show latitudinal variation in life-cycle corresponding to synchronization with seasonal fluctuations in resources. In particular, insects often vary clinally in voltinism (the number of generations per year) which is determined by the timing of diapause release. These phenotypic gradients in life-cycle have rarely been linked to genetic variation at specific loci. We studied genetic variation along a latitudinal cline in the European corn borer (Ostrinia nubilalis), which varies in the number of generations per season in the United States, from one generation in the north to three in the south. We found that voltinism is closely associated with allelic variation in cryptochrome, a gene in the circadian clock pathway. Period, another circadian gene, showed a sawtooth cline and varied both among voltinism types and within the bivoltine type. Our study suggests that these circadian genes are key to seasonal timing and may be involved in variation in diapause termination, traits which are associated with temporal isolation between Ostrinia strains.

Genome-wide rates of molecular evolution are higher in mutualistic plant-nesting ants

Benjamin Rubin, Corrie Moreau

2C_304-Insect Evolution
Sunday, June 22, 2014 1:45 PM-2:00 PM

The obligate mutualism between ants in the genus Pseudomyrmex and acacia trees is one of the most well known of any ant-plant relationship. In this particular mutualism, ants nest in and feed on the hollow thorns, food bodies, and extra-floral nectar provided by the acacia. In exchange for these resources, resident ants aggressively protect their hosts by attacking herbivores, trimming encroaching plants, and removing pathogenic fungi. This ant defense is incredibly effective and their absence ensures plant death. In addition to the acacia specialists, the Pseudomyrmex ant genus includes two other obligate mutualistic clades that nest in trees from the genera Triplaris and Tachigali. These trees have hollow trunks and leaf petioles, respectively, instead of thorns and do not provide direct food rewards, as do acacias. Instead, ants feed on honeydew from plant-sucking insects cultivated inside the plants. Despite the differences in diet and nest structure, these ants behave in the same way as acacia-nesters, aggressively biting and stinging any intruders. Amazingly, these three groups of plant-ants evolved mutualistic behavior convergently. We present three newly sequenced Pseudomyrmex genomes representing species from each mutualistic clade as well as four genomes of closely related non-mutualistic Pseudomyrmex species. Despite their independent evolutionary origins, all three mutualistic species show genome-wide signatures of elevated rates of molecular evolution. This pattern is present in both coding and non-coding sequence and is not the result of genetic drift due to generation time or population size, suggesting that mutation rates are higher in mutualists. We also find a small set of genes with consistent signatures of positive selection in all mutualists, suggesting their involvement in the evolution of mutualistic behavior. Our findings provide a detailed understanding of the genetic features involved in and, possibly, resulting from, the evolution of this complex behavior.

Differential expression of carotenoid biosynthesis genes may underlie function in gall midges

Cassidy Cobbs, Patrick Abbot, Jeremy Heath, John Stireman

2C_304-Insect Evolution
Sunday, June 22, 2014 2:00 PM-2:15 PM

Carotenoids are conjugated isoprenoid molecules with a number of important physiological functions in organisms, including roles in photosynthesis, oxidative stress reduction, vision, diapause, photoperiodism, and immunity. Until recently, it was believed that only plants, microorganisms, and fungi were capable of synthesizing carotenoids and that animals acquired them from their diet, but studies have demonstrated that three arthropod clades (aphids, spider mites, and gall midges) acquired via lateral gene transfer a pair of genes homologous to those required for the initial steps of carotenoid biosynthesis. To assess the functional significance of the gene transfer and subsequent gene duplication events within various gall midge (Diptera: Cecidomyiidae) lineages, we examined phytoene synthase, phytoene desaturase, and lycopene cyclase expression by real-time quantitative PCR in larvae, pupae, and adult Asteromyia carbonifera flies. We also examined general expression differences between A. carbonifera and five other ecologically diverse gall midge species using RNA-seq. Gene expression information was correlated with insect carotenoid composition to develop a proposed model for the revised carotenoid biosynthesis pathway in gall midges.

The Diversification of Insects, a phylogenetic perspective

James Rainford

2C_304-Insect Evolution
Sunday, June 22, 2014 2:15 PM-2:30 PM

Hexapoda (insects and their relatives) is the most diverse terrestrial group of organisms on the planet and collectively comprise over half of all described species. Any attempt to understand the history of life on land and the assembly of terrestrial ecosystems is thus incomplete without consideration of the pattern of hexapod diversification and how the potential drivers of this richness have acted through evolutionary time. Previous work on understanding the history of hexapod diversification has either focused on patterns within the fossil record, which for hexapods is highly incomplete, or has been taxonomically restricted and so unable to consider the wider phylogenetic context. Here I present a first attempt to explore patterns of diversification within hexapods using an explicit dated phylogenetic hypothesis for the group and the application of birth-death models. These models confirm the roles of flight and complete metamorphosis as key innovations driving hexapod diversification. Subsequent reductions in diversification are recovered for several relic groups previously identified as having a higher fossil diversity during the Mesozoic. In addition a number of recently derived taxa are found to have radiated at an elevated rate following the development of flowering plant (angiosperm) floras during the mid Cretaceous. Taken together these results identify key developmental innovations responsible for hexapod richness and differing responses of various hexapod groups to environmental changes from the mid Cretaceous floral transition to the present day.

Life history response to juvenile stress in Apis mellifera

Daniel Smith, Olav Rueppell, Juan Collazo, Babak Yousefi

2C_304-Insect Evolution
Sunday, June 22, 2014 2:30 PM-2:45 PM

Developmental cues can induce phenotypic plasticity which increases subsequent survival and reproduction. However, juvenile stress adversely affects later life in many species, including humans. In social species such adverse effects can be buffered by social environment. We were therefore interested in studying the effect of juvenile stress on the life history of the highly social honey bee, Apis mellifera. Two stressors were selected to test the hypothesis that early life stress impacts adult behavior and life expectancy. The parasitic mite, Varroa destructor, was used to induce disease stress in the 5th larval instar and subsequent development. Secondly, the oxidative stressor paraquat was applied to newly emerged bees. Cohorts of individually tagged worker bees were introduced in a common observation hive environment for life-long monitoring. Both stressors increased mortality during the first half of life but the effects on behavior were weak and inconsistent, and no behavior consistently influenced subsequent mortality risk. These results demonstrate lasting mortality effects of early life stress. However, the effects did not last until old ages, which may be due to demographic selection or a social buffering. However, we did not find evidence for behavioral shifts that could have potentially compensated for the earlier stress in these long-lived bees. More research is needed to understand the interactions between stress, social behavior, and life history in the honey bee model.

The effect of genetic quality on the mutation rate, estimated from genome sequences of mutation accumulation lines

Nathaniel Sharp, Aneil Agrawal

2C_305A-Mutation
Sunday, June 22, 2014 1:30 PM-1:45 PM
The deleterious mutation rate plays a key role in evolution, but mutation rate variation is poorly understood. We tested for an effect of genetic quality on spontaneous mutation in Drosophila melanogaster using a mutation accumulation approach. Genotypes constructed to carry deleterious alleles on one chromosome during mutation accumulation showed an elevated rate of fitness decline on a different chromosome. This elevation was correlated with the effect of the treatment alleles on body mass, suggesting that mutation rate is condition dependent. In a follow-up study, we now examine genome sequences from about 100 lines to assess the effect of genetic quality on the rate of point mutations, indels, transposable element insertions, and gene conversion events.

The role of induced mutations as steps toward a Fisherian optimum in Arabidopsis thaliana under field conditions

Frank Stearns, Charlie Fenster

2C_305A-Mutation
Sunday, June 22, 2014 1:45 PM-2:00 PM
Mutations are the ultimate source of genetic variation, allowing natural selection to act. Recent efforts in the study of adaptation genetics have focused on ways to predict how new mutations will contribute to the process of adaptation, most notably relying on mathematical extensions of Fisher’s Geometric Model (FGM) and tests of these mathematical findings through experiments with microorganisms. The results have been very encouraging. One prediction of the FGM that has received less attention suggests that less fit lineages are more likely to benefit from new mutations than organisms that have higher fitness in a particular environment. There is some disagreement in the literature; some authors report mathematical models that predict no change in mean fitness due to new mutations regardless of starting fitness and others showing experimental evidence that mutations are more harmful in lineages under stressful conditions. To our knowledge, there has been no experimental study explicitly addressing this aspect of the FGM. We test this using 18 accessions of Arabidopsis thaliana from across the species distribution. All accessions were mutated using the chemical mutagen EMS and planted in one field plot along with their pre-mutated founder accessions. Fitness was estimated as fruit set x survivorship. Preliminary analyses support Fisher’s prediction that less fit lineages will benefit more from new mutations than more fit lineages.

Patterns of amino acid sequence evolution across various time scales in the mitochondrial genomes of sexual and asexual snails

Joel Sharbrough, Meagan Luse, Jeffrey Boore, John Logsdon, Maurine Neiman

2C_305A-Mutation
Sunday, June 22, 2014 2:00 PM-2:15 PM
Understanding how mutations affect phenotype is of paramount importance in evolutionary biology but remains poorly understood in all but a few model systems. A particularly interesting setting in which to evaluate genotype-phenotype connections is provided by asexual vs. sexual organisms: asexual lineages are expected to exhibit accelerated deleterious mutation accumulation relative to sexual counterparts. While a number of asexual taxa have been shown to accumulate putatively harmful mutations more rapidly than related sexuals, it is still unclear whether mutation accumulation affects fitness enough to contribute to the evolutionary maintenance of sex or asexual lineage extinction. Because amino acid sequence represents a primary measure of phenotypic function, we can generate important inferences about genotype-phenotype connections and thus the consequences of mutation accumulation by evaluating the rates and patterns of amino acid sequence evolution. Here, we compared the rate of radical nonsynonymous evolution (i.e., amino acid changes between biochemical groups) to the rate of conservative nonsynonymous evolution (i.e., amino acid changes within biochemical groups) in the mitochondrial genomes of seven sexual and 24 asexual lineages of Potamopyrgus antipodarum, a freshwater snail in which sexuals and asexuals coexist and compete. We performed these comparisons at relatively long (divergence data), intermediate (polymorphism and divergence data), and relatively short (polymorphism data) time scales, which allowed us to evaluate how the rates and patterns of these mutations change across time. We found that the rate of conservative substitution is significantly higher than that of radical substitution, that radical mutations are significantly less likely to contribute to divergence than conservative mutations, and that radical polymorphisms exist at similar frequencies as conservative polymorphisms within P. antipodarum. These results indicate that conservative nonsynonymous mutations are substantially less harmful than radical mutations, suggesting that treating all nonsynonymous mutations as a single, monolithic class may be inappropriate, but also indicate that the evolutionary differences between radical and conservative mutations are not apparent at relatively short time scales. Furthermore, asexual P. antipodarum appeared to exhibit higher rates of conservative, but not radical, substitution than their sexual counterparts, consistent with the hypothesis that reduced efficacy of purifying selection in the absence of sex should result in an increased rate of accumulation of mildly deleterious mutations.

Redefining the context in context-dependent mutation

Premal Shah, Arjun Krishnan, Michael Gilchrist, Joshua Plotkin

2C_305A-Mutation
Sunday, June 22, 2014 2:15 PM-2:30 PM
Biases in mutation rates between nucleotides have long been implicated in large-scale variation in GC content across genomes. Recent evidence suggests that such biases might exist at even finer scales of individual genes. However, decoupling the effects of biased mutation from that of natural selection in observed genomic patterns remains a challenging hurdle.

Patterns of biased codon usage provide an excellent avenue to explore the role of mutation biases and selection for translation efficiency/accuracy shaping genomic sequences. By combining a mechanistic model of protein translation with a population genetic model, we show how the effects of biased mutation can be decoupled from that of selection for efficiency/accuracy in explaining patterns of codon usage biases. Furthermore, by applying this methodology to several bacterial genomes, we show evidence for widespread mutation biases even within individual genes. The biases in mutation rates within a gene depend highly on the context of the encoding amino acid. However, the context around a given nucleotide - often taken to be adjacent nucleotides on either side - is grossly insufficient in explaining the rate and even directionality of biased mutation rates.

Susceptibility of Caenorhabditis elegans to a bacterial pathogen is a typical quantitative trait with an atypical mutational bias

Veronique Etienne, Erik Andersen, Charles Baer

2C_305A-Mutation
Sunday, June 22, 2014 2:30 PM-2:45 PM

Understanding the genetic basis of disease susceptibility is an important goal of medical genetics and of evolutionary biology. A key first step toward understanding the genetics and evolution of any phenotypic trait is characterizing the role of mutation. However, the extent to which mutation introduces genetic variation for disease susceptibility has, as far as we know, never been quantified in any organism. Here we quantify the mutational variance (VM) for susceptibility to one strain of the pathogenic bacterium Pseudomonas aeruginosa in the nematode Caenorhabditis elegans. VM is a composite parameter dependent on the mutation rate, the size of the mutational target, and the magnitude of allelic effects on the trait. We find that VM for susceptibility to P. aeruginosa is on the order of, or slightly less than VM for a wide variety of life-history and morphological traits in this strain of C. elegans, but is well within the range of reported values for those kinds of traits. Perhaps surprisingly, the average susceptibility did not change significantly over 250 generations of mutation accumulation. Consistent with that finding, selection gradient analysis reveals that selection has both a directional and a stabilizing component, which implies that mutant alleles that increase susceptibility to P. aeruginosa come with a fitness cost. The standing genetic variation (VG) for susceptibility to P. aeruginosa in a worldwide collection of wild isolates of C. elegans is very similar to typical values of VG for life-history and morphological traits in a variety of taxa, and comparison of VM to VG suggests an average strength of selection against mutations affecting susceptibility to P. aeruginosa of a few tenths of a percent. We conclude that, in this system, pathogen susceptibility presents a fairly large mutational target under relatively weak asymmetric stabilizing selection. These results should inform more realistic models of the evolutionary genetics of pathogen susceptibility.

Adapterama @ BadDNA.org - DNA sequencing sample prep for Illumina instruments made easy (amplicons, RADseq, sequence capture & genomes)

Travis Glenn, Brant Faircloth, Troy Kieran, Todd Pierson, John Finger

2C_305B-Genomics
Sunday, June 22, 2014 1:30 PM-1:45 PM

Next-generation DNA sequencing (NGS) presents a potential cornucopia of benefits for studies in evolutionary biology, but easy low-cost preparation of many samples for sequencing remains a constraint. In Adapterama, we present methods for preparing many uniquely tagged (indexed) samples for NGS. Although many sample preparation methods exist, most of these methods rely upon a limited number of commercially available adapters or require single-purpose, custom adapters that require substantial initial investment (e.g., thousands of dollars of oligos to facilitate pooling dozens to hundreds of samples). We demonstrate cheap combinatorial methods to create double-, triple-, and quadruple indexed samples that can be pooled & sequenced with standard Illumina libraries to produce high quality reads for mitochondrial and genome assemblies, microsatellite identification, sequence capture, amplicon sequencing and restriction digest libraries in as many combinations as one desires. The result is that sequencing for many projects in evolutionary biology can be achieved by using these methods, and that the sequencing costs for many projects can become so trivial that being nice to your colleagues can replace the need for everyone winning the grant lottery.

Transposable element and genome size evolution in sexual and functionally asexual evening primroses

Arvid Ågren, Jesse D Hollister, Marc Johnson, Stephen Wright

2C_305B-Genomics
Sunday, June 22, 2014 1:45 PM-2:00 PM

Genome size varies more than 1200-fold across the flowering plants. Despite plenty of theoretical and empirical attention, little consensus exists on the main factors underlying this variation. Several studies have demonstrated that a major contributor to genome size difference between closely related species is differential accumulation of transposable elements. Furthermore, there appears to be a strong correlation between the proportion of the genome made up of transposons and genome size in plants. Given the key role of transposon abundance in driving genome size variation, transposon dynamics should be central to attempts to understand genome size evolution. Much population genetic theory predicts that the reproductive system of the host organism will be an important factor in transposon dynamics. However, whether sexual reproduction should be associated with an increase or decrease in transposon copy number remains unclear. On the one hand, asexuality may lead to a decrease because insertions cannot spread to new lineages through syngamy. On the other hand, Mueller’s ratchet-like processes may result in higher transposon accumulation in asexual lineages. Here, we use a combination of transcriptome sequencing and flow cytometry to compare transposon activity and genome size evolution in some thirty species of differing reproductive systems in the plant genus Oenothera, the evening primroses. Functional asexuality, the absence of recombination and segregation, is estimated to have evolved independently approximately 20 times in the genus. Moreover, in contrast with many other asexual species, functionally asexual species tend to share the same ploidy level with their sexual relatives The effect of reproductive system is therefore decoupled from the effect of ploidy level, which is also expected to affect transposon evolution, making Oenothera particularly suitable for this kind of comparative analyses.

Genome evolution and transposable element dynamics in wild sunflower species

Hannah Tetreault, Mark C Ungerer

2C_305B-Genomics
Sunday, June 22, 2014 2:00 PM-2:15 PM

Transposable elements (TEs) are ubiquitous mobile DNA found in both prokaryotes and eukaryotes and in large part explain genome size variation in higher eukaryotes. The vast majority of repetitive DNA in plant genomes is derived from the proliferation of TEs, specifically class I long terminal repeat (LTR) retrotransposons. These elements are capable of proliferating in their host genome via a copy-and-paste mechanism and have achieved exceptionally high copy numbers in many plant lineages. Understanding the diversity and evolutionary dynamics of these sequences among different plant lineages is of considerable importance in the study of plant genomes and genome evolution. Modern DNA sequencing technologies combined with improvements in bioinformatic tools has facilitated studies of TE biology. Wild sunflower species in the genus Helianthus provide an excellent system for studying TE evolutionary dynamics in the context of genome size expansion and evolution. Genome sizes of 8 diploid sunflower species representing major lineages in the phylogeny (and an outgroup Phoebanthus species) have been determined by flow cytometry; genome sizes range from an estimated 6.9 to 24.2pg. Total genomic DNA of the 9 species under study was sequenced via an Illumina platform yielding approximately 0.2 to 0.6x coverage per species. Genome size was shown to correlate with estimated DNA repetitive fraction ($p=0.0023$ $r=0.9005$). Groups of related LTR retrotransposons were identified and their relative abundances among species determined using a graph based clustering algorithm. A reference panel of full-length LTR retrotransposons mined from BAC data of the common sunflower Helianthus annuus was utilized to identify potential proliferative LTR retrotransposon lineages. This study demonstrates the feasibility of combining analysis of short read sequencing data with existing TE reference information to gain insights into TE evolutionary dynamics across species.

Studying genetic variation in three species of sapsuckers using next generation sequencing

Ashley Curtis, Theresa Burg

2C_305B-Genomics
Sunday, June 22, 2014 2:15 PM-2:30 PM

Yellow-bellied (Sphyrapicus varius), red-breasted (S. ruber) and red-naped (S. nuchalis) sapsuckers are three species that make up the varius sapsucker superspecies complex. All three species are phenotypically distinct and are widely distributed throughout North America with minimal overlap to their ranges where hybrid zones occur. Genetic studies to date are limited to allozyme and mitochondrial studies that are unable to conclusively differentiate between the three species. Due to limited genetic evidence, classification of the congeners as individual species is instead a result of phenotypic differentiation, distinct geographic distribution, and evidence of assortative mating within contact zones. Our study uses genotyping by sequencing (GBS) to study speciation in the varius complex and provide evidence of a genetic basis for species identification. Samples have been collected at various sites throughout North America for each of the species. We are examining these samples to initially determine if the three species are genetically distinct. Our second question focusses on the level of introgression in each species and whether it is a result of recent hybridization or ancient admixture.

Paternity in the NGS era

Kritika Garg, Balaji Chattopadhyay, Uma Ramakrishnan

2C_305B-Genomics
Sunday, June 22, 2014 2:30 PM-2:45 PM

Understanding patterns of parentage assignment is essential to comprehend various processes in natural systems. Till now most our understanding of paternity analysis in wild animals has been based on microsatellite data. In present study we test the utility of reduced representation whole genome sequencing (WGS) for parentage analysis, especially for low quality samples. Using short-nosed fruit bat as a study species we compare the power of WGS data in assigning paternity. We compare the parentage assignments based on WGS data to previously published microsatellite based assignment. We further utilize WGS data to understand mate choice in this species. Our previous work suggested a role of post-copultory mate choice for genetic compatibility. We extend our finding based on whole genome patterns.

Early Evolution of the Genetic Basis for Soma in the Volvocine Green Algae

Erik Hanschen, Patrick Ferris, Bradley Olson, Richard Michod

2C_306A-Phylogenies and Phylogenetics
Sunday, June 22, 2014 1:30 PM-1:45 PM

To understand the hierarchy of life in evolutionary terms we must explain why groups of one kind of individual evolve into a new higher-level individual as observed in the evolution of eukaryotes, multicellular organisms, and eusocial societies. In the evolution of multicellularity, a fundamental step is the division of labor into reproductive germ and non-reproductive soma. In the volvocine green algae, a well developed model system for the evolution of multicellularity, the regA gene determines the fate of somatic cells in multicellular Volvox carteri. The Volvox regA gene has a homolog in unicellular Chlamydomonas containing a conserved protein domain thought to down regulate growth in poor environments. We sought to determine when the somatic cell fate determining protein, regA, evolved in the Volvocales. We report the sequence of regA-like genes and several syntenic markers from divergent species of Volvox. We show that regA evolved early in the Volvocales, after group formation but before the evolution of cellular differentiation. We predict that lineages with and without soma descended from a regA-containing ancestor. The variation in presence of soma may be explained by multiple lineages independently evolving soma utilizing regA or alternate genetic pathways. Our prediction that the genetic basis for soma exists in species without somatic cells raises a number of questions, most fundamentally, under what ecological conditions would species with the genetic potential for soma not evolve these traits. We conclude that the evolutionary history of somatic cells in the volvocine algae is more complicated and labile than previously appreciated on theoretical grounds.

Phylogeny and biogeography of two North American lamioid mint lineages (Lamiaceae)

TILOTTAMA ROY, Charlotte Lindqvist

2C_306A-Phylogenies and Phylogenetics
Sunday, June 22, 2014 1:45 PM-2:00 PM

The angiosperm family Lamiaceae is considered one of the most distinctive and derived angiosperm lineages of major ecological, evolutionary, cultural, and economic importance. Its second largest subfamily, Lamioideae, encompasses two lineages with members in the New World, the tribes Stachydeae and Synandreae. Stachydeae is a widespread and taxonomically complex lineage with 470 species, exhibiting remarkable morphological, ecological, biogeographical, and chromosomal diversity, and includes the globally distributed Stachys, as well as one of the largest Hawaiian angiosperm radiations, the endemic mints. Our recent studies with chloroplast (cpDNA) and ribosomal DNA (rDNA) loci suggested two independent migration events of Stachys to the New World and that dispersal to Hawaii appears to have happened only once, from their closest, contemporary relatives in Southwestern US, around approximately 4 Mya. Results from cpDNA and rDNA loci show incongruence, suggesting a possible hybrid origin for the Hawaiian mints involving different New World Stachys lineages. The South American Stachys appear to have diversified from within two Mesoamerican lineages and could have arisen from hybridization events as well. In order to overcome the biases from maternally inherited cpDNA, and concerted evolution in rDNA markers, and to better resolve the relationships between the Hawaiian mints and their New World Stachys relatives, we utilized independently inherited, nuclear-encoded low copy loci. Although the individual gene trees from the different loci are incongruent, the topology of the species tree derived from a combined coalescent analysis reflects that of the rDNA tree derived from our previous study, showing a reticulate origin of the Hawaiian mints from temperate North American Stachys species. The tribe Synandreae, the only other lamioid lineage native to the New World, consists of five genera, which seemingly arose from an independent colonization of the New World, although single closest lamioid relative is yet to be defined. Through phylogenetic and biogeographic analyses of low copy nuclear markers, we attempted to disentangle the relationships within this tribe, and its position among other lamioid mints. Our results corroborate previous studies, and strongly support the monophyly of Synandreae, distantly related to Stachydeae. Such comparative studies of the mints into the Americas may increase our understanding of processes involved in the origin, establishment and diversification of early angiosperms globally, as well as help elucidate the broader evolutionary aspects of how major early angiosperms lineages colonized and established in the Americas.

An integrated phylogenomic approach toward pinpointing the origin of mitochondria

Martin Wu

2C_306A-Phylogenies and Phylogenetics
Sunday, June 22, 2014 2:00 PM-2:15 PM

Overwhelming evidence supports the endosymbiosis theory that mitochondria originated once from the a-proteobacteria. However, its exact position in the tree of life remains highly debated. This is because systematic noise including sparse taxonomic sampling, sequence composition biases and high evolutionary rates has long plagued the mitochondrial phylogenetics. In this study, we address this issue by 1) increasing the taxonomic representation of a-proteobacterial genomes by sequencing 18 phylogenetically novel species. They include 5 Rickettsiales and 4 Rhodospirillales, two orders that have shown close affiliations with mitochondria previously, 2) using a set of 29 slowly evolving mitochondria-derived nuclear genes that are less biased than mitochondria-encoded genes as the alternative “well behaved” phylogenetic markers, 3) applying site heterogeneous mixture models that account for the sequence composition bias. With the integrated phylogenomic approach, we are able to for the first time place mitochondria unequivocally within the Rickettsiales order, as a sister clade to the Rickettsiaceae and Anaplasmataceae families, all subtended by the Holosporaceae family. Our results suggest that mitochondria most likely originated as an endosymbiont in the Rickettsiales lineage, but not from the distantly related free-living Pelagibacter and Rhodospirillales. In addition, the multiple diverse Holosporaceae genomes sequenced in this project will provide novel insights into the genetic complement of mitochondrial ancestor.

The genome of the ctenophore Mnemiopsis leidyi: bringing resolution to the phylogenetic position of the ctenophores

Joseph Ryan, Christine Schnitzler, Evan Maxwell, Kevin Pang, Warren Francis, Stephen Smith, Tyra Wolfsberg, James Mullikin, Steven Haddock, Casey Dunn, Mark Martindale, Andreas Baxevanis

2C_306A-Phylogenies and Phylogenetics
Sunday, June 22, 2014 2:30 PM-2:45 PM

Until recently, Ctenophora (the comb jellies) was the only non-bilaterian animal phylum without a sequenced genome, and the phylogenetic position of the ctenophores has remained highly controversial. To understand the molecular innovations that drove the outbreak of diversity in the early evolution of animals, we have sequenced, assembled, annotated, and analyzed the 150 megabase genome of the ctenophore, Mnemiopsis leidyi. The availability of this high-quality whole-genome sequence data has enabled us to perform detailed phylogenetic analyses based on both sequence data and gene content, with the goal of bringing clarity to the long-standing debate regarding the phylogenetic position of the ctenophores. The results of our comprehensive analyses, involving multiple lines of evidence, strongly suggest that ctenophores are the likely sister group to all other extant animals. This finding significantly affects our thinking regarding early animal evolution. For example, it appears that neural cell types were lost in poriferans, despite the fact that the sponge (Amphimedon queenslandica) possesses many of the neural components that are also present in Mnemiopsis. Further, the mesodermal cell types found in ctenophores and in the bilaterians may have evolved independently, based on a comparison of the inventory of genes associated with these cell types. Sequence data from the deeply sequenced transcriptomes of seven other ctenophores also provide support for the possibility of some degree of independent evolution. These new sequence data, coupled with the inherent complexity of non-bilaterian species such as Mnemiopsis, open up the intriguing possibility that these animal species have the potential to provide a strong foundation for translational studies focused on specific human diseases. Using a comparative genomics approach, we find that non-bilaterian animals have the potential to serve as viable models for studying various important classes of human diseases.

Improving model-based phylogeographic inference by developing new spatially-explicit summary statistics

Diego Alvarado-Serrano, *Michael Hickerson*

2C_306B-Methodology
Sunday, June 22, 2014 1:30 PM-1:45 PM

Improving our understanding of the relative contribution of different historical processes on structuring populations and species is at the forefront of phylogeographic research. Such understanding is of pressing importance in light of the drastic ongoing landscape and climate changes. To assess the relative likelihood of different plausible evolutionary histories, it is often useful to distill raw population genetic data into a small set of summary statistics that capture information relevant to competing evolutionary histories. However, the traditional population genetic summary statistics used overlook the spatial component of genetic variation, and to overcome this limitation, we present a large set of novel and informative spatially explicit summary statistics focused on assessing the degree of spatial distribution and autocorrelation of genetic variation. We then use spatial demographic and genetic simulations to illustrate their utility for model-based phylogeography by assessing their behavior and performance under two alternative classes of demographic histories that involve expansion and admixture from multiple refugia: cyclical expansion and single expansion. A comparison of the two classes of demographic histories show that both histories could be distinguished by a combination of new and classical summary statistics under a range of parameter values, although they were almost indistinguishable when employing only classical summary statistics. In line with this finding, spatial summary statistics constituted more than 75% of the top 10 most discerning statistics in discriminant function analyses. These results, which were consistent under two different simulated scenarios of cyclical and single expansion, confirm that the use of spatially explicit summary statistics has the potential to substantially improve our ability to use geo-referenced genetic data to test alternative complex species histories. Together with classical non-spatial summary statistics, this new set of spatial statistics offer a valuable instrument to understand how past events shapes genetic diversity. Future developments in the selection of meaningful sets of statistics together with further integration of spatial analyses into statistical inference approaches are expected to provide valuable insights into species and community responses to environmental changes.

Keywords: climate change, model-based phylogeography, range expansion, summary statistics

---

Inferring Very Recent Population Growth Rate from Population-Scale Sequencing Data Using a Large-Sample Coalescent Estimator

Hua Chen, *Kun Chen, Jody Hey*

2C_306B-Methodology
Sunday, June 22, 2014 1:45 PM-2:00 PM

Large-sample or population-level sequencing data provides unprecedented opportunities for inferring detailed population histories, especially recent demographic histories. On the other hand, it challenges most existing population genetic methods: simulation-based approaches require intensive computation, and analytical approaches are often numerically intractable when the sample size is large. We proposed a computationally efficient method for simultaneous estimation of population size and growth rate in the very recent history, using the pattern of the total number of segregating sites as a function of sample size (TNSFS). Coalescent simulation shows that it can accurately and efficiently estimate the rate and the onset time of the recent population growth from large-scale data. This approach has the flexibility to model population history with multiple growth stages or other epochs, and it is robust when the sample size is very large or at the population scale, for which the Kingman's coalescent assumption is not valid. This approach is applied to two recently published data and estimates the recent population growth rate in the European population to be 2.4% with the onset time 5.8Kyr ago, and the rate in the African population to be 1.44% with the onset time 8.5Kyr ago.

Simulation tests of probabilistic models for historical biogeography: DEC and DEC+J

Nicholas Matzke

2C_306B-Methodology
Sunday, June 22, 2014 2:00 PM-2:15 PM

Several phylogenetic models for historical biogeography are in widespread use, e.g. character mapping, Dispersal-Vicariance Analysis (DIVA), and Dispersal-Extinction-Cladogenesis (DEC). In addition, new models have become available: BayArea, and the variety of models implemented in the R package BioGeoBEARS. These include DEC+J (which adds founder-event speciation to DEC) and DIVALIKE (a likelihood interpretation of DIVA; a DIVALIKE+J model is also available). There has been very little testing of biogeographical models against simulated data in the situation when the true model is substantially different than the assumed inference model. Also, all of the above models assume that the observed tree is the true tree, ignoring possible missing speciation/extinction events, and dependence of speciation/extinction rates on geographic range. These possibilities are taken into account by the GeoSSE and ClaSSE models, but at the cost of many more free parameters, which may strain typically small biogeographic datasets. To test the accuracy of DEC and DEC+J inference on datasets simulated under different biogeographical and SSE models, I jointly simulated phylogenies and geographic range under 6 macroevolutionary models. The first three assumed speciation/extinction were independent of geographic range: (1) Yule process (pure-birth, no extinction); (2) Birth-Death (BD) process with extinction rate 1/3 of the speciation rate; (3) BD process with extinction equal to speciation. The next three assumed an SSE model where the base speciation rate was multiplied by the number of areas occupied, and base extinction rate was divided by the number of areas occupied. This produced (4) SSE with speciation but zero extinction rate; (5) SSE with with the base extinction rate 1/3 of the speciation rate; and (6) SSE with base rates of speciation and extinction equal. For each of the 6 macroevolutionary models, all combinations of low/middle/high values were used for these biogeographic parameters: d (rate of range-expansion), e (rate of range-contraction), and j (relative weight of founder-events versus traditional DEC cladogenesis events at speciation). The datasets (138 parameter combinations, 100 simulations each with 50 living species) were subjected to inference under DEC and DEC+J. DEC and DEC+J were distinguishable under all 6 models, except when j was very small and d very high. DEC artificially raises d and e when DEC+J is the true model, and shows significantly reduced accuracy in inferring ancestral range. These results indicate that the fact that DEC+J is favored over DEC by many empirical datasets is not likely to be an artefact of missing SSE processes.

Extending BAMM: a computer program for analyzing complex macroevolutionary dynamics on phylogenetic trees

Carlos Anderson, Dan Rabosky

2C_306B-Methodology
Sunday, June 22, 2014 2:15 PM-2:30 PM

The phylogenetic history and the distribution of current phenotypes of a group of species has been shaped by sequences of past macroevolutionary events. These events may include changes in the rate of speciation, extinction, or phenotypic evolution. Events occur in various locations on a phylogenetic tree and each one has specific parameters, such as whether the speciation rate increased or decreased through time. BAMM is a computer program that identifies macroevolutionary events that have occurred in the phylogenetic history of a group of species. Here we describe extensions to the software that improve our ability to reconstruct complex histories of speciation, extinction, and phenotypic evolution. We also apply our software to an empirical phylogeny and propose ways in which our methods may be improved or extended.

The Impact of the Rate Prior on Bayesian Estimation of Divergence Times with Multiple Loci

Mario dos Reis, Tianqi Zhu, Ziheng Yang

2C_306B-Methodology
Sunday, June 22, 2014 2:30 PM-2:45 PM

Bayesian methods provide a powerful way to estimate species divergence times by combining information from molecular sequences with information from the fossil record. With the explosive increase of genomic data, divergence time estimation increasingly uses data of multiple loci (genes or site partitions). Widely used computer programs to estimate divergence times use independent and identically distributed (i.i.d.) priors on the substitution rates for different loci. The i.i.d. prior is problematic. As the number of loci (L) increases, the prior variance of the average rate across all loci goes to zero at the rate 1/L. As a consequence, the rate prior dominates posterior time estimates when many loci are analysed, and if the rate prior is misspecified, the estimated divergence times will converge to wrong values with very narrow credibility intervals. Here we develop a new prior on the locus rates based on the Dirichlet distribution that corrects the problematic behaviour of the i.i.d. prior. We use computer simulation and real data analysis to highlight the differences between the old and new priors. For a dataset for six primate species, we show that with the old i.i.d. prior, if the prior rate is too high (or too low), the estimated divergence times are too young (or too old), outside the bounds imposed by the fossil calibrations. In contrast, with the new Dirichlet prior, posterior time estimates are insensitive to the rate prior and are compatible with the fossil calibrations. We re-analysed a phylogenomic data set of 36 mammal species and show that using many fossil calibrations can alleviate the adverse impact of a misspecified rate prior to some extent. We recommend the use of the new Dirichlet prior in Bayesian divergence time estimation.

Phylogenomics of deep-sea octocorals: new approaches to solve long-standing problems

Santiago Herrera, Timothy Shank

2C_306C-Phylogenetic Systematics
Sunday, June 22, 2014 1:30 PM-1:45 PM

The sub-class Octocorallia, is one of the least studied groups within the phylum Cnidaria. In general, the taxonomy, phylogenetic relationships and population-level variability within this group are poorly understood. Morphologically-based species identification and classification are extremely challenging for non-specialists, and are difficult to replicate among taxonomists. Variations in octocoral colony architecture and micro-skeletal structures have been historically used as diagnostic characters. Studies over the last 15 years have shown that many of these morphological traits keep little to no correspondence with the patterns of relatedness inferred using low-variability mitochondrial and ribosomal DNA sequence markers. As such, these traditional molecular markers have been remarkably insufficient to resolve relationships at all taxonomic levels within the octocorals. These have been long-standing problems with no solution, leaving fundamental questions regarding species differentiation, classification, and biogeography of cold-water octocorals unresolved.

Recent technical advances allow the implementation of next-generation sequencing technologies for the rapid detection and genotyping of genome-wide Single Nucleotide Polymorphisms (SNPs) in non-model organisms. These technologies open a new frontier in molecular studies, not only providing rich information for species identifications and taxonomy, but also the promise of providing profound insights into the population genomics, phylogeography, and evolution of deep-sea species.

We employed Restriction-site-Associated DNA sequencing (RAD-seq) to identify SNPs in individuals from 13 putative octocoral coral species from the clade of families Paragorgiidae, Corallidae, and Alcyoniidae. Through phylogenomic analyses we produced a completely resolved and well-supported evolutionary tree for the group, which spans divergence times greater than 50 million years. Our approach demonstrates the great potential of RAD-seq for untangling the genetic relationships of deep-sea organisms, particularly those that have traditionally been difficult to study due to low levels of genetic variation.

Genome-wide RAD data yields fine resolution species relationships in embiotocid surfperches

Gary Longo

2C_306C-Phylogenetic Systematics
Sunday, June 22, 2014 1:45 PM-2:00 PM

Advances in next generation sequencing technology (NGS) along with decreased costs have led to a rapid expansion in the field of population genomics. A particularly attractive approach that requires no prior genomic information and that simultaneously genotypes while sequencing is restriction-site associated DNA (RAD) markers. Although this technique has been used alongside population genomics to do things such as identify candidate loci under selection and parallel adaptation, there have been relatively few RAD phylogenomic studies. In order for RAD data to provide phylogenetically informative data, a sufficient number of orthologous restriction sites must be retained across taxa. Recent simulations suggest that sufficient orthologous RAD markers exist within relatively young taxonomic groups to correctly infer “known” phylogenies for drosophila (≤40-60 mya) and primates (~22 mya). Additionally, recent work has resolved species relationships and boundaries in Lake Victoria cichlids using RAD data. Here, we use phylogenetically informative RAD data to infer relationships among all genera and 22 species of surfperches (Embiotocidae), resulting in the most complete and well supported surfperch phylogeny to date. There are currently 24 valid species divided into 13 genera, seven of which contain only one species. 20 species are found in the eastern Pacific along the western coast of North America from southern Alaska to central Baja, Mexico, with one freshwater species found in the central valley of California. The other four species reside in the western Pacific along the coasts of Japan and Korea. The highest density of surfperch species can be found between latitudes 32°N and 38°N off the coast of California. It is likely that ancestral surfperches radiated north and south out from California coastal waters and colonized the western Pacific during an interglacial warming period. To better understand this radiation, we generated robust, well-supported phylogenies by drawing from over 150,000 phylogenetically informative SNPs from across the genome in our largest RAD data sets. This allowed for high-resolution species relationships and clarified previously unresolved and low support branches from earlier embiotocid molecular phylogenies. This phylogeny sheds new light on the processes of adaptive radiation in this family.

Convergence of nodes and internodes: Assessing the monophyly of bamboo corals (Cnidaria, Octocorallia, Isididae) and their diversity in the deep sea

Esprit Heestand Saucier, Les Watling, Scott France

2C_306C-Phylogenetic Systematics
Sunday, June 22, 2014 2:00 PM-2:15 PM

Bamboo corals are immediately recognizable by their jointed axial skeleton (dark proteinaceous nodes alternating with white calcareous internodes), however there have been many questions about the evolutionary relatedness of the four isidid subfamilies as well as the placement of some “problematic” genera. The subfamily Isidinae is restricted to shallow waters while the other three subfamilies, Keratoisidinae, Mopseinae and Circinisidinae, are primarily found in the deep sea. Keratoisidinae has a worldwide distribution and is the most speciose subfamily, whereas Mopseinae and Circinisidinae have a more restricted geographic range, being found only in the Southwest Pacific and Southern Ocean.

We assess the monophyly of Isididae and investigate the placement of the problematic genera Sclerisis and Isidoides using genetic analyses of over 250 colonies collected in the North Atlantic, Caribbean, Southwest and Central Pacific, and Indian Oceans. Our results, based on mitochondrial DNA sequence data, show the Isididae as polyphyletic. In particular, the subfamily Isidinae, which contains the type genus (Isis) of the family, forms a clade with members of an entirely different suborder, Holaxonia. Members of the strictly deep-sea subfamily Keratoisidinae form a well-supported monophyletic clade, and are further characterized by a unique mitochondrial gene arrangement; there are more clades and diversity among the keratoisidins than there are currently described genera. Mopseinae and Circinisidinae specimens used in our analysis are intermixed in a single clade that did not cluster with Keratoisidinae; our taxon sampling is inadequate to assess the monophyly of these two subfamilies, however they are not a sister taxon of Keratoisidinae. Sclerisis haplotypes (n=2) were intermixed with specimens in the Mopseinae/Circinisidinae clade. Isidoides is consistently recovered as the sister taxon to the Keratoisidinae and not with the other genera of deep-sea chrysogorgids (which form their own monophyletic clade) with which they are currently classified. Our molecular phylogeny suggests that “bamboo corals” represent at least three independent evolutionary radiations, and that a jointed axial skeleton with sclerite-free proteinaceous nodes is therefore convergent.

The Ruby Seadragon, a spectacular new species of seadragon (Syngnathidae)

Josefin Stiller, Greg Rouse, Nerida G. Wilson

2C_306C-Phylogenetic Systematics
Sunday, June 22, 2014 2:15 PM-2:30 PM

The discovery of a new large, ornamental vertebrate is a rare occurrence. Seadragons are elaborately camouflaged marine fish belonging in Syngnathidae. The clade is endemic to coastal seas along southern Australia. Two species are currently recognized; the Common Seadragon (Phyllopteryx taeniolatus), and the Leafy

Seadragon (Phycodurus eques), both from fairly shallow waters. Here we present a new species of seadragon from slightly deeper water, which shows a characteristic red coloration. We therefore called it the Ruby Seadragon. We present evidence from molecular genetics, comparative morphology, and ecology that supports the designation of a new species.

Genetic differentiation was examined using three nuclear markers and several mitochondrial regions . All markers showed considerable genetic differences between the Ruby Seadragon and the other seadragons, of a magnitude to suggest it is a discrete species. Phylogenetic analysis (4386 bp total) confidently placed the Ruby Seadragon in Phyllopteryx as the sister to Phyllopteryx taeniolatus, with Phycodurus eques as the sister-group to this clade.

Morphological analysis using a high-resolution micro-computed tomography scan (micro CT) of the new species revealed clear skeletal differences that distinguish it from its relatives. Animated three-dimensional reconstructions of the species were used to outline shared traits with the other seadragons and morphological novelties unique to the Ruby Seadragon. Tracing of morphological characters in light of the molecular phylogeny allowed us to investigate evolutionary trends in the body organization of seadragons.

Even though the Ruby Seadragon seems to inhabit similar areas on the Western Australian coast as the other two species, they are potentially bathymetrically separated. The new species may be isolated by inhabiting deeper waters: Three of four specimens were collected from 50 to 72 meters of depth, which is considerably deeper than the usual depth range of other seadragons. It is likely that the occurrence beyond recreational scuba diving depths hindered previous discovery. Therefore, the Ruby Seadragon is a glowing example of the importance of biodiversity studies and scientific collections: some of the specimens were housed in museum collections for almost a century but never recognized as a new species.

Further research is needed on this enigmatic new species to establish the distributional and bathymetric range of the Ruby Seadragon, to study the biology of this species in its habitat, and to assess its conservation needs.

Assessing the intraspecific systematics of the Cotton Mouse, Peromyscus gossypinus, using a highly variable region of the mitochondrial genome

Sean Beckmann

2C_306C-Phylogenetic Systematics
Sunday, June 22, 2014 2:30 PM-2:45 PM

High morphological plasticity within and among species presents an ongoing challenge to the identification of taxonomic units. This is particularly true in generalist rodent species where plasticity is the norm, not the exception. One such species, the cotton mouse, Peromyscus gossypinus, consists of five extant, morphologically identified subspecies. Studies of morphological and allozyme variation have suggested these may not represent distinct taxonomic units. This study applied DNA sequencing technology to assess the taxonomic status of extant subspecies of P. gossypinus and elucidate the species' intraspecific phylogeny. The D-loop of the mitochondrial control region was sequenced in 527 organisms from throughout the species range including all known insular populations. Phylogenetic reconstructions, genetic distances, and analysis of molecular variance were performed on the resulting data. Results were compared to currently recognized subspecies to identify congruence and assess taxonomic validity. Reconstructions identify three primary clades within P. gossypinus with varying support and do not correspond to the current taxonomy. Within clades several insular populations are distinct, indicating a lack of gene flow with mainland populations. Finally, results indicate a pattern of diversity that corresponds with historic biogeographic events. These results suggest the need to overhaul the current intraspecific systematics of P. gossypinus.

Keywords: Systematics, Phylogeography, Intraspecific, Peromyscus

---

Division of labor in insect societies: Genetic components and physiological regulation

Romain Libbrecht

2C_BalC-ASN Young Investigators' Symposium: Jasper-Loftus Hill Award
Sunday, June 22, 2014 1:15 PM-1:45 PM

Division of labor is central to the organization of social insects (ants, termites and some species of bees and wasps) and is thought to be at the root of their ecological success. There are two main levels of division of labor in insect societies. The first relates to reproduction and involves the coexistence of queen and worker castes: while reproduction is usually monopolized by one or several queens, functionally sterile workers perform all the tasks to maintain the colony, such as nest building, foraging or brood care. The second level of division of labor, relating to such non-reproductive duties, is characterized by the performance of different tasks or roles by different groups of workers. The aim of my research is to better understand the mechanisms underlying division of labor in insect societies, by investigating how genes and physiology influence caste determination and worker behavior in ants. I have first used the Argentine ant Linepithema humile to conduct controlled crosses in the laboratory, which revealed the existence of non-additive genetic effects, such as parent-of-origin and genetic compatibility effects, on caste determination and worker behavior. Second, I have performed experimental manipulation of hibernation, hormonal treatments, gene expression analyses and protein quantification in Pogonomyrmex harvester ants, which revealed the physiological pathways regulating maternal effects on caste determination. Additionally, comparing gene expression between queens, nurses and foragers in Pogonomyrmex ants revealed the role of vitellogenin in regulating division of labor. Finally, I am currently focusing on the epigenetic regulation of behavior and reproduction in the clonal raider ant Cerapachys biroi. Overall, the results gathered so far provide important insights into the role of genes and physiology in the regulation of division of labor in social insect colonies, helping to better understand the organization, evolution and ecological success of insect societies.

Convergences and divergences during adaptive radiation

Travis Ingram

2C_BalC-ASN Young Investigators' Symposium: Jasper-Loftus Hill Award
Sunday, June 22, 2014 1:45 PM-2:15 PM

Adaptive phenotypic evolution in diversifying clades can result in multiple classes of macroevolutionary pattern. First, divergent selection associated with ecological speciation can result in trait differentiation linked to speciation events (nodes) in a phylogenetic tree. Alternatively, attraction to the same phenotypic optima or adaptive peaks can result in convergent trait evolution between multiple lineages. I will describe recent methodological advances that allow us to investigate both divergent and convergent evolution with phylogenetic comparative data, and will demonstrate these approaches using adaptive radiations of Pacific rockfish and Caribbean anoles. I will compare the support for divergence vs. convergence in traits related to different aspects of the niche, and discuss the potential for general principles of macroevolutionary trait diversification.

Climate change ecology and evolution in the sea

Malin Pinsky

2C_BalC-ASN Young Investigators' Symposium: Jasper-Loftus Hill Award
Sunday, June 22, 2014 2:15 PM-2:45 PM

Will species respond similarly in the ocean and on land to the impacts of climate change? While the same ecological and evolutionary processes operate in both environments, marine ecosystems have substantially different physical conditions, geographic patterns, and taxonomic diversity than ecosystems on land. Here, we use genetic estimates of dispersal combined with long-term ecological data to suggest that marine species can generally keep up with climate velocities (the rate and direction that temperatures move across the seascape), while many terrestrial species appear to be lagging behind. In addition, meta-analysis and modeling suggests that there are important interactions between climate and other anthropogenic impacts in the ocean that are distinct from those on land. Heavily fished species, for example, may suffer from reduced ability to adapt to climate change while simultaneously shifting their geographic distributions faster than would otherwise be expected. This is a substantially different effect than imposed by habitat fragmentation, the dominant anthropogenic impact on land. Small species with fast life histories are also more likely to have collapsed to low abundance in the ocean than on land. Cross ecosystem comparisons provide a fascinating opportunity to test ecological and evolutionary theory while improving our understanding of future climate impacts.

Population-genomic correlates of inbreeding depression in outcrossing Caenorhabditis species

Luke Noble, Matthew Rockman, Annalise Paaby, Max Bernstein, M. Victoria Cattani, Taniya Kaur

2D_201-Fitness and Selection
Sunday, June 22, 2014 3:15 PM-3:30 PM

Inbreeding depression is one of the most familiar examples of genetics at work. Basic parameters such as mating system, population size and metapopulation dynamics are expected to interact with the underlying genetic architecture and distribution of selective effects, with the potential for different outcomes for different evolutionary histories. The Caenorhabditis genus provides extreme examples: while the outcrossing C. remanei suffers strong inbreeding depression, outbreeding depression is seen for the predominantly selfing, androdioecious C. elegans. We have found substantial variation in inbreeding depression both within and among outcrossing species C. remanei, C. sp. 28, C. sp. 29 and C. kamaaina (C. sp. 15), measured as time to extinction across replicate lines for 20 generations of sib-mating. Sequencing and annotation of surviving inbred line genomes, along with the founding populations from which they were derived, allows accurate measurement of relative nucleotide diversity and estimation of the functional impact of a large sample of segregating mutations. Surprisingly, we find no correlation between diversity and the severity of inbreeding depression. Fitness estimates and variant effect prediction efforts are ongoing, and initial results suggest inbreeding may be better predicted by the load of highly deleterious mutations, and by correlates of selection efficacy such as codon bias.

Conserving genomic variability in amphibians: estimating effective population size and population growth trends

Schyler Nunziata, Stacey Lance, David Scott, David Weisrock

2D_201-Fitness and Selection
Sunday, June 22, 2014 3:30 PM-3:45 PM

Recent advancements in genetic techniques now make it possible for thousands of single nucleotide polymorphisms (SNPs) to be assayed across the genomes of non-model species. Because accuracy and precision in estimating effective population size (Ne) and genetic diversity increases rapidly with the number of loci used, this could lead to powerful studies of population health and viability. However, before these estimates can be applied to conservation questions, it is necessary to understand the evolutionary processes and mechanisms regulating genetic diversity. Ne and other measures of genetic diversity can be used to detect changes in population abundance and identify conservation needs. However, calculating Ne requires restrictive assumptions about population processes such as stable population size, no age structure, and no gene flow. Amphibians have complex population structuring, violating many of the assumptions in models used to estimate Ne. It is unclear what the true Ne is under these circumstances because current equations do not take into account all factors simultaneously. We use stochastic population simulation models under representative demographic conditions to estimate true Ne and quantify genetic diversity loss. We evaluated model results with empirical data, using both demographic and genetic methods to estimate Ne in two populations of salamanders, Ambystoma opacum and A. talpoideum in an isolated wetland, on the Savannah River Site (SC) over a 20-yr period. These two species represent opposite growth rate trends, with A. opacum population steadily expanding over the course of the study and A. talpoideum declining. The numbers of breeding adults (N) and their offspring are known for 30 years for each population. To calculate Ne with demographic models we used field estimates of longevity, sex ratio, generation time, and breeding success. For genetic estimates we used double-digest RAD sequencing to generate several thousand SNP markers to estimate Ne and other classical population genetic parameters (Ho, HE, allelic richness) using temporally collected genetic data over 20 years for each species. Our results provide important information on what factors should be incorporated into models for estimating Ne.

Demographic inference and genetic diversity in isolated urban and rural populations of white-footed deermice in New York City

Stephen Harris, Jason Munshi-South

2D_201-Fitness and Selection
Sunday, June 22, 2014 3:45 PM-4:00 PM

Urbanization is often characterized by extreme fragmentation of native habitats and is a likely driver for adaptation in the non-model organism, Peromyscus leucopus, in New York City (NYC). The white-footed deermouse is an abundant small mammal native to eastern North America and in NYC, is representative of an urban-adapter. We examined genetic structure and the demographic history of white-footed mice in NYC and looked for evidence of local adaptation in isolated urban populations. We utilized next generation sequencing (NGS) of restriction site-associated DNA (RADseq) to generate thousands of putatively neutral RAD tags and assembled the nearly complete P. leucopus transcriptome from RNA sequencing. This dataset was generated from equal numbers of deermice in undisturbed protected rural habitat and several urban park sites, and population genetic statistics were calculated in protein coding regions. Demography is difficult to construct from historical records, but new techniques that utilize the joint allele frequency spectrum allow for demographic inference from genomic data. Using the RADseq loci we looked at genetic structure and estimated demographic parameters for populations of white-footed deermice in and around NYC and then complimented this history with a scan for genetic diversity across transcriptome contigs containing RAD tags. We find evidence of selection in genes that might be driving local adaptation in NYC P. leucopus populations and uncover the demographic history of white-footed deermice in a fragmented urban habitat.

Genomic differences reflect fitness over a small-scale thermal gradient in reef-building corals

Rachael Bay, Stephen Palumbi

2D_201-Fitness and Selection
Sunday, June 22, 2014 4:00 PM-4:15 PM

Local adaptation was traditionally thought to be rare in high gene flow systems, such as marine environments, as the influx of migrants would drown out any signal of natural selection. However, next-generation sequencing techniques have been used to uncover population substructure at a number of selected loci even in populations previously thought to be panmictic. This begs the question, what is the smallest spatial scale at which adaptation can occur? If selection is strong enough, can it act within a single population? We explore an extreme case of selection in the face of gene flow in reef-building corals, where the spatial scale of environmental heterogeneity is orders of magnitude smaller than the average dispersal distance. We combine whole-transcriptome sequencing with reciprocal transplantation to examine adaptation to microclimate temperature regimes within a single reef in the tabletop coral, Acropora hyacinthus. We identified single nucleotide polymorphisms (SNPs) associated with temperature regime, even in the presence of gene flow. We found that rare variants representing a broad range of cellular pathways were maintained in more thermally stressful microclimates, evidence for balancing selection in a heterogeneous environment. Survival and growth measurements from transplant experiments mirror genetic data, suggesting some genotypes are more resilient in the face of heat stress than others. These results provide information on possible mechanisms for coral resilience as well as the potential for populations to adapt as ocean temperatures increase.

Clonal Selection in a Unisexual Vertebrate

Amber Makowicz, Ingo Schlupp

2D_201-Fitness and Selection
Sunday, June 22, 2014 4:15 PM-4:30 PM

Kin selection theory states that individuals should favor their kin at the cost of their own fitness when the benefits of inclusive fitness outweigh the costs. In clonal species, relatedness is high and kin selection would predict stronger selection favoring identical clones when compared to other clonal lineages. I studied this theory using the clonal fish the Amazon molly (Poecilia formosa). Females produce daughters that are identical to themselves and each other, and are sexual parasites to their parental species. They overlap and compete in many aspects of their ecological niche, behavioral, and life history parameters. Understanding the maintenance of sexual/unisexual species is a challenge because it violates competition theories. Behavioral differences between sexual/unisexual species may play a prominent role in allowing these species to overlap in the same ecological niche, such as aggression regulated via kinship. Here, I demonstrate that these females can recognize and prefer sister clones over non-sister clones. Familiarity was ruled out as viable explanation. Furthermore, I was able to show that Amazon mollies were using a combination of sensory channels to discriminate between sister and non-sister clones. Females responded strongest to visual only cues; however, they were more active when chemical cues were present. Moreover, I found that Amazon mollies could even adjust their aggressive behaviors between different clonal lineages. Together, this data suggests that Amazon mollies are able to identify identical clonal sisters using both visual and chemical cues and regulate their aggressiveness towards them when compared to non-sister clones and their sexual host.

Morphological Diversity Patterns of Mammals Prior to the K-Pg Extinction Event

David Grossnickle

2D_206-Deep Time
Sunday, June 22, 2014 3:15 PM-3:30 PM

The end-Cretaceous extinction of non-avian dinosaurs opened ecological niche space that was subsequently exploited by Cenozoic mammals. However, some evidence suggests mammals had begun to diversify prior to the Cretaceous-Paleogene (K-Pg) boundary (66 million years ago). Diversification of mammals into new ecological niches would have led to a greater variety of diets, and, consequently, an increase in morphological disparity of molars. To assess the possibility that mammals began to diversify prior to the K-Pg boundary, I examined morphological disparity patterns of Cretaceous therians, the mammal group that gave rise to diverse placentals and marsupials. Two-dimensional landmark data from occlusal surfaces of individual molars belonging to 60 crown therian and stem boreosphenidan genera were studied using geometric morphometric techniques, including a Procrustes analysis and principal components analysis. Therian genera were assigned to Cretaceous time bins based on the temporal range of their fossil occurrences, and morphological disparity of molar shape was calculated for each time bin. To explore evolutionary trends on a regional scale, taxa from North America and Asia were separated and results were considered independently for the two continents. An additional measure of therian disparity was obtained from body mass estimates, which were calculated using the dimensions of the first lower molar. Results indicate that morphological disparity was low for much of the Cretaceous and then experienced a rapid increase during the Campanian (84-72 million years ago). Disparity results based on the global data set show a decrease in disparity during the Maastrichtian (72-66 million years ago), but results based solely on North American taxa suggest that disparity continued to increase during the Maastrichtian. This difference may be due in part to the Maastrichtian fossil record being dominated by North American fossils, resulting in Maastrichtian disparity values that are less reflective of a global trend. Based on the current fossil record, it is concluded that therian mammals experienced a morphological diversification during the Late Cretaceous, although it remains uncertain as to whether this diversification trend was maintained until the K-Pg boundary.

Measuring phylogenetic conservatism of extinction in vertebrates: deep-time signals and methods

Laura Soul, Matt Friedman

2D_206-Deep Time
Sunday, June 22, 2014 3:30 PM-3:45 PM

Interactions between extinction risk, heritable traits that confer vulnerability, and phylogenetic relationships among taxa are an important focus of neontological research in extinction and conservation. The fossil record offers a unique deep-time perspective on these patterns that is unavailable to us from extinctions in recorded history alone. Unfortunately differences in time scale, the type of data available, and research intensity for different clades have so far made unification of neontological and palaeontological studies of extinction problematic. Here I present a study focussing on vertebrate groups, to determine whether phylogeny can be used as a proxy for extinction-linked, non-fossilising traits in the geological past. I used three metrics – Fritz and Purvis' D, Pearson's ρ and Moran's I – to examine the pattern of phylogenetic clustering in extinction in three tetrapod groups (synapsids, temnospondyls and parareptiles) through the Permo-Triassic (P/T) mass extinction. In addition, given the potential for distortion of macroevolutionary patterns in the fossil record caused by poor sampling, I used simulations to test how robust the methods are to palaeontological data. By simulating 'true' phylogenies, then sampling them to represent time-scaled cladograms that we can reconstruct from the fossil record, I measured the degree to which measurements co-vary on true and fossil trees. Results show that there was a progressive shift towards more clustered extinctions leading into the P/T boundary, and all three clades show the most significantly clustered extinction at the boundary itself. This is in line with previous work on invertebrate groups. The results of the simulations indicate that strong phylogenetic clustering of extinction can be correctly identified when it is present, and that estimates tend to be conservative. However, I also found instances where results from the true trees and fossil trees were inconsistent. A measurement on a fossil tree can show significant phylogenetic clustering of extinction when the measurement on the true tree shows phylogenetically random extinction for the same time bin. Therefore, results must be interpreted with caution and in the context of long-term signals. Consistent selection against heritable traits over long timescales leads to a disproportionate loss in biodiversity. This occurred in the geological past and an increase in extinction intensity amplified the effect.

Cenozoic mammals and the biology of extinction

Peter Smits

2D_206-Deep Time
Sunday, June 22, 2014 3:45 PM-4:00 PM

Extinction is expected to be non-random with respect to biology. Determining how different traits, both alone or in concert, influence extinction risk is extremely important for understanding the differential diversification of taxa. Traits relating to environmental preference are good candidates for modeling differential extinction because it is expected that, based purely on stochastic grounds, taxa which prefer rare environments would have a greater extinction risk than taxa which prefer abundant environments. Importantly, the Law of Constant Extinction posits that extinction risk is random with respect to taxon age. This statement has come increasingly under fire and its generality is possibly suspect. By fitting different theoretical distributions of survival to empirically observed durations, the generality of this statement can be tested.

Trait mediated survival was studied at both the generic and specific level for the record of Cenozoic mammals using dietary and locomotor categories, as well as body size. These traits were selected because they relate directly to environmental preference. Preliminary analysis of specific level survival as predicted from dietary and locomotor categories indicated that North American and European mammals had fundamentally different patterns of taxon duration. North American species survival was best predicted by locomotor category while European species survival was best predicted by dietary category. Also, the distribution of North American species durations was best modeled as exponentially distributed (constant extinction risk) while European species durations were better modeled by a Weibull distribution (monotonic nonconstant extinction risk). Even with further refinements to this analysis, these results do highlight how regional level processes may shape taxonomic patterns in fundamentally different ways

Ants in the age of dinosaurs: a history from amber

Phil Barden

2D_206-Deep Time
Sunday, June 22, 2014 4:00 PM-4:15 PM
Over the past ten years, several fossil discoveries have painted a new picture of early ant history. Cretaceous taxa are now known to have been remarkably diverse, many exhibiting morphological innovations not found in any groups living today. These stem-group ants offer new insight into early ant evolution, in particular, valuable morphological data and information regarding their ecology, diversity, and sociality. Here, ancient ant taxa are contextualized through morphometric and phylogenetic analyses to evaluate the placement of fossil species and infer their role in paleoenvironments.

Biting into it: Occlusion and development force correlations and anticorrelations in dental characters

Liliana Davalos, Omar Warsi, Edward Li, Samuel Gochman, Nancy Simmons, Paul Velazco

2D_206-Deep Time
Sunday, June 22, 2014 4:15 PM-4:30 PM
Since fossils are indispensable to date phylogenies and answer comparative questions, scoring morphological characters from the best remains available is a critical step in many evolutionary studies. Among mammals, teeth are exceptionally well-preserved and important sources of characters for phylogenetic analyses. We simulated character matrices based on a matrix of 278 dental characters that was designed to infer the phylogeny of very incomplete Miocene fossils from an ecologically hyperdiverse clade of mammals. Compared to the simulated matrices, the observed data had clusters of extremely high and low similarity, indicating both correlations and anticorrelations in character states. Analyses of character ontology revealed occluding premolars and molars were significantly more likely to encode identical character states, while dental features from adjacent locations were more likely to encode completely dissimilar patterns. We propose that selection for functional occlusion underlies the excess similarity in molar and premolars, and developmental programs for individual dental loci explain the extreme dissimilarity in character states. Out results reject the assumption of character independence implicit in the vast majority of analyses integrating phenotypic characters, and caution against collecting large matrices under the presumption that more is more.

Global Influenza A/H3N2 Migration under Changing Prevalence throughout the Year

Daniel Zinder, Mercedes Pascual

2D_301A-Viral/Microbial Evolution
Sunday, June 22, 2014 3:15 PM-3:30 PM
Influenza A/H3N2 is a highly seasonal, single stranded, segmented RNA virus that has been circulating in the human population since 1968 and is the cause of considerable morbidity and mortality. A fundamental question in the dynamics of seasonal H3N2 influenza is identifying the relationship between changing prevalence throughout the year and the level and timing of immigration and emigration of the virus between global communities. This question has remained elusive because we have lacked a methodological framework to address seasonal, as opposed to constant phylogeographic migration rates. Here, we build and expand upon recently developed methods to infer migration rates which differ from season to season, and to calculate the expected number of migration events between global communities throughout the year. Our results reveal clear patterns of seasonal migration within regions and globally, with rapid local turnover and windows of immigration and emigration mapping to epidemic spread and decline respectively. At a global level, strain persistence, as manifested through the trunk of the phylogenetic tree of H3N2, is strongly correlated with reduced seasonal variability in incidence within the global communities which were examined. One main implication is that the current emphasis on connectivity, including air travel, should be complemented with a better understating of the conditions and timing required for the successful establishment of migrants. Our approach provides a basis to better understand seasonal drivers, to expand prediction horizons and to improve vaccine updating by identifying strains that not only escape immunity but also have the seasonal opportunity to establish themselves. In addition, our inference framework can inform the study of seasonal phylogeographic migration patterns in other pathogens and in microbes in general.

Host range expansion of MERS-Coronavirus and the permissivity of receptor orthologs

Kayla Peck, Adam Cockrell, Boyd Yount, Trevor Scobey, Ralph Baric, Mark Heise

2D_301A-Viral/Microbial Evolution
Sunday, June 22, 2014 3:30 PM-3:45 PM
Dipeptidyl peptidase IV (DPP4) has been identified as the receptor for MERS-Coronavirus (MERS-CoV) infection, with bat, monkey, and human DPP4 able to mediate MERS-CoV infection. Other DPP4 orthologs, including those from traditional small animal models such as mouse, ferret, and guinea pig, do not permit infection. In order to understand the evolutionary mechanisms of host range expansion, it is important to identify key determinants in DPP4 that govern MERS-CoV host range. First, we demonstrate that mouse DPP4 (mDPP4) cannot support MERS-CoV infection. However, we identified a combination of two key mutations in mDPP4 that allows the molecule to confer infection at a level approaching that observed with human DPP4. We test whether these two residues regulate species specificity more broadly by similarly mutating the ferret and guinea pig DPP4 orthologs. Interestingly, in mDPP4, one

of the key mutations disrupts a non-conserved glycosylation site. Similar to mDPP4, sequence alignments and predictive structural studies indicate that both ferret and guinea pig DPP4 harbor non-conserved glycosylation sites within the region of DPP4 that interacts with the MERS-CoV receptor binding domain. Therefore, we explore the contribution of glycosylation sites in preventing infection in these DPP4 orthologs, particularly whether disruption of glycosylation at the key site in mDPP4 is responsible for allowing infection. Analysis of the conservation of glycosylation sites across DPP4 orthologs may help explain the evolution of host range for MERS-CoV. We reveal whether glycosylation is an important mechanism by which species resist MERS-CoV infection and the implications for development of small animal models, as well as the potential for DPP4 orthologs to support adaptation of MERS-CoV.

Spatial variation of microbial communities in the gastrointestinal tract of natural populations of house mice

Taichi Suzuki, Michael Nachman

2D_301A-Viral/Microbial Evolution
Sunday, June 22, 2014 3:45 PM-4:00 PM

Host-associated microbial communities (microbiota) play an important role in evolution. Characterizing the microbiota along different portions of the gastrointestinal (GI) tract may help us understand the mechanisms shaping the composition of microbial communities. Here we describe the microbiota across the GI tract in natural populations of house mice (Mus musculus) and discuss factors that might be structuring these microbial communities. We collected GI samples from six individuals from Tucson, Arizona. Microbes were characterized by 16S rRNA sequencing. DNA was extracted from 10 locations along the GI tract from each individual including mouth, esophagus, stomach, duodenum, ileum, proximal cecum, distal cecum, colon, rectum, and feces. We found major shifts in diversity and relative abundance of microbial taxa between the upper and lower GI tract. The lower GI tract (cecum to feces) showed greater microbial diversity and greater relative abundance of anaerobic taxa compared to the upper GI tract (mouth to ileum). Microbial communities are clustered by host genotype only in the lower GI tract but not in upper GI tract. Fecal samples were similar to the microbiota of the lower GI tract where the majority of digestion takes place in hindgut fermenters.

Cyanobacterial host response to infection by a novel cyanopodophage, and inferred co-evolutionary interactions in the environment

Siobhan Watkins, Catherine Putonti

2D_301A-Viral/Microbial Evolution
Sunday, June 22, 2014 4:00 PM-4:15 PM

Cyanophages, viruses which infect cyanobacteria, are known to critically influence population diversity and functional activity of their hosts in the oceans, however, as yet, little is known regarding interactions over time between phages and cyanobacteria in freshwaters. Cyanophages were isolated from freshwater locations known to support cyanobacterial blooms in Southern England. Of the cyanophages isolated, the majority infected a single host. Some, however, were found to have a broader host range, and one, designated ϕMHI42, was infectious to strains of both Microcystis and Planktothrix. Using transmission electron microscopy (TEM), ϕMHI42 was shown to be morphologically similar to members of the Podoviridae, with a very large capsid: the size estimation was supported by analysis under atomic force microscopy (AFM). It was not possible to generate amplicons from phage DNA using previously published primer sets. Attempts made to sequence the viral genome has also presented a unique set of problems. Characterization of host growth after infection with ϕMHI42 was assessed under a range of conditions, and the phage was found to demonstrate different lifestyle strategies across a number of strains of cyanobacteria belonging to the genera Microcystis and Planktothrix. Furthermore, infection of the host by a virus appeared to increase cell growth rate and metabolism. Preliminary data also suggested that changes in temperature can alter phage infection characteristics. These results combine to suggest that ϕMHI42 demonstrates high novelty, confirming that freshwaters are likely to represent a rich reservoir of as yet uncharacterized bacteriophages. Furthermore, a complex relationship between endemic populations of cyanobacteria and cyanophages is likely to have resulted in differing host response to infection. We hypothesize that within these samples a large community of specialist cyanophages are present that are divergent in terms of their ability to switch hosts over time. Freshwater cyanophages are often touted as a solution to the control of harmful cyanobacterial blooms in the environment. However, these results begin to demonstrate the highly dynamic co-evolutionary responses between cyanobacterial host and virus (in an aquatic environment which is likely to be considerably more diverse than the marine), as well as the considerable and immediate effect certain environmental parameters can have between the two. This information has clear implications for the use of phages to control naturally occurring populations of bacteria.

Macroevolution, phylomorphospace and directional evolution in burrowing scallops

Emma Sherratt, Dean C. Adams, Jeanne M. Serb

2D_301B-Convergent Evolution
Sunday, June 22, 2014 3:15 PM-3:30 PM

Examining patterns (modes) of change in natural systems offers the opportunity to understand how biological diversity is both created and maintained. Bivalved scallops (Pectinidae) are a particularly good system to study evolutionary patterns of morphological change: they are a speciose clade, their members display an array of shell morphologies, they are found in a wide range of habitats, and they are broadly organized into five functional groups which vary in their level of mobility (cementing, byssal attaching, recessing, free-living, and long-distance swimming). Previous work has shown that in scallops there is strong convergent evolution in shell shape among unrelated long-distance swimming species. In this study we characterized morphological patterns of shell shape in 121 species of scallops representing lineages from differing contemporary functional groups to gain a more complete picture of the degree of morphological similarity among different functional groups. For this we combined morphological data on shell shape derived from landmark-based geometric morphometric methods with a phylomorphospace approach, a phylogenetic comparative method to infer evolutionary change along branches of a phylogeny. We evaluate the predictions that the scallop morphospace is partitioned according to shell morphologies defining the five functional groups, suggesting substantial convergent evolution. Our results find species of two of the five life-habits have evolved similar morphological shape from inhabiting similar environments at different geographic locations: we confirm convergent evolution of long-distance swimming species, and find convergent evolution among species that are recessers (a burrowing behavior). Furthermore, out results find a striking trend of directional morphological evolution in one clade of recessers, along an axis that describes a progressively convex shell shape. Variation in shell shape among recessers is predicted to be due to functional differences in burrowing behavior. We discuss these results in terms of the implications for understanding scallop biology and evolutionary history, and more broadly, in terms of evolutionary processes driving invertebrate diversity.

The evolution of phenotypic convergence in fishes of the lower Congo River

Liz Alter

2D_301B-Convergent Evolution
Sunday, June 22, 2014 3:30 PM-3:45 PM

Phenotypic convergence provides powerful insight into how morphological diversity is shaped by selection. A striking instance of multi-trait convergence is found across a broad phylogenetic spectrum of fishes endemic to the lower Congo River (LCR), a complex, high-energy hydrological system characterized by some of the most extensive and powerful rapids on Earth. In this extreme selective environment, representatives of distantly related fish lineages have independently evolved complex suites of convergent traits including depigmentation, microphthalmia or eye loss, body depression with metameric increase, enhanced latero-sensory anatomy, and hypertrophied jaw and branchial musculature. To better understand the evolution of these phenotypes, we developed a Bayesian molecular phylogenetic framework for one of the groups, spiny eels of the genus Mastacembelus. Our analysis demonstrates that depigmentation and microphthalmia have independently evolved multiple times in this genus, representing distinct colonizations of the LCR by both lacustrine and riverine lineages. Analysis of divergence times indicates these phenotypes arose within a narrow window, concurrent with newly available habitat in the LCR. This study represents one piece of a novel comparative framework for this newly discovered system, as we move toward the goal of understanding the evolutionary context of phenotypic convergence across multiple levels of biological organization.

Are tenrecs an adaptive radiation?

Sive Finlay, Natalie Cooper

2D_301B-Convergent Evolution
Sunday, June 22, 2014 3:45 PM-4:00 PM

Adaptive radiations have always attracted the interests and attentions of naturalists. Some of the most famous examples include Darwin's finches, cichlid fish and Caribbean Anolis lizards. These groups appear to have evolved diverse phenotypes and fill a wide variety of ecological niches. However, to determine whether apparent diversity in a clade is a true adaptive radiation, it is important to test whether it exhibits exceptional phenotypic and ecological diversity.

Tenrecs (Afrosoricida, Tenrecidae) are often cited as an example of an adaptively radiated family yet this claim has not been tested quantitatively. Here we assess the evidence for whether the apparent morphological variety within the tenrec family should be considered to be the product of an adaptive radiation.

If tenrecs are exceptionally morphologically diverse they should follow two predictions; morphological diversity (measured as disparity) should be greater than that expected to evolve by chance and tenrec disparity should be significantly higher than their nearest relatives, the golden moles. We used a combination of geometric morphometric and phylogenetic comparative method approaches to test these assumptions. We find that tenrecs are more diverse than their closest relatives but they show significantly less diversity than expected to evolve by chance. Although these are preliminary findings which will need to be supported by further morphological and ecological studies, our results cast doubt over whether tenrecs should be considered to be an adaptive radiation under strict definitions of the term. These findings highlight the vital importance of testing our common assumptions about patterns of evolution within apparently diverse groups.

"All roads lead to Rome" in the development of a vestigial eye: Convergent evolution between Eurycea rathbuni and Astyanax mexicanus

Ruben Tovar, Dana Garcia

2D_301B-Convergent Evolution
Sunday, June 22, 2014 4:00 PM-4:15 PM

The south central Texas Eurycea clade exhibits a continuum of karst salamander phenotypes. The Texas blind salamander (E. rathbuni) is considered a stygobiont because it completes its life cycle in the aquatic subterranean habitat of the Edwards Aquifer where it lives in perpetual darkness. Consequently, E. rathbuni exhibits a broad head, gracile limbs, limited pigmentation and highly reduced eyes. In contrast, the Barton Springs salamander (E. sosorum) is epigean and is endemic to surface habitats; it exhibits small robust limbs, pigmentation, and well developed eyes. To determine the sequence of events during development that lead to widely disparate ocular outcomes and to gain insights into the molecular mechanisms responsible, embryos at various stages of development were obtained from the two species (E. sosorum and E. rathbuni) and sectioned using a Shandon cryotome. Five developmental stages of E. sosorum, and six developmental stages of E. rathbuni were identified, and sections taken from these embryos were labeled for Pax6 and Shh using immunohistochemistry. Images were obtained using an Olympus FV-1000 scanning confocal microscope. Expression of Pax6 and Shh proteins is observed in both morphotypes represented by E. rathbuni and E. sosorum. Eurycea sosorum maintained expression of pax6 and shh through embryogenesis and into a juvenile stage. Decreased labeling of Pax6 protein was observed during later stages of E. rathbuni development, while Shh protein labeling was increased in a select subset of cells surrounding the brain and eye. Interestingly, these results parallel pax6 and shh expression in two morphotypes explored in Astyanax mexicanus, suggesting some degree of convergent evolution in the developmental mechanisms that lead to the development of vestigial eyes.

Convergent evolution of the conspicuously colored tail in lizards: implications for the evolution of color signals

Charles Watson, Christopher Buttermore, Christian L Cox

2D_301B-Convergent Evolution
Sunday, June 22, 2014 4:15 PM-4:30 PM
Conspicuous coloration in animals has often evolved as a signal to deter predators or for social communication. Understanding how conspicuous color signals are gained and lost in a phylogenetic context can provide insight into the conditions that favor their evolution. One such color signal among lizards is a highly-contrasting, conspicuously colored tail that is present in at least seven lizard families on four continents. We used non-phylogenetic and phylogenetic comparative analyses of 686 lizards (skinks and their allies in the infraorder Scincomorpha) to estimate the frequency of gains and losses of the conspicuously colored tail and the number of evolutionary transitions between tail colors. We found that 8.2% of these lizards have a brightly colored tail with 68% blue-tailed, 25% red-tailed, and 7% with a bright yellow tail. The conspicuous tail is lost as adults in 30% of these lizards. We also found that there are multiple gains and losses of the brightly colored tail, and several evolutionary transitions between each tail color. Our research demonstrates the evolutionary dynamics of a color signal in lizards and may have implications for understanding selective pressures that lead to the evolutionary gain and loss of conspicuous coloration.

The dynamics of autotetraploid formation in Arabidopsis arenosa

Brian Arnold

2D_302A-Plant Evolution
Sunday, June 22, 2014 3:15 PM-3:30 PM
Whole-genome duplication (WGD), which results in polyploidy, is a significant evolutionary force throughout the tree of life, but is curiously common in plants. Understanding the evolutionary relationships between polyploids and their diploid progenitors can give us important insights into the dynamics of polyploid formation, establishment, and the generation of biological diversity. We focus on autopolyploids, which contain duplicated but equally homologous chromosomes. This chromosome duplication allows for greater intra-individual allelic diversity and potentially larger effective population sizes. Demographic analyses can help us address how polyploid formation varies across the landscape of potential diploid progenitors and how it alters the evolutionary trajectory of species. We investigate the dynamics of autotetraploid formation and evolution in Arabidopsis arenosa, a close relative of A. thaliana and a new model for molecular understanding of polyploidy. We performed demographic analyses using coalescent-based models on three genomic datasets that have different yet complementary ascertainment biases: (1) Restriction-Associated DNA sequencing (RADseq), (2) whole-genome sequencing of pooled samples, and (3) individual whole-genome sequencing. Although the separate datasets yield different interpretations for some details of population history, all analyses agree that particular diploid gene pools preferentially contribute to autotetraploid diversity, suggesting frequent polyploid formation events and/or interploidy gene flow from specific diploid genotypes. Moreover, our analyses show some autotetraploid lineages exhibit altered patterns of purifying selection and have experienced relatively recent, rapid demographic expansions and colonization of new niches.

Evolution of petal fusion in asterids core eudicots

Jinshun Zhong, Stacy Jorgensen, Sarah Powell, Beck Powers, Jill Preston

2D_302A-Plant Evolution
Sunday, June 22, 2014 3:30 PM-3:45 PM
Petal fusion (sympetaly) is hypothesized as a key innovation that enhances pollinator specialization, hence promoting speciation. Sympetaly has evolved multiple times during the diversification of angiosperms. However, the most striking plant lineage with ancestrally fused petals is the asterid clade of core eudicots that comprises one fourth of angiosperm diversity. Though the genetic basis of sympetaly remains poorly known, studies in the model species Arabidopsis thaliana (Brassicaceae, rosid) and petunia (Petunia x hybrida, Solanaceae, asterid I) have revealed candidate genes that may have evolved a function in the origin and maintenance of sympetaly. Specifically, we hypothesize that orthologs of A. thaliana floral organ boundary genes have diversified in expression and/or function to affect the transition to sympetaly in asterids. To test this hypothesis we are conducting qRT-PCR, in situ hybridization, and virus-induced gene silencing of NAC and WOX family genes in distantly related sympetalous asterids, petunia and lettuce (Lactuca sativa, Asteraceae, asterid II), and an outgroup that lacks fused petals (carnation, Dianthus caryophyllus, Caryophyllaceae). Our data thus far support a role for at least some of these genes in asterid sympetaly, suggesting their recruitment to a novel and ecologically important developmental function.

Assessing the Polyploid origin of the genus Erythrina (Fabaceae)

Ashley N Egan, Jeff J. Doyle

2D_302A-Plant Evolution
Sunday, June 22, 2014 3:45 PM-4:00 PM
Commonly known as Coral Trees, Erythrina is a pantropical genus comprising ~130 species and is of polyploid origin. Their striking inflorescences and flowers have lead to a wide use of several species in the horticultural industry where they are planted as street and park trees. The genus also boasts several chemical properties currently being investigated for anti-anxiety and anti-malarial properties. These same compounds are used ‘recreationally’ as hallucinogens, often with fatal consequences. To estimate the timing of polyploidy we sequenced the transcriptome of 2 Erythrina species spanning the evolutionary breadth of the genus using 454 pyrosequencing. We also sequenced the winged

bean, Psophocarpus tetragonolobus, as an outgroup. We used the distribution of Ks for paralogous gene pairs created by polyploidy to help bound the time of polyploidization. Our results suggested that progenitor genomes diverged around 14 mya. To further bound this, we used the same method to estimate divergence times between the two Erythrina species as well as each species to Psophocarpus. We conclude that polyploidy took place between 5 and 15 mya in an ancestoral lineage, preceeding the radiation of the genus Erythrina.

Evolution of tomato fruit ripening traits

Ian Gillis

2D_302A-Plant Evolution
Sunday, June 22, 2014 4:00 PM-4:15 PM

Through ripening, fleshy fruits like tomato go through many phenotypic changes, which are believed to increase the possibility of animal mediated seed dispersal. Fruit traits that change during the course of ripening include color, firmness, flavor and toxicity. These changes allow the fruit to have different functions based on maturity, such as protection of forming seeds when unripe, and animal attraction when the seeds are fully mature. However, even closely related species often vary widely in fruit ripening traits, and not all fleshy fruits appear obviously palatable when ripe. Little is known about the evolutionary processes acting on fruit ripening traits, and the genetic basis of such traits has not been adequately explored. The clade of species that includes the cultivated tomato, Solanum section Lycopersicon, is a good model for study of the evolution of fruit ripening traits, as the 13 species in the clade vary in several fruit-specific traits. To increase our understanding of the evolutionary processes affecting fruit evolution, we are currently characterizing all species in the tomato clade for color, firmness, sugar content and alkaloid content at two stages of fruit maturity. Color change upon ripening is relegated to the most recently diverged species, which show a range of colors from yellow to orange to red. Our results also suggest that firmness on maturity shows variation throughout the clade with no correlation to phylogeny; for instance the species with the hardest and softest fruits measured are sister species. The amount of softening also varies widely with some species ripening to 70% of their unripe firmness, while others do not show significant levels of softening. Sugar levels also show considerable variation in total content as well as amount of change in sugar content through ripening. Alkaloids are still underway for investigation into variation in alkaloid degradation during ripening, as well as identifying whether this trait is found throughout the clade.

Genetic variation for photosynthetic traits within and among populations of the C3-C4 intermediate Mollugo verticillata.

Joe Hereford

2D_302A-Plant Evolution
Sunday, June 22, 2014 4:15 PM-4:30 PM

Photosynthetic adaptations such as evolution of C4 and CAM are some of the most convergent adaptations in biology. The most widely known examples of photosynthetic adaptations are CAM and C4 photosynthesis. These adaptations have likely arisen to limit photorespiration by increasing the concentration of CO2 within the leaf. C4 photosynthesis alone has evolved more than 60 times from the ancestral C3 mode of photosynthesis. C4 species are more common in hot-dry environments suggesting that this mode of photosynthesis arose as adaptation to limit photorespiration in hot-dry climates. There have been many studies demonstrating physiological variation between C4 and C3 species. In addition, many studies have demonstrated macroevolutionary patterns among plant families or species in photosynthetic traits. However, we do not know much about variation within species or within populations of a single species for traits that underlie photosynthetic adaptations. If there is variation within and among populations, we can begin to study the microevolutionary aspects of the evolution of photosynthetic adaptations. Here I quantify genetic variation within and between populations of the C3-C4 intermediate Mollugo verticillata for CO2 compensation point. CO2 compensation point is the internal CO2 concentration where photorespiration and photosynthesis are balanced. The two study populations located in alternate climatic environments within California. One population is located in near the coast under a cool climate, and the other population is located inland under a hotter climate. I measure the CO2 compensation point of both populations under hot and cool temperatures to test the hypothesis that there are genetically based differences between populations, and I quantify genetic variation within each population. This study demonstrates how characters that are usually studied in a macroevolutionary context can vary at the microevolutionary scale. From here we can begin to examine the microevolutionary aspects of how photosynthetic adaptations evolve.

HOST BIRDS COMBAT CUCKOO MIMICRY BY EVOLVING RECOGNIZABLE EGG PATTERN SIGNATURES

Mary Stoddard, Rebecca Kilner, Christopher Town

2D_302B-Trait Evolution
Sunday, June 22, 2014 3:15 PM-3:30 PM
HOST BIRDS COMBAT CUCKOO MIMICRY BY EVOLVING RECOGNIZABLE EGG PATTERN SIGNATURES

Mary Caswell Stoddard*, Rebecca M. Kilner, Christopher Town

The Common Cuckoo (Cuculus canorus) is a brood parasite that deposits its eggs in the nests of unrelated host species. As part of this coevolutionary arms race, many host species have evolved egg rejection defenses in response to cuckoo parasitism. In turn, many host-specific races of the Common Cuckoo have evolved egg mimicry. Once egg mimicry has evolved, how can hosts improve their chances of distinguishing and rejecting foreign cuckoo eggs? In theory, hosts subjected to cuckoo egg mimicry should evolve egg patterns which are highly recognizable, yet evidence for this has been mixed, in part because we lack appropriate tools for quantifying egg pattern information. We developed a pattern recognition tool which, in a way that is analogous to vertebrate vision, extracts important features from a visual scene. We applied this algorithm to images of eggs laid by hosts of the Common Cuckoo to determine whether hosts subjected to intense cuckoo mimicry have evolved the most recognizable egg patterns. Our results support the hypothesis that many hosts have evolved recognizable egg patterns as a defense against cuckoo mimicry, lending new support to the idea that host egg patterns play a major role in the arms race interactions between cuckoos and hosts. However, our analysis revealed several surprises: for example, not all recognizable patterns share the same features. In this presentation, we provide an in-depth analysis of the key features that appear critical for the evolution of recognizable egg patterns. We also relate these findings to broad questions about the evolution of recognition among rivals, neighbors and kin in other animal taxa.

The geographical and community context of mutualism dynamics: fig-pollinator-parasite interactions in the Sonoran Desert

John Nason

2D_302B-Trait Evolution
Sunday, June 22, 2014 3:30 PM-3:45 PM

Mutualisms are ubiquitous and profoundly influential in shaping ecological and coevolutionary interactions of plants and animals. Our understanding of mutualism, however, has suffered from a lack of spatial (geographical) and ecological (community) context, a context that must be considered to fully understand the fitness costs and benefits of mutualism and its persistence over ecological and evolutionary time. This talk investigates how plant population size and reproductive traits are influenced by environmental gradients and how their variation influences local- and geographical-scale dynamics in a pollination mutualism subject to parasitism. We focus on a fig-fig wasp mutualism composed of Ficus petiolaris and its species-specific fig wasp pollinator, as well a well-defined community of parasites comprised of seed-eating fig wasps that do not function as pollinators, and a nematode parasite of the pollinator. Sonoran Desert populations of F. petiolaris, a rock strangler, are often small and spatially isolated and, according to theory, subject to high risk of local pollinator extinction and mutualism failure. We test the hypothesis that where host populations are small, mutualism may be stabilized by reproductive adjustments in the fig; namely increased intra-crown asynchrony in flower and fruit production and longer receptivity of individual flowers to pollinators. We also test the hypothesis that these reproductive adjustments may have significant costs by potentially benefiting parasites that negatively impact fig seed and pollinator production. The patchy distribution of F. petiolaris, its high within-crown flowering asynchrony (atypical of figs) and high parasite loads, as well as potential interactions among these factors, make this an interestingly complex yet well-defined system for evaluating these hypotheses and the impact of environmental and biotic stressors on the fitness and persistence of mutualism.

Genome-wide evidence of genetic associations in eclosion timing in Rhagoletis fruit fly host races

Peter Meyers, *Scott Egan, Thomas Powell, Glen Hood, Meredith Doellman, Daniel Hahn*

2D_302B-Trait Evolution
Sunday, June 22, 2014 3:45 PM-4:00 PM

Seasonal timing of reproduction is a key selective trait that drives ecological speciation in phytophagous insects. The apple maggot fly, Rhagoletis pomonella (Diptera: Tephritidae), provides a textbook example, with ancestral hawthorn-infesting host races eclosing later than a recently evolved host race that infests earlier-fruiting apples. We have identified a suite of RADseq genetic markers that strongly associate with both eclosion timing and host race differentiation. Largely overlapping sets of loci control the trait in both host races, though the data suggest that the genetic basis of early eclosion timing may not be straightforward, potentially requiring a rearrangement or modification of formerly adaptive linkage relationships.

Multicellular evolution in the volvocine algae evolved through genetic permanence of a predator evasion response in unicellular Chlamydomonas

Bradley Olson, *Chris Berger, Sarah Cossey*

2D_302B-Trait Evolution
Sunday, June 22, 2014 4:00 PM-4:15 PM

The current view of multicellular evolution is that ecological pressures such as predation and/or scarce resources drive genetic permanence of cellular cooperation. It has been assumed that the simplest mechanism to evolve multicellularity is clonal development, where incomplete cell division results in cell-cell attachment forming a multicellular organism. Since clonal development is thought to be easy to evolve the presumption is that this mechanism underlies multicellular evolution in most taxa, including plants and animals. Aggregative cooperation is another mechanism of multicellular evolution that is observed in social amoeba, slime molds, and other organisms, where cells in the environment aggregate in response to stress, which provides them safety in numbers, and motility advantages. As this behavior is thought to be genetically complex, the assumption is that aggregative cooperation has a higher barrier for its evolution and thus is a less common mechanism of multicellular evolution. However, we found that predation of unicellular Chlamydomonas cells results in cellular aggregative cooperation within minutes of predator treatment. We have found that interaction of Chlamydomonas with predators causes the algae to release a signal that when added to naive Chlamydomonas cell causes them to aggregate. Moreover, Chlamydomonas will only aggregate with genetically similar strains, not other species with in the same genus, nor other closely related algae. This suggests that the aggregation signal elicits a self-self recognition mechanism for aggregation. Subsequently, we have performed RNA-seq on a time-course of predator treatment and identified genes important for the predator response. Finally, by analyzing the orthologs to these genes in Chlamydomonas to those in its multicellular relatives such as Gonium and Volvox we have determined the evolutionary history of genes important for multicellular evolution. In summary, our data reveal an unrealized mechanism by which unicellular Chlamydomonas communicates the presence of predators and allows them to interpret this signal to determine if they should aggregate, resulting in groups that are more resistant to predation. These data suggest aggregative cooperation may be a more common mechanism of multicellular evolution than currently thought. We also have the first insight between selective pressure and the underlying genetic mechanism by which multicellularity evolved in the volvocine algae.

Dispersal transiently alters the expression of immune-related genes in male rhesus macaques (Macaca mulatta)

Noah Snyder-Mackler, James Higham, Shauna Morrow, Sean Coyne, Dario Maestripieri, Jenny Tung

2D_302B-Trait Evolution
Sunday, June 22, 2014 4:15 PM-4:30 PM

Dispersal is a challenging transition in a male rhesus macaque's life history, associated with the stress of losing past social ties, forming new ones, extended periods of solitude, and usually becoming the lowest-ranking male in a new social group. The stress associated with dispersal may therefore be reflected in lasting physiological differences between pre- and post-dispersal animals. Alternatively, if male macaques have evolved to be resilient to dispersal-related stress—a normal component of rhesus macaque life history—dispersal may produce only transiently experienced physiological costs. Here, we investigated changes in genome-wide gene expression levels in peripheral blood mononuclear cells between pre- and post-natal dispersal male rhesus macaques, members of a well-studied free-ranging population on the island of Cayo Santiago. We identified no significant differences between pre- and post-dispersal males, suggesting no long-term gene regulatory signature of dispersal. Instead, we found a strong signature of a short-term effect of dispersal on the expression of 3.6% (317/8,909) of the genes that we measured. Specifically, males sampled close to (within 300 days of) natal dispersal exhibited changes in expression of genes involved in the immune response, consistent with immunomodulatory effects of elevated glucocorticoids and testosterone. Our findings suggest that dispersal bears immunological costs detectable on the level of gene regulation, but that male macaques can recover from these costs during more stable periods of their life history.

Genomic evidence for reduced sexual selection in plumage-dichromatic birds

Huateng Huang, Dan Rabosky

2D_302C-Sexual Selection
Sunday, June 22, 2014 3:15 PM-3:30 PM

Sexual dichromatism - the tendency for sexes to differ in colour pattern - represents a striking form of within-species morphological variation. Conspicuous intersexual differences in colour pattern are generally thought to result from Darwinian sexual selection, to the extent that dichromatism is often treated as a surrogate for the intensity of sexual selection in phylogenetic comparative studies. Some evidence suggests that sexual dichromatism is correlated with social mating system in birds, but little direct evidence links the intensity of sexual selection to the magnitude of sexual dichromatism. Here, we show that the genomic signature of sexual selection is greater in avian species that lack pronounced intersexual plumage differences. We compared levels of genetic variation on sex chromosomes and autosomes in matched pairs of dimorphic and monomorphic bird species. Analyses of ~900,000 restriction-site associated loci from each of 24 individual birds demonstrates that monomorphic species show a consistent reduction in sex-linked genomic variation relative to closely-related dimorphic species. This implies greater variance in male reproductive success - and more intense sexual selection - within those species lacking conspicuous intersexual plumage differences. These results challenge assumptions about the primacy of sexual selection in driving intraspecific color differences in birds.

Modality interactions alter call trait preferences in gray tree frogs

Gerlinde Höbel, Michael Reichert

2D_302C-Sexual Selection
Sunday, June 22, 2014 3:30 PM-3:45 PM

Animal displays often comprise various modalities, and the presence of one display component can alter receiver responses to other components. Sometimes additional components merely increase the probability of response, but receivers may also prefer different trait values or show different selectivity depending on whether a component is presented in isolation or as part of a multimodal display. I conducted playback trials with female frogs to test the hypothesis that receiver responses are affected by modality interactions. I obtained preference functions for several call traits under two experimental conditions, (i) unimodal = auditory stimulation only, and (ii) multimodal = auditory + visual stimulation, and describe variation in preference function shape and preference traits (i.e., preferred value, selectivity, responsiveness). I show that receiver preferences differ as a function of available signal modalities, and that the effect of adding a visual cue to an auditory signal varies depending on the call trait in question. I also compare the unimodal and multimodal preferences with the trait distribution of males, to test which preference function best predicts display trait distribution. Finally, I discuss the consequences of modality interactions for sexual selection and signal evolution.

Reassessing natural selection patterns and shapes in the wild: the case of an honest insect signal

Roberto Munguia-Steyer, Alex Córdoba-Aguilar, Alejandra Barceló-Atilano, Isaac González-Santoyo, Daniel González-Tokman

2D_302C-Sexual Selection
Sunday, June 22, 2014 3:45 PM-4:00 PM

A key assumption in sexual selection theory is that further elaboration of a sexually selected trait (SST) will be constrained by survival. However, assessing such cost in the wild has been problematic as: a) longevity has been frequently computed as the last day the individual was recorded in the field; b) if imperfect detection is not included explicitly in survival analyses, longevity estimates are going to be biased, being the bias more extreme in less detected individuals (i.e females, alternative male morphs). c) previous studies have not included other traits than the SST in question, that may also contribute to fitness. We have solved these drawbacks using modern mark-recapture techniques entering imperfect detection and other traits that correlate with the expression of a SST. For this, we studied survival effects of an exaggerated SST (wing spot) and a related non-SST (wing length) in calopterygid adults in the wild. Size of wing spots in calopterygids is sexually selected and is an honest indicator of condition in terms of physiology and survival. These findings, however, have been somehow confounded by a correlation between wing spot and wing length. Here we show that control and experimental individuals with an increased wing spot area in both sexes present a lower survival probability which illustrates a natural selection constrain for exaggerated SST expression. Furthermore, we also found a significant effect of dismissing imperfect detection and individual heterogeneity in survival and recapture rates via simulation, being the bias higher in females. Finally, we demonstrate a linear selection acting on wing spot area but not on wing size or correlational selection between both variables. Our work not only clarifies that a survival cost exists for an exaggerated SST, but that such cost and imperfect detection should be properly analyzed in evolutionary studies.

Love "bugs"? Exposure to parasites increases promiscuity in a freshwater snail

Deanna Soper, Curt Lively, Kayla King, Daniela Vergara

2D_302C-Sexual Selection
Sunday, June 22, 2014 4:00 PM-4:15 PM

Under the Red Queen hypothesis, outcrossing can produce genetically variable progeny, which may be more resistant, on average, to locally adapted parasites. Mating with multiple partners may enhance this resistance by further increasing the genetic variation among offspring. We exposed Potamopyrgus antipodarum to the eggs of a sterilizing, trematode parasite and tested whether this altered mating behavior. We found that exposure to parasites increased the number of snail mating pairs and the total number of different mating partners for both males and females. Thus, our results suggest that, in host populations under parasite-mediated selection, exposure to infective propagules increases the rate of mating and the number of mates.

Sexual selection and the evolution of the Major Histocompatibility Complex

Tony Wilson, Angela Bahr, Maciej Ejsmond, Jacek Radwan

2D_302C-Sexual Selection
Sunday, June 22, 2014 4:15 PM-4:30 PM

The Major Histocompatibility Complex (MHC) is an essential component of the vertebrate adaptive immune system, responsible for the recognition and presentation of foreign antigens. The genes of the MHC are exceptionally polymorphic, a condition thought to be mediated by a combination of pathogen-mediated selection and disassortative mating preferences. Recent simulation results indicate that natural and sexual selection may interact in a non-additive fashion, generating levels of MHC variation in excess of those expected under either process in isolation, and highlighting the potential importance of sexual selection in the maintenance of ecologically-relevant genetic variation. Sex-role reversed species, in which the conventional patterns of male competition and female choice are inverted, offer a potential opportunity to experimentally partition the forces of natural and sexual selection and to better understand their involvement in the generation and maintenance of genetic diversity. I will describe the recent characterization of the genes of the Major Histocompatibility II loci in the sex-role reversed seahorse, Hippocampus abdominalis, with the aid of next-generation sequencing technologies, and detail a series of behavioral experiments aimed at clarifying the role of sexual selection in generating MHC diversity in this species. The results of these experiments are counterintuitive, and may help to shed light on how genetic variation for ecologically-relevant traits can be maintained in the face of strong directional selection.

Identifying Drivers of Island Speciation on an Ancient Tropical Island Using Next Generation Sequencing Data

Kyle O'Connell, Matthew Fujita, Eric Smith, Awl Riyanto, Nia Kurniawan

2D_303-Speciation and Divergence
Sunday, June 22, 2014 3:15 PM-3:30 PM

Tropical ecosystems often harbor diverse and ancient lineages that have accumulated over the course of their long history. This allows them to serve as excellent models to test hypotheses regarding biotic diversification. The Sunda Shelf region of Indonesia is exceptional for the study of tropical systems because of its dynamic geological history paired with a climatological stability that presents a unique opportunity to study island diversification in an ancient tropical setting. We have chosen Sumatra as a site to test island diversification models, specifically comparing in situ diversification against vicariance and dispersal. Using data collected entirely from next-generation sequencing technologies, including full mitochondrial genomes, we examine these models using dense sampling of two species complexes: frogs from the genus Rhacophorus and geckos from the genus Cyrtodactylus. Likelihood and Bayesian analyses reveal evidence for in situ diversification within Sumatran Rhacophorus, but the traditional vicariance and dispersal model within the Cyrtodactylus. This work will help to identify the types of speciation processes most important to tropical diversification.

Locating a selection signature inside chromosomal rearrangements for tests of adaptive divergence in Anopheles gambiae

Qixin He, L. Lacey Knowles

2D_303-Speciation and Divergence
Sunday, June 22, 2014 3:30 PM-3:45 PM

As the primary malaria vector that is widely distributed in sub-Sahara, Anopheles gambiae s. str. utilizes many different microhabitats where human reside. Its fast adaptation is partly attributed to polymorphic inversions within or between populations in the species. Theory predicts that large paracentric inversions, which do not directly affect individual fitness, can facilitate local adaptation by suppressing recombination among co-adapted genes captured by inversions. While stable clines and associations between inversions and specific environmental factors are suggestive of causal relationships, finding specific gene or regions which confer the fitness advantage of the inversions is difficult because of high levels of linkage disequilibrium and/or low nuclear diversity within young inversions.

In this study, wild mosquito samples were collected from five populations in transitional ecozones between forest and savanna in Cameroon and genome-wide SNPs identified from barcoded Rad sequencing. Departure from Hardy-Weinberg equilibrium of two common polymorphic inversions, 2La and 2Rb, suggests the existence of divergent selection in different habitats, with the inverted chromosomes predominating in dry habitats and the standard chromosomes in wet habitats. Fst comparisons showed that within inverted regions (i) Fst (average 0.4-0.5) is significantly higher than collinear regions (

Wallace under scrutiny: role of the fluvial barriers in the diversification of Amazonian Amphibians

Santiago Ron, Marcel Caminer, Daniela Pareja, Daniel Rivadeneira

2D_303-Speciation and Divergence
Sunday, June 22, 2014 3:45 PM-4:00 PM

The Amazon region harbors the most speciose communities on Earth and yet the processes that originated that diversity are poorly understood. One of the oldest hypotheses to explain Amazon diversity is the Riverine Barrier Hypothesis, which postulates that the large rivers of the Amazon basin have acted as barriers to gene flow, promoting genetic differentiation and, as a result, speciation. We tested the Riverine Barrier Hypothesis in amphibians by analyzing genetic differentiation in nine amphibian species sampled along 200 km of the Napo River in Amazonian Ecuador. Samples were collected on both banks of the river at 20 km intervals. We also included samples collected up to 100 km away from the banks. Between one and four mitochondrial genes were sequenced per species. Phylogenetic trees were obtained under the maximum likelihood optimality criterion and a parametric bootstrap test was applied on each species to test the hypothesis of reciprocal monophyly between banks of the river. In eight out of nine species, our results show lack of support for the Riverine Barrier Hypothesis (i.e., opposite banks of the river are genetically similar and are not monophyletic). However, we found strong and statistically significant differentiation between banks in the treefrog Hypsiboas cinerascens. In conclusion, our results indicate that large rivers have played a minor role in the diversification of Amazonian amphibians. However, a small proportion of species may have formed by the vicariant effect of Riverine Barriers.

Investigating modes of speciation in trans-Isthmian fishes

Hannah Owens

2D_303-Speciation and Divergence
Sunday, June 22, 2014 4:00 PM-4:15 PM

Traditionally, geminate taxon pairs are thought to arise through allopatry when a geographic barrier emerges, bisecting a taxon’s geographic range and preventing gene flow between the now-separated populations. However, incipient parapatric speciation prior to final barrier emergence is also possible. In the case of the former scenario, one may expect the ecological niche tolerances of geminate species to be conserved, whereas in the latter, niche tolerance divergence is expected to be correlated with genetic divergence. Grunts in the family Haemulidae present a possible example of pre-isolation speciation; evidence from previous studies have suggested possible non-simultaneous divergence in four marine geminate pairs separated by the formation of the Isthmus of Panama. To investigate this idea, I pursued two lines of inquiry. First, I developed ecological niche models for each of the eight taxa by integrating locality data from several observational and specimen databases with ecological data from the World Ocean Atlas. The resulting models were then projected into their sister taxon’s geographic range, and the power to accurately predict observations of the sister taxon was assessed. Second, I measured similarity between modeled ecological niche tolerances of geminate taxa and calculated the degree to which niche divergence and genetic divergence were correlated. Generally, niche models of one taxon did not accurately predict its geminate, and niche and genetic divergence were correlated. While equivocal, my results suggest that speciation in haemulid geminate pairs may have begun parapatrically prior to final isolation by the completion of the Isthmus of Panama.

Divergent and geographically distinct mitochondrial lineages occur despite apparent nuclear gene flow in the Texas Coralsnake, Micrurus tener

Jeffrey Streicher, Eric Smith, Todd Castoe

2D_303-Speciation and Divergence
Sunday, June 22, 2014 4:15 PM-4:30 PM

Incongruent geographic patterns of mitochondrial (mtDNA) and nuclear (nDNA) variation have been previously demonstrated in diverse groups of vertebrates, including squamate reptiles. The causes of this phenomenon are often thought to be sex-biased gene flow, adaptation, introgression, or demographic shifts, although these explanations have only rarely been tested. Here we describe an exceptional case of mito-nuclear discordance in the venomous Texas Coralsnake, Micrurus tener. This species occurs from Louisiana and Texas in the United States southward to northern Mexico. To characterize geographic patterns of DNA variation in M. tener, we generated a multilocus mtDNA dataset and a large nDNA genome-wide Single Nucleotide Polymorphism (SNP) dataset. Specifically, we sequenced two mtDNA gene fragments for 80 snakes (ca. 1,500 bp) and used double-digest RADseq to collect a nDNA SNP set for 43 snakes. The mtDNA data identified two divergent lineages within M. tener that are essentially geographically distinct, and that were rendered paraphyletic by its sister species, M. fulvius. In stark contrast, the nDNA SNPs suggest panmixia among individuals belonging to these two divergent M. tener mtDNA lineages. To identify historical and/or demographic scenarios most likely to have produced mito-nuclear discordance in M. tener, we used a partial Micrurus genome assembly, morphological measurements, and climate data, to test for patterns associated with competing explanations. Our results highlight the utility of reduced representation genome sampling to evaluate population genetic and phylogeographic questions, and to test hypotheses based on mtDNA data.

Utilizing genotyping-by-sequencing to elucidate Neotropical army ant evolution

Max Winston, Daniel Kronauer, Corrie Moreau

2D_304-Insect Evolution
Sunday, June 22, 2014 3:15 PM-3:30 PM

As keystone predators in Neotropical forests, hundreds of vertebrate and invertebrate organisms associate with the 12 known species of Eciton, which exert strong top-down effects on community structure in the leaf litter. Despite their clear ecological importance and strong history of research, a comprehensive phylogenetic and biogeographic study is lacking for the important clade. This absence of phylogenetic resolution has been a substantial impediment to determining ecological and evolutionary dynamics, and presents an opportunity to investigate broader mechanisms of diversification in the Neotropics. Using the high-throughput method genotyping-by-sequencing (GBS), we harvested SNPs from across the Eciton genome to infer the clade's phylogenetic history and their colonization of Neotropical habitats. This work contributes both to a better understanding of the ecological impact of Neotropical army ants as well as the significance of biogeographic processes in macroevolutionary dynamics.

A new method of colour pattern analysis helps explain the existence of inaccurate mimics in an insect community

Christopher Taylor, Tom Reader, Francis Gilbert

2D_304-Insect Evolution
Sunday, June 22, 2014 3:30 PM-3:45 PM

A "Batesian mimic" is a harmless organism that resembles a more dangerous "model", thus deceiving potential predators into leaving it alone. Scientists have long been fascinated by the astonishing level of similarity that some mimics have evolved. Lately, however, attention has turned to those at the other end of the scale: why do some mimics have only a passing resemblance to their models, when we expect natural selection to drive them to increasing accuracy? Plenty of theories have been put forward, but testing them has been hampered by the difficulty of quantifying similarity between a mimic and its model.

Since models are almost always aposematic, their colour pattern is a highly salient feature of their appearance. However this is often ignored when assessing mimetic accuracy because it is difficult to analyse, with the focus instead on morphometric features. We recently developed a method to calculate similarity among colour patterns, and showed that this captures a high proportion of the variation that observers use to distinguish harmful from harmless prey. We applied our method to data from a community of wasps and bees (models) and hoverflies (mimics) in order to calculate mimetic accuracy for nearly 500 individuals of more than 40 mimic species.

The mimic species in our study all have similar levels of phenotypic variation, which suggests that inaccurate mimics are not in a transitional evolutionary state, nor are they constrained by a lack of genetic variation. It is likely, therefore, that a trade-off limits the evolution of mimetic accuracy. Our data suggest two possibilities. Firstly, in contrast to morphometric studies, we find that some mimics do occupy an intermediate position between two or more model species. They may benefit from increased protection as a result, and increased similarity to one model would mean lower accuracy to another.

Secondly, we find an association between patterns with a higher proportion of black and low mimetic accuracy. Dark abdominal colours may be important to hoverflies for thermoregulation, and therefore species that evolve highly wasp-like patterns may be limiting their ability to regulate temperature. This tallies with the observation that more accurate mimicry tends to evolve in larger species, which may be better able to retain heat.

As we demonstrate, the ability to compare colour patterns effectively has opened up a new set of possibilities in the study of mimetic communities, which creates novel insights into well-studied systems.

Timing the diversification of the Amazonian biota: butterfly divergences are consistent with Pleistocene refugia

Ivonne Garzon, Jennifer Benetti-Longhini, Andrew V.Z. Brower

2D_304-Insect Evolution
Sunday, June 22, 2014 3:45 PM-4:00 PM

Rejection of the Pleistocene refugium hypothesis (PRH) as an explanation for the high biodiversity of Neotropical forest is based in part on the assertion that biotic elements of these forests evolved during the Neogene. That argument is justified, in turn, by the ages of crown groups (the age of the most recent common ancestor of extant species of a clade). We consider the use of crown ages as a metric to reject the PRH to be an unfair test, because the circumscription of crown groups of interest is arbitrary, and their ages represent overestimates of the time of species formation. I will present divergence times between pairs of sister species (131 pairs), and among pairs of sister species and their closest relative (56 triplets), from 35 genera of Neotropical butterflies, aiming to refocus the discussion about the timing of diversification of the Neotropical biota on the time of the formation of extant species, a metric that is consistent and comparable across taxa. Results from our study show that 72% of speciation events leading to the formation of butterfly sister species occurred within the last 2.6 Myr, a result consistent with the temporal predictions of the PRH, suggesting that the PRH cannot be completely discarded as a driver of Neotropical diversification.

The Co-evolution Between Mitochondrial and Nuclear Genes in Insects

Yiyuan Li

2D_304-Insect Evolution
Sunday, June 22, 2014 4:00 PM-4:15 PM

Co-evolutionary interactions between the mitochondrial (mt) and nuclear (nuc) genomes can play a significant role in the evolutionary dynamics of both genomes. However, the co-evolutionary process in a broad range of insects is largely unknown. One of the most tightly interacting pathways is the oxidative phosphorylation (OXPHOS) system, which involves both mt and nuc genes. As mt genes exhibit a high mutation rate, related nuc genes might have compensatory adaptation to maintain OXPHOS function. As a result, nuc-OXPHOS genes may be under strong selection pressure and evolve more rapidly than nuclear genes that are not involved in mitochondrial-nuclear interactions.

Hymenopterans show exceptionally high rates of mitochondrial molecular evolution compared to other insects, making this taxon an excellent model to test for evidence of compensatory evolution driven by genome-genome interactions. This co-evolutionary interaction consequently elevates the evolutionary rate of both nuclear and mitochondrial genes in hymenopterans compared to other insects. We tested this hypothesis by comparing the evolutionary rates (synonymous substitution rate and nonsynonymous substitution rate) among three gene groups (mt-OXPHOS, nuc-OXPHOS, and nuc) in holometabolous insects, including Hymenoptera, Coleoptera, Lepidoptera, and Diptera. Relevant gene orthologs were annotated from transcriptomes generated by the 1,000 Insect Transcriptome Evolution (1KITE, www.1kite.org) project.

Based on the combined analysis of 28 OXPHOS subunits across 33 species, we want to address the following two questions: 1) Is there compensatory evolution on nuc genes driven by mt genes? 2) Does a haplodiploid sex determination system lead to higher evolutionary rates on OXPHOS genes compared to other sexual determination system.

Social context of disease resistance: Interactions among social and individual immune defense mechanisms in honey bees

Michael Simone-Finstrom, David Tarpy

2D_304-Insect Evolution
Sunday, June 22, 2014 4:15 PM-4:30 PM

Organisms have evolved numerous defenses to resist or tolerate parasitic infection, including both individual physiology and structural based defenses and behavioral, group-level defenses. The over-arching goal of this research is to examine the social context of parasite-resistance mechanisms and better understand the evolution of physiological and behavioral immunity in social systems. There is a paucity of information concerning how the suite of individual and social defenses interact to affect parasite transmission and colony fitness in honey bees. Since multiple defenses can act against the same parasite, how do colonies invest in these differing defenses? Determining the potential costs and benefits of maintaining both individual and social immune defenses—and any trade-offs that exist among them—is key to understanding disease resistance in a social context. Colonies were established with varying levels of genetic diversity (each headed by a queen that mated with 4-30 males). Analyses were conducted to determine a colony's ability to resist disease (the fungal pathogen Chalkbrood), level of hygienic behavior (diseased brood removal), grooming rates, level of antimicrobial resin collection both prophylactically and in response to a pathogen challenge, and larval immune response to a bacterial pathogen. Results suggest that there are no clear trade-offs among the social immune traits measured and specifically that hygienic behavior and resin use is decoupled in honey bees. However hygienic behavior and larval immune response to a bacterial challege was positively correlated suggesting that these traits may be linked. The role of genetic diversity influencing these traits was modest at the levels examined in this study. The results indicate that the mechanism by which genetically diverse colonies are better able to resist disease as compared to likely stems from a combination of both individual and social immunity, and we found no clear trade-offs among the different traits that can contribute to colony health.

Transfer of Non-coding DNA Drives Regulatory Rewiring in Bacteria

Yaara Oren

2D_305A-Evolution of Regulatory Systems
Sunday, June 22, 2014 3:15 PM-3:30 PM

The rapid pace of evolution in bacteria is widely attributed to the promiscuous transfer and recombination of protein-coding genes. However, it is not known whether the same forces also drive the evolution of non-coding regulatory regions. Through the analysis of 270,000 regulatory regions across 247 bacterial genomes, we demonstrate that regulatory 'switching' to non-homologous alternatives is ubiquitous, occurring across the bacterial domain. Using comparative transcriptomics, we show that at least 16% of the expression divergence between E. coli strains can be explained by this regulatory switching. Among other mechanisms, we found that switching can occur through horizontal transfer of regulatory regions. We experimentally show that regulatory transfer facilitates rapid phenotypic diversification of a human pathogen. This regulatory mobility enables bacterial genes to access a vast pool of potential regulatory elements, facilitating efficient exploration of the regulatory landscape.

Modeling tumorigenesis in the intestinal crypt: The distribution of fitness effects in somatic tissue fundamentally alters tumor incidence curves.

Vincent Cannataro, Scott McKinley, Colette St. Mary

2D_305A-Evolution of Regulatory Systems
Sunday, June 22, 2014 3:30 PM-3:45 PM

Tumors are the product of increased proliferative capacity in somatic cell lineages. This increase in cellular fitness is the result of the accumulation of mutations and genomic alterations in a selective context. The distribution of fitness effects (DFE) of new mutations has been characterized in several whole organisms (single celled and multicellular), although comparably little work has characterized the DFE in somatic tissue within multicellular organisms. The presence of tumor suppressor genes and oncogenes, as well as other genes involved in regulating the cell division cycle, suggests that the DFE in somatic tissues may be fundamentally different from the DFE of whole organisms, which are selected to maximize reproductive rate. The goal of this work is to estimate the DFE in evolving pools of somatic stem cells and investigate the implications of alternative somatic DFE in tumorigenesis. We propose a novel model of stem cell regulated intestinal crypt dynamics using recent empirical findings of stem cell homeostasis and explore the evolution of fitness in the small pools of cells that continually divide and reconstitute the intestinal epithelium. As cells divide they have a chance to mutate and those mutations may affect the division and/or differentiation rate of a stem cell lineage. Further, mutations become fixed via the action of drift and selection. Preliminary analysis suggests that characteristics of the DFE, as well as the specific cellular processes that the DFE influences, fundamentally affect the shape and magnitude of predicted tumor incidence curves. Understanding how new mutations govern cellular proliferation over time will shed light on the evolution that occurs in cell populations within organisms and how this evolution can lead to cancer and aging.

Epistatic interactions are prevalent in Drosophila 3’UTR evolution

Ying Zhen, Peter Andolfatto

2D_305A-Evolution of Regulatory Systems
Sunday, June 22, 2014 3:45 PM-4:00 PM

Untranslated-transcribed regions (UTRs) contain cis-regulatory information allowing post-transcriptional control of mRNA and protein levels. Evolutionary analyses in Drosophila have revealed that UTRs are highly constrained sequences and have been inferred to be the targets of frequent adaptive substitution. We develop a powerful transgenic assay to quantify the effects of 3’UTR sequence divergence between two closely-related Drosophila species on transcript and protein abundance. We find that the expression divergence encoded by 3’UTR sequence divergence is frequently associated with non-additive interactions among substitutions that distinguish the two species. We further show that the extent and direction of non-additivity can vary depending on the level of regulation and in a tissue-specific manner. Our results have important implications for the rate and trajectories of adaptive regulatory evolution as well our ability to reliably predict phenotype from genotype.

Bioenergetics of transcription-factor evolution: pleiotropic constraint, compensation and a sweet spot for hybrid incompatibility

Sasha Tulchinsky, Norman Johnson, Adam Porter

2D_305A-Evolution of Regulatory Systems
Sunday, June 22, 2014 4:00 PM-4:15 PM

Hybrid incompatibility can result from gene misregulation when interacting pairs of transcription factors and their cis-regulatory targets differentially coevolve in separate populations. Pleiotropy ought to constrain the evolution of incompatibility because transcription factors (TF's) that serve multiple functions should be less likely to diverge. How profound is this constraint?

We applied a bioenergetic model of molecular interaction wherein gene expression is determined by fractional occupancy of a TF bound to its cis-regulatory target. Occupancy is in turn determined by bioenergetic parameters: free energy of binding between interacting allelic variants, the number of TF molecules available, and competition for the TF from sequence-similar sites in the genomic background. We represented alleles by bit strings, and binding energy depended on their match. Combinations of parameter values determined the genotype-phenotype (G-P) map – a sigmoidal relationship between allelic mismatches and phenotypic expression. Misregulation occurs when a phenotype differs from its optimal value.

We simulated a pleiotropic regulatory pathway involving a conserved and a directionally selected trait, regulated by a shared TF, with two populations evolving in parallel. Pleiotropy indeed slowed the evolution of the TF, shifting more of the response to the cis-regulatory locus of the directionally selected trait, but compensatory evolution still occurred at the cis-regulatory locus of the conserved trait. Both traits contributed to hybrid misregulation.

The shape of the G-P map, and therefore its underlying bioenergetic parameters, determined much of the evolutionary dynamics of hybrid misregulation. Pleiotropic constraints on hybrid misregulation became prohibitive when the G-P map became too steep. Likewise, phenotypic change was insensitive to mismatches when the G-P map became too plateaued, with hybrids showing little misregulation despite the lack of constraint. Between these extremes, a broad 'sweet spot' existed, permitting the evolution of substantial hybrid incompatibility in both traits in the presence of pleiotropy.

Tempo and mode of regulatory evolution in Drosophila

Joseph Coolon, C. Joel McManus, Kraig Stevenson, Brenton Graveley, Patricia Wittkopp

2D_305A-Evolution of Regulatory Systems
Sunday, June 22, 2014 4:15 PM-4:30 PM

Genetic changes affecting gene expression contribute to phenotypic divergence, thus understanding how regulatory networks controlling gene expression change over time is critical for understanding evolution. Prior studies of expression differences within and between species have identified properties of regulatory divergence, but technical and biological differences among these studies make it difficult to assess the generality of these properties or to understand how regulatory changes accumulate with divergence time. Here, we address these issues by comparing gene expression among strains and species of Drosophila with a range of divergence times and use F1 hybrids to examine inheritance patterns and disentangle cis- and trans-regulatory changes. We find that the fixation of compensatory changes has caused the regulation of gene expression to diverge more rapidly than gene expression itself. Specifically, we observed that the proportion of genes with evidence of cis-regulatory divergence has increased more rapidly with divergence time than the proportion of genes with evidence of expression differences. Surprisingly, the amount of expression divergence explained by cis-regulatory changes did not increase steadily with divergence time, as was previously proposed. Rather, one species (D. sechellia) showed an excess of cis-regulatory divergence that we argue most likely resulted from positive selection in this lineage. Taken together, this work reveals not only the rate at which gene expression evolves, but also the molecular and evolutionary mechanisms responsible for this evolution.

Population genetic and genomic identification of locally adapted loci

Jeremy Yoder, Peter Tiffin

2D_305B-Genomics

Sunday, June 22, 2014 3:15 PM-3:30 PM
Increasing availability of genomic data for non-model organisms has led to a proliferation of landscape genomic methods, which seek to identify locally adapted gene regions using high-density marker data sampled across a species's range. Using simulated data, I compare the power of several proposed methods to distinguish selected loci from the rest of the genome. I contrast different models of the relationship between genetic variants and environmental conditions, examine the effects of collecting data from populations in non-equilibrium conditions, and determine how consideration of genomic context improves the detection of locally adapted loci.

One-generation viability experiments have little power to detect selection in genome scans

David Hall

2D_305B-Genomics
Sunday, June 22, 2014 3:30 PM-3:45 PM
Utilizing a single bout of within-generation viability selection to identify selected loci across the genome is quick, conceptually straightforward and relatively inexpensive. Unfortunately, it is also extremely limited in its ability to detect selected loci, even when sample sizes are extremely large. The primary problem is the trade-off between detecting selection at a locus and the cost of viability selection in terms of numbers of surviving individuals. Given this trade-off, within-generation viability experiments to detect selected loci in genome-wide scans should be carefully reconsidered and perhaps abandoned.

Snake genomes provide insight into the molecular evolutionary origins of a phenotypically distinct vertebrate clade

Todd Castoe, Jason de Koning, Daren Card, Drew Schield, Jacobo Reyes Velasco, Audra Andrew

2D_305B-Genomics
Sunday, June 22, 2014 3:45 PM-4:00 PM
Snakes possess many extreme and unique morphological and physiological adaptations that make them among the fundamentally different among amniote vertebrates. The uniqueness of the form and function of snakes motivates the analysis of how evolution has uniquely shaped snake genomes, and how these genomic changes have led to the unique physical characteristics and adaptations of snakes. Here we link major evolutionary shifts in metabolic protein function to extreme feats of metabolism and physiology observed in snakes. We describe evidence that snake genomes have undergone unprecedented levels of positive selection to change protein function, and the genes identified as targets of selection seem clearly related to the evolution of snake-specific characteristics. The structure and evolution of snake genomes, on the whole, are shown to be unique among vertebrates, which indicates snakes are an exciting and valuable model system studying the detailed interactions of multiple inter-related genomic attributes and features (e.g., epigenetics, transposable elements, mutation rates, recombination, etc.). These findings collectively provide new evidence for the diversity of evolutionary genomic changes that may underlie major phenotypic evolutionary shifts in vertebrates.

Genetic mapping of horizontal stripes in Lake Victoria cichlid fishes: benefits and pitfalls of using of dense linkage mapping using RAD markers

Frederico Henning, Hyuk Je Lee, Paolo Franchini, Axel Meyer

2D_305B-Genomics
Sunday, June 22, 2014 4:00 PM-4:15 PM
The genetic dissection of naturally occurring phenotypes sheds light on many fundamental and longstanding questions in speciation and adaptation and is a central research topic in evolutionary biology. Until recently, forward-genetic approaches were virtually impossible to apply to non-model organisms, but the development of next-generation sequencing techniques made this now possible. Here, we apply the ddRAD-seq method to map a color trait with a known adaptive function in cichlid fish, well-known examples of rapid rates of speciation and phenotypic diversification. A suite of morphological traits are related to speciation and adaptation in cichlids, among which body coloration features prominently. The focal trait of the present study, horizontal stripes are rare in cichlids, but evolved in several cichlid radiations repeatedly and are associated with an elongated body shape and piscivorous foraging behavior. Additionally, we directly quantify the genotyping error rates in RAD markers and offer guidelines for identifying and dealing with errors in NGS-based datasets. We conducted interspecific crosses between two endemic cichlid fish from Lake Victoria in East Africa, Haplochromis sauvagei and H. nyererei, and constructed a saturated linkage map with 867 SNP markers distributed on 22 linkage groups and total size of 1130.63cM. Lateral stripes are inherited as a Mendelian trait and map to a single genomic interval of 300Kb that harbors 15 genes, among them a paralog of a gene with known function in stripe patterning. Dorsolateral and midlateral stripes were always inherited together and are thus probably under the same genetic control. Uncritical marker selection was found to severely impact accurate linkage map construction. Fortunately, by applying appropriate quality control steps, a genotyping accuracy of >99.9% can be reached. Thus, allowing for efficient linkage-mapping of evolutionarily relevant traits.

Genomic insights into a specialized pathogen of the fungus-growing ant symbiosis

Nicole Gerardo

2D_305B-Genomics
Sunday, June 22, 2014 4:15 PM-4:30 PM
The highly evolved agricultural lifestyle of leaf-cutting ants has attracted particular attention because these ants cultivate a symbiotic fungus in specialized chambers of their nests. The ants cut leaves, preprocess them into small pieces, and feed them to the symbiotic fungus, which, in turn, serves as their major food source. These ant farmers have been cultivating fungi for at least 50 million years. Like human agriculture, ant agriculture is hampered by disease. The ants' fungal crops are attacked by fungal pathogens in the genus Escovopsis, which are believed to have evolved in association with the ants and their fungi for millions of

years. Escovopsis infection can have detrimental impacts on garden health and, consequently, on the survival of ant colonies. Escovopsis spp. have never been isolated outside of fungus-growing ant colonies, and different strains of Escovopsis are capable of attacking the fungi grown by different fungus growing ant species. The long term, specialized evolutionary history of the association between Escovopsis spp. and their hosts provides a unique venue for exploring the consequences of host specialization on pathogen genome evolution. Analysis of the first available genome sequence of an Escovopsis strain isolated from a fungus-growing ant colony indicates that the pathogen has a small genome compared to those of previously sequenced ascomycete fungi. Escovopsis is also predicted to have fewer genes than close relatives and is missing genes thought to be important in breaking down plant material. In contrast, Escovopsis has maintained several genes coding for terpene synthases, which could facilitate breakdown of its host fungus. These insights provide a starting point for investigating the genomic changes that underlie pathogen specialization across this ancient symbiotic association.

Small Genome Attraction Obfuscates Phylogenetic Signal

Jonathan Foox, Rob DeSalle, Mark Siddall

2D_306A-Phylogenies and Phylogenetics
Sunday, June 22, 2014 3:15 PM-3:30 PM
The increased availability of whole genomic data has spurred phylogenetic reconstruction through gene family presence/absence matrices. This method is attractive for its reductive power of enormous datasets that make analyses more tenable, as well as its robustness against homoplasy, given that gene loss and regain is unlikely. However, it has been observed that highly reduced genomes will have an overrepresentation of absences in such matrices, and that species in a given matrix will "attract" each other, leading to spurious phylogenetic inferences. The overdetermination of absences is explored, both through simulation and with respect to empirical datasets in recent publications. A new metric is proposed to test for significance value of small genome attraction and hidden signal in the dataset.

Assessing the utility of whole genome amplified DNA for next-generation phylogeography and population genomics

Christopher Blair, Christopher Campbell, Anne Yoder

2D_306A-Phylogenies and Phylogenetics
Sunday, June 22, 2014 3:30 PM-3:45 PM
Low quantity DNA is often a limitation when working in the fields of clinical research and forensic science. However, DNA limitation can also be a hindrance in ecological and evolutionary research programs due to a range of factors including tissue type and preservation method. A potential solution to low quantity DNA lies in whole genome amplification (WGA) techniques that can substantially increase DNA yield throughout the genome. Although early Sanger-based studies suggest that many WGA methods yield highly unbiased genome representation and allelic concordance with genomic DNA (gDNA), few studies have quantified how these patterns scale with genome-level data. As more laboratories begin to utilize next-generation DNA sequencing methods in their individual research programs, additional studies are needed to examine and quantify the potential bias of WGA. Here, we use multiple displacement amplification and double-digest RAD sequencing on the grey mouse lemur (Microcebus murinus) to test the null hypothesis of no difference in genome coverage or SNP concordance between WGA DNA and gDNA. Our results show extremely high SNP concordance between samples when genotyping both de-novo and with a reference genome when specifying a minimum coverage depth of 20x. Genome coverage is also similar between WGA DNA and gDNA and allelic dropout is not observed. We also examine how SNP concordance varies based on coverage threshold and results suggest that SNP genotyping without a reference should be based on a minimum of 12x coverage, whereas when genotyping with a reference the same level of congruence is obtained with 8x coverage. At 20x coverage we observe no significant difference in the number of shared loci with SNPs and percent identical SNPs when genotyping de-novo versus with a reference. These results suggest that WGA may be a suitable solution for next-generation population genomic studies when DNA quantity would otherwise be a limiting factor.

Phylogenomics of Amphibia

Paul Hime, Emily Lemmon, Alan Lemmon, Brice Noonan, Scott Keogh, Stephen Donnellan, Alex Pyron, Rachel Mueller, David Green, David Weisrock

2D_306A-Phylogenies and Phylogenetics
Sunday, June 22, 2014 3:45 PM-4:00 PM
Myriad genomic advances are now allowing unprecedented resolution of many challenging questions in Evolutionary Biology and among them, targeted sequence capture is becoming a popular approach for gathering gene sequence data across large numbers of taxa. In this talk, I will discuss our ongoing efforts to develop and implement methods for generating phylogenomic data by anchored hybrid enrichment in amphibians which confront challenges posed by both extreme variation in genome size and by deep evolutionary divergences between lineages. Primary goals of this work are to broadly sample representatives of each major amphibian lineage, to collect hundreds of orthologous loci for coalescent species-tree estimation, and to test hypotheses about the relationships between rates of amphibian lineage diversification and rates of molecular evolution across the genome.

New phylogenetic tools for studying the phenotypic axis of diversification

Liam Revell

2D_306A-Phylogenies and Phylogenetics
Sunday, June 22, 2014 4:00 PM-4:15 PM
Over the past three decades or more phylogenies have become central in the study of evolution. In this presentation, I will describe work on some new tools for studying trait evolution using phylogenetic trees. Specifically, I will discuss an approach for identifying the position of one or multiple shifts in the rate of evolution through time; I will propose and illustrate a simple approach that can be used to test the hypothesis that the state of one continuous trait affects the rate of a second; and I will describe a method for reconstructing ancestral states of a discretely valued

character trait under the threshold model from evolutionary quantitative genetics.

The evolution of Acacia and biogeographic connections of the Australian continent

Daniel Murphy, Joe Miller, Gillian Brown

2D_306A-Phylogenies and Phylogenetics
Sunday, June 22, 2014 4:15 PM-4:30 PM

The Acacia s.s. clade is a dominant element of the Australian flora, with over 90% of the c. 1000 species having a distinctive phyllodinous leaf type. In contrast, there are relatively few phyllodinous Acacia species found outside the Australian continent; these comprise 18 taxa found in Malesia and on islands of the Pacific and Indian Oceans. Dating divergences of the Acacia clade allows investigation of what were the drivers for the lineage's diversification and the timing of biogeographical links between Australia and Malesia (and beyond). Acacia has rarely been used for such studies due to the large sampling of taxa needed to make meaningful biogeographical conclusions, and there have also been difficulties in dating divergences, due to the paucity of fossils for age calibrations. This has meant that this critical Australian lineage has been little represented in understanding the biogeography of the Australasian region. In this study, we extensively sample the diversity of Acacia species found within and outside Australia, use multiple DNA regions, and apply a reliable age constraint, obtained from the extensive microfossil pollen record, in order to co-estimate phylogenetic relationships and molecular divergence dates for the Acacia clade. Using these chronograms we demonstrate that most major clades of Acacia diversified in the Miocene. Divergence dating of Acacia species found outside Australia reflects two main patterns: a recent Pleistocene connectivity of taxa, especially those found across the Sahul shelf between Malesia and Australia, and in contrast, a pattern of relationship indicating older Austral-Malesian-Pacific links.

Species tree methods and ultraconserved elements (UCEs): a case study in galliform birds

Edward Braun, Kelly Meiklejohn, Rebecca Kimball, Brant Faircloth, Travis Glenn

2D_306B-Methodology
Sunday, June 22, 2014 3:15 PM-3:30 PM

Sequence capture using probes for ultraconserved elements (UCEs) followed by next-generation sequencing has become a popular method to collect data for phylogenetic analyses in vertebrates. Although powerful overall, many individual UCEs exhibit limited variation, especially when the amount of flanking DNA is limited or when UCEs from closely related taxa are compared. This can result in poorly resolved estimates of gene trees when individual UCEs are analyzed. The poor resolution of individual gene trees presents a challenge for phylogenetic analyses that summarize gene trees using a multispecies coalescent framework. We present the result of analyses using UCE data from a set of galliform birds (pheasants and partridges) that underwent a relatively recent evolutionary radiation. The data matrix we collected comprised almost 1,500 loci and more than 600 kb of data. Multiple phylogenetic analyses of concatenated data and individual gene trees were conducted and the results of these analyses will be discussed, demonstrating conditions under which specific coalescent-based methods can prove to be problematic.

Accounting for Horizontal Gene Transfer in Coalescent-based Phylogenetic Inference in Multi-locus Viral Genome Using a Pruning Algorithm

Arindam RoyChoudhury

2D_306B-Methodology
Sunday, June 22, 2014 3:30 PM-3:45 PM

Horizontal gene transfer is a fairly common feature in viral genome. Most traditional coalescent framework does not have an explicit mechanism for taking into account of horizontal gene transfer; as a result, the viral phylogenetic trees estimated based on such framework are often inaccurate. Here we present a novel phylogenetic technique that accounts for horizontal gene transfer in phylogenetic inference in a coalescent-based model of viral evolution. First, the likelihoods of local phylogenetic sub-tree are computed for each locus using a pruning algorithm. Then, the likelihood at each locus at each sub-tree is tested for identifying outliers (i.e. evidence for horizontal gene transfer), and then the final tree overall is estimated excluding the identified regions and loci consisting of horizontal gene transfer. Later these regions and loci are analyzed separately to identify the nature of horizontal gene transfer. While estimating the overall tree and sub-trees, a pruning algorithm based likelihood approach is used. Our method does not use MCMC algorithms, and as a result the process is computationally fast. We also establish through simulation studies that these estimation process has a high degree of accuracy.

Detecting Evolution in Action: Composite Likelihood Method for inferring Incomplete Selective Sweeps Using DNA Sequence Polymorphism

Thi Ha My Vy, Yuseob Kim

2D_306B-Methodology
Sunday, June 22, 2014 3:45 PM-4:00 PM

Adaptive evolution of a species occurs when a rare mutation that produces an advantageous phenotype spreads across population by natural selection. How, when and where in the genome such an evolutionary event occurs is a fundamental question in evolutionary biology. It is possible to detect ongoing positive selection because it generates complex patterns of DNA sequence variation. When a beneficial mutation is on the way to fixation, individuals (homologous chromosomes) in the population are divided into two groups: one group of individuals carrying the beneficial allele with low polymorphism, high linkage disequilibrium, excess number of high frequency derived alleles nearby the locus under selection, and another group of individuals carrying the ancestral allele with neutral level and pattern of sequence variation. The population genetic difference between two groups is therefore considered as the signal of ongoing positive selection. Several tests have been proposed and conducted to detect this kind of signal. However, they do not offer robust statistical test with accurate estimates of strength of selection and the location of selection.

In order to manage those obstacles, in this study, we propose a new statistical test, named Mapping Incomplete Sweep using Composite Likelihood test (MISCL), which detects ongoing positive selection based on the analytic prediction of sample configuration. We first derived the joint sampling probabilities for allele frequencies of two groups as a function of strength of selection and recombination rate. Then a parametric test is conducted to polymorphic sites which are most likely under ongoing selection, Tested against simulated data, this method yielded higher statistical power and more accurate parameter estimates compared to other available method. This procedure was also applied to Drosophila melanogaster genomes and discovered new candidate genes under ongoing positive selection.

Public threshold game: a new game to model social behavior in animals

Masoud Mirmomeni, Arend Hintze, Eli Strauss, Christoph Adami

2D_306B-Methodology
Sunday, June 22, 2014 4:00 PM-4:15 PM

The evolution of cooperation has been a conundrum in evolutionary biology because cooperation is vulnerable to selfish cheaters. One example of this dilemma is the “tragedy of the commons”, where individuals can either contribute to a public good or abstain. Since the public good is distributed to everyone regardless of an investment or not, those individuals who abstain will always fare better, unless the public goods multiplier (the synergy) is unrealistically high. While it is possible in principle to enforce cooperation via costly punishment, we found that even though punishment shifts the cooperation regime to emerge at lower synergy thresholds, individuals evolve to become pure cooperators who do not need to punish. This means that the threat of punishment alone is sufficient to drive cooperation, while actual punishment is rare. On the contrary, in natural systems we often observe vigorous punishment. Another difference between the public goods game and (some) natural systems and is that in the public goods game the payoff is a linear function of the amount paid in, while in natural systems often a threshold determines how much individuals need to contribute in order to obtain a fixed payoff that does not depend on the number of contributors who ultimately trigger it (more wolves hunting in a pack does not increase the size of the moose: you either get the moose or you don’t).

To remedy these discrepancies between the public goods game and the game-theoretic dilemma observed for example in collective hunting strategies, we introduce the “public thresh- old game” as an extension to public good game where a fixed payoff is distributed equally once enough individuals cooperate (number of contributors ≥ threshold). This alteration changes the game dramatically. Here, if the investment in the public good exceeds a given threshold, everyone (contributors as well as cheaters) receives an equal share (R/n), where R and n is the fixed payoff and the number players in the game respectively, while if the investment does not reach the threshold, the investment is lost. We find that effective punishment emerges as a stable strategy in this game, which in return facilitates cooperation. This suggests that the “public threshold game” is a better model for natural gambles that are “all-or-nothing”, and in which the triggered payoff does not depend in a linear fashion on the number of investors.

Estimating uncertainty in multivariate responses to selection

John Stinchcombe, Anna Simonsen, Mark Blows

2D_306B-Methodology
Sunday, June 22, 2014 4:15 PM-4:30 PM

Predicting the responses to natural selection is one of the key goals of evolutionary biology. Two of the challenges in fulfilling this goal have been the realization that many estimates of natural selection might be highly biased by environmentally induced covariances between traits and fitness, and that many estimated responses to selection do not incorporate or report uncertainty in the estimates. Here we describe the application of a framework that blends the merits of the Robertson–Price Identity approach and the multivariate breeder's equation to address these challenges. The approach allows genetic covariance matrices, selection differentials, selection gradients, and responses to selection to be estimated without environmentally induced bias, direct and indirect selection and responses to selection to be distinguished, and if implemented in a Bayesian-MCMC framework, statistically robust estimates of uncertainty on all of these parameters to be made. We illustrate our approach with a worked example of previously published data. More generally, we suggest that applying both the Robertson–Price Identity and the multivariate breeder's equation will facilitate hypothesis testing about natural selection, genetic constraints, and evolutionary responses.

Reliability of estimating phylogenies using quantitative characters

Ceferino Varón González, Simon Whelan, Chris Klingenberg

2D_306C-Methodology
Sunday, June 22, 2014 3:15 PM-3:30 PM

Species are often studied using a set of quantitative multidimensional characters, for example their shape or their pattern of gene expression. These species can be represented then in a multidimensional space in which each dimension takes up the variation in each variable. In empirical studies, squared-change parsimony is usually used to reconstruct the position of the internal nodes in this multidimensional space and pick the shortest possible topology. In this study we assess the reliability of this choice. In the simplest case, in which four species are studied, there are three possible topologies that can recover the correct unrooted phylogeny. We simulate the evolution of four species in the multidimensional space following one specific topology, then we try to reconstruct the correct phylogeny as one empirical study would do and check whether we choose the topology we have simulated or a different one. This method is analogous to the one used by Huelsenbeck and Hillis for molecular data. In our simulations we use different combinations of branch lengths and we first use a Brownian motion model of evolution, so parsimony gives equivalent results to maximum-likelihood. The results suggest a positive effect of the length of the central branch and the dimensionality over the phylogenetic reliability. Therefore, using more independent quantitative variables to describe the species increases the chances of obtaining the correct phylogeny. We also find long-branch attraction when few dimensions are used. Much evolution in two terminal branches can overwrite the signal established by a long central branch. This effect is especially concerning when covariation between the quantitative variables (i.e. integration) is assessed in the simulations. Integration decreases the effective dimensionality and therefore the reliability, which is poor with few dimensions. The attempts to transform the multidimensional space to take into account the account the integration and therefore to increase the reliability require big sample sizes, even in the unlikely situation in which the correct evolutionary integration pattern is known. Finally, stabilizing selection is also tested. The results are the worst in this situation, since convergence systematically happens. Unfortunately, both integration and stabilizing selection have been considered widespread features in the evolution of phenotypic quantitative characters.

Bayesian inference of population sizes, migration rates and divergence times based on importance sampling of coalescent trees

Yujin Chung, Vitor Sousa, Jody Hey

2D_306C-Methodology
Sunday, June 22, 2014 3:30 PM-3:45 PM

Estimating the demographic history of a group of populations has been a major focus in population genetics. Hey and Nielsen (2007) developed a method to estimate the demographic parameters under an Isolation with Migration model (implemented in the IMa and IMa2 programs). Under this method, genealogies and divergence times are first jointly sampled from a Markov chain Monte Carlo (MCMC) simulation in which other demographic parameters are integrated out analytically. Then the joint posterior density of population sizes and migrations rates are approximated from the sampled genealogies. However, the MCMC simulations in this approach are computationally expensive because of a large state space and because the correlation between genealogies and divergence times causes poor mixing.

We propose here a new Bayesian model which improves the MCMC part of the original method without introducing biases in demographic parameter estimations. By applying importance sampling, we first simulate by MCMC over coalescent trees rather than over genealogies and divergence times. The coalescent tree space is much smaller than the genealogy space, since coalescent trees do not carry the information about migration events. As a second step, the joint density of all the demographic parameters is approximated from the sampled coalescent trees. For a given demographic history, it is required to compute the conditional probability of a coalescent tree. This computation is analytically done by considering a coalescent tree as a continuous-time Markov chain of lineages in a population tree (Andersen et al., 2013). A comparison between the original and new methods will be presented.

The effects of partitioning on phylogenetic inference

David Kainer, Robert Lanfear

2D_306C-Methodology
Sunday, June 22, 2014 3:45 PM-4:00 PM

In this study we investigate the effects of partitioning on phylogenetic inference. Partitioning is a commonly used phylogenetic method that aims to accommodate variation substitution patterns among sites. Most phylogenetic studies use one of a small number of approaches to choose a partitioning scheme: no partitioning, partitioning by gene and codon position, or optimising a partitioning scheme using the BIC or the AICc. But despite partitioning's popularity, there have been few systematic studies of its effects on phylogenetic inference, and there have been no studies that compare different approaches to partitioning across many datasets. In this study, we applied four partitioning schemes to each of 34 publicly available empirical datasets, and compared the topologies, branch lengths, and branch support estimated with each scheme in a maximum likelihood framework. We find that the choice of partitioning scheme almost always affects tree topology, particularly when partitioning is omitted. Most notably, we find occasional instances where the use of a sub-optimal partitioning scheme produces highly supported but incorrect nodes in the tree. Branch lengths and bootstrap support are also affected by the choice of partitioning scheme, sometimes dramatically so. We discuss the reasons for these effects and make some suggestions for best practice.

Clustering Genes by Phylogenetic Similarity

Kevin Gori

2D_306C-Methodology
Sunday, June 22, 2014 4:00 PM-4:15 PM

The abundance of sequence data due to high-throughput sequencing has the potential to make phylogenetic inference more accurate by enabling the simultaneous analysis of multiple loci to be used in constructing a tree. However, if the loci do not share the same history, due to events such as horizontal gene transfer, it can be misleading to describe the entire data set by a single tree. We propose a system by which data can be described by multiple trees, potentially aiding the discovery of distinct evolutionary histories.

Our method, treeCl, partitions a set of sequence alignments into one or more classes, where each class represents a distinct phylogenetic history and comprises the loci that share that history. The method is "process-agnostic" in that no specific model of the biological processes causing evolutionary heterogeneity is assumed, and so escapes biases that may affect approaches that assume particular mechanisms of non-congruent evolution.

I present a survey of clustering methods by which the partitioning can be achieved, show how the quality of the results can be assessed by maximum likelihood, and use a series of simulation experiments to rank the methods. I also show a means of searching the partition-space to optimise the partition for a fixed number of classes. Also included in treeCl are ways of visualising distributions of trees in tree-space, which can be used to indicate whether a dataset is a candidate for phylogenetic partitioning, and a statistical means of determining the optimum number of classes.

In an example study, I apply the method to a set of 344 proteins from 18 yeast species and identify a subset of genes whose evolutionary history departs from the species tree in the placement of a single species. This may be related to a whole-genome duplication in yeast.

Relaxing the molecular clock to different degrees for different substitution types

Hui-Jie Lee, Nicolas Rodrigue, Jeffrey Thorne

2D_306C-Methodology
Sunday, June 22, 2014 4:15 PM-4:30 PM

Because point mutations can arise from a variety of molecular mechanisms, the change in substitution rate over time can differ among substitution types. To quantify this variation among substitution types and to improve divergence time estimation, we sample histories of homologous sequences according to their posterior distribution. These histories allow us to infer "branch lengths" for each combination of branch and substitution type on a phylogenetic tree. We can then examine the degree to which substitution types vary in their tendency to change rates. In addition, we can use this information to infer divergence times. A nice feature of the approach is that context-dependent substitution (e.g., CpG hotspots) can be accommodated.

Individual recognition and the maintenance of phenotypic and genetic diversity

Michael Sheehan

2D_BalC-ASN Young Investigators' Symposium: Jasper-Loftus Hill Award
Sunday, June 22, 2014 3:15 PM-3:45 PM

Individual recognition requires phenotypic variation; otherwise distinguishing between individuals is impossible. How does the phenotypic variation required for individual recognition evolve? Does individual recognition lead to increased phenotypic and genetic diversity? Provided that individuals benefit by being recognizable, selection is predicted to favor the evolution of distinctive, easily recognizable phenotypes called identity signals. I first describe a series of behavioral experiments and comparative studies demonstrating the variable facial color patterns used by Polistes fuscatus paper wasps are identity signals. Notably, I experimentally show that identity-signaling traits are under negative-frequency dependent selection - individual wasps benefit when they have rare, recognizable phenotypes receiving less aggression than wasps with common, indistinguishable appearances. Moreover, I demonstrate that the identity-signaling color patterns are heritable in P. fuscatus, suggesting that selection for distinctive appearances also maintains genetic variation. My findings contribute to a growing number of studies supporting the hypothesis that individual recognition can favor the maintenance of elevated phenotypic and genetic diversity. A number of important questions, however, remained unexplored including the relative contributions of coding and regulatory variation to individual identity signals and the evolutionary dynamics of identity signal associated loci. I address these questions using population genomic data in house mouse urinary scent marks and human faces. Wild house mice excrete individually distinctive combinations of major urinary proteins (MUPs) in their urine. By comparing the Mup genes and transcripts to the excreted proteins in the urine for F1 progeny of wild-caught mice I document the relative importance of coding versus regulatory differences among individuals in generating the information content of identity signals. While scent is key for mouse recognition, humans rely disproportionately on faces for individual recognition. By combining morphological analyses of patterns of facial diversity with population genomic analyses of SNPs recently identified to influence normal facial morphology, I demonstrate that human facial identity has evolved under negative-frequency dependent selection, consistent with identity signaling. Face-associated SNPs with the strongest evidence of selection tend of be old and of African origin, with some variants predating the split between the human and Neanderthal lineages. These studies of wasps, mice and humans argue for identity signaling as a potentially widespread selective force maintaining phenotypic and genetic diversity in social animals. Future research examining the evolution of vocal, visual and chemical identity signals holds promise for understanding the link between social interactions and phenotypic diversity in animals.

Drosophila, reproductive isolation, and speciation

Daniel Matute

2D_BalC*-Dobzhansky Prize Winner Lecture
Sunday, June 22, 2014 -

Speciation involves the evolution of one or more reproductive isolating mechanisms that split a single species into two that no longer interbreed. Thus, contact between nascent species determines their fate, and represents a crucial step in the evolution of reproductive isolation. The study of evolutionary biology has experienced a strong revival of interest in speciation in the last 25 years and has made substantial progress in helping to understand biogeographic patterns, in producing a body of data that has fueled theories about speciation, and in some cases, has led to the identification of genes causing reproductive isolation as well as adaptive differences among species. My research is a systematic study of the genetic basis of reproductive isolation and my ultimate goal is to produce a comprehensive summary of the natural history of reproductive isolation in the Drosophila group.

Recombination suppression helps hybridizing species persist, and perils of a career in evolutionary biology

Mohamed Noor

2E_BalC-SSE Presidential Address
Sunday, June 22, 2014 -

Many species retain their overall distinction despite hybridizing with a congener for long periods of time. This research examines the potential impact of recombination suppression in hybrids (as by chromosomal inversions) in allowing distinct "types" to persist, using Drosophila pseudoobscura and D. persimilis as a model system. Both sequence divergence and genetic mapping of species differences support this conclusion. Since this is a late talk and immediately preceding the poster session, it will be aimed light and general, and some parts are intended as humorous (always a risky maneuver).

The impact of breeding protocol on inbreeding, genetic diversity, and adaptation to captivity as measured in experimental populations of deer mice

Janna Willoughby, Robert Lacy, J. Andrew DeWoody

3A_201-Population Genetics
Monday, June 23, 2014 8:30 AM-8:45 AM

The goals of captive breeding programs are often to prevent extinction and/or extirpation while maintaining genetic diversity and fitness until reintroductions or supplementation of wild populations can occur. However, due to genetic changes that occur in captive populations, approximately one-third of such conservation programs fail to successfully establish new populations or contribute genes to existing populations. We evaluated such genetic changes in captive populations using pedigree information and neutral microsatellite loci that should reflect evolution due to drift and inbreeding. We bred six populations of white-footed mice (Peromyscus leucopus) for 20 generations using two replicates of three protocols: minimizing mean kinship (MMK), random mating (RAN), or selection for docility (DOC). After 20 generations, inbreeding (as measured by the pedigree) increased in all 6 captive populations, and was strongest in the first few generations. We found that MMK resulted in the slowest rate of loss of genetic diversity whereas the RAN and DOC protocols resulted in a more rapid loss of genetic diversity (with more variance across replicate populations). At the end of the captive program, the MK populations retained ~60% of the allelic diversity found in the source population compared to 48% and 45% in the RAN and DOC protocols, respectively. By comparing simulated populations to empirical data, we found evidence for adaptation to captivity via genetic hitchhiking of neutral microsatellites to nearby genes under selection, although these results varied by breeding protocol. Our results suggest that MMK reduces the loss of alleles due to drift, inbreeding, and selection more effectively than random mating or docility selection, and thus MMK should be the gold standard breeding protocol for threatened and endangered species reared in captivity.

Localized population samples reveal discordant patterns of genetic diversity among Mojave lizard species

Mike Hague, Eric Routman

3A_201-Population Genetics
Monday, June 23, 2014 8:45 AM-9:00 AM

Genetic diversity is the basic currency of evolution: only genetically variable loci are capable of evolutionary change. Nonetheless, the forces that maintain patterns of genetic variation in wild populations are poorly understood. Neutral genetic diversity is generally thought to increase with population size, but this relationship can be confounded by natural selection and genetic draft. Selection is more efficient in larger populations, so one might expect selected loci, and linked neutral loci, to be less variable in larger populations. The goal of this study was to measure how population levels of genetic diversity differ among similar sympatric species. We collected localized population samples of two contrasting groups of lizard species that differ in a suite of life history traits. We compared zebra-tailed lizards and western banded geckos, which are abundant and short-lived, to chuckwallas and desert iguanas, which are less common and long-lived. At neutral loci, we found that the two abundant species had significantly higher levels of diversity than the less common species. But, the nuclear RAG1 marker showed signatures of selection and homogenous levels of diversity across the four species. High variation at the neutral loci is likely due to large effective population size and gene flow; however, uniform variation at RAG1 highlights the fact that genetic diversity does not simply scale with population size. Selection may confound estimates of demography from presumably neutral loci. Future studies should utilize high throughput sequencing to measure how patterns of genetic diversity vary intraspecifically among loci and interspecifically among similar species.

---

ddRAD-seq analyses of population structure in brood parasitic indigobirds (Vidua spp.)

Jeffrey DaCosta, Christopher Balakrishnan, Jean-Bernard Dongmo, Michael Sorenson

3A_201-Population Genetics
Monday, June 23, 2014 9:00 AM-9:15 AM

The African indigobirds (Vidua spp.) are exceptional in that learning and mimicry of host vocalizations leads to adult behaviors that result in assortative mating and host fidelity. These behaviors provide a mechanism for rapid sympatric speciation via host shifts. Host shifts imply a non-zero rate of host infidelity, however, and the same behavioral mechanisms may lead to hybridization if eggs are laid in the nest of a host species already associated with another indigobird species. Thus, it is not clear if the morphological and genetic similarity of indigobird species is due to their recent common ancestry or ongoing hybridization. We addressed this question using “double-digest” restriction site-associated DNA sequencing (ddRAD-seq) to collect genomic data for three indigobird species (one of which has two host races) in Cameroon. Samples from all species were collected at two sampling localities, and we conducted population genetic analyses to determine if local gene flow or interspecific divergence best explains patterns of genomic variation. Results indicate that there is considerable divergence among species and species cohesion between sampling localities. Conspecific host races, however, are genetically similar and analyses of rare, derived alleles suggest that they continue to hybridize locally. Whether these incipient populations will eventually diverge into diagnosable species despite ongoing gene flow remains an open question.

Genetic population structure of Blanding’s turtle (Emydoidea blandingii) in southeastern Wisconsin

Sean Murphy, Gregory Mayer

3A_201-Population Genetics
Monday, June 23, 2014 9:15 AM-9:30 AM

The genetic population structure of Blanding’s turtle (Emydoidea blandingii), a threatened species through much of its range, was examined in southeastern Wisconsin using nine microsatellite loci in three populations (N=35). A low but significant value of FST (0.05212) indicated low levels of population structure. Deviations from Hardy-Weinberg equilibrium within populations provided little evidence for within-population structure. An M-Ratio test for recent genetic bottlenecks in the populations under study showed low ratios of allelic diversity to allelic size ranges in two of three populations, indicating possible genetic bottlenecks. Genotype assignment tests indicated that all turtles were most likely from their source populations. Effective population sizes for all populations were similar and large (759-815). These data suggest that Blanding's turtle was once widely distributed in southeastern Wisconsin, but that recent habitat fragmentation and loss has contributed to a genetic bottleneck in the resulting subpopulations.

Male-beneficial genotypes harbor deleterious genetic architecture

Karl Grieshop, David Berger, Göran Arnqvist

3A_206-Genetic Architecture
Monday, June 23, 2014 8:30 AM-8:45 AM

When constructing inbred lines, the majority of lineages one attempts to inbreed typically go extinct prior to achieving the desired inbreeding coefficient. The two most widely accepted mechanisms of extinction due to inbreeding are increased homozygosity for partially recessive deleterious mutations (the partial dominance hypothesis) and increased homozygosity for alleles at loci with heterozygote advantage (the overdominance hypothesis). Starting with a population of 41 isofemale lines/genotypes of the seed beetle Callosobruchus maculatus showing sexually antagonistic (SA) genetic variation, 20 replicate lineages of each isofemale line were subject to single-pair full-sib inbreeding for 10 consecutive generations. Approximately 80% of these lineages had gone extinct by the end of 10 generations of inbreeding. Survival analyses revealed that the pattern of extinction was variable across the different isofemale lines and was non-linear (i.e. attributable to inbreeding per se and not simply cumulative stochastic extinction). A mixed-effects Cox regression revealed that male-beneficial genotypes suffered relatively greater extinction rates than female-beneficial genotypes. Likewise, multiple regression revealed that replicate lineages from male-beneficial genotypes were significantly more likely to be extinct after 10 generations of inbreeding relative to those from female-beneficial genotypes. Insights as to the mechanism(s) responsible for this observation are provided by causal details of lineage extinctions recorded throughout the experiment, as well as a follow-up experiment comparing female fecundity and male fertility in extant lineages from genotypes at opposite extremes of the continuum from male-beneficial/low-survival to female-beneficial/high-survival. Explanations for these results are discussed in the context of the partial dominance and the overdominance hypotheses described above. These results provide insights into the nature of SA genetic architecture, but also suggest that certain components of genetic variation are likely underrepresented or even completely lacking from panels of inbred lines.

Payoffs and Tradeoffs

Lindsey McGee, Darin Rokyta

3A_206-Genetic Architecture
Monday, June 23, 2014 8:45 AM-9:00 AM

The genetic architecture of many phenotypic traits is such that genes often contribute to multiple traits, and mutations in these genes can therefore affect multiple phenotypes. These pleiotropic interactions often manifest as tradeoffs between traits where improvement in one property entails a cost in another. The life cycles of many pathogens include periods of growth within a host punctuated with transmission events, such as passage through a digestive tract or a passive stage of exposure in the environment. Populations exposed to such fluctuating selective pressures are expected to acquire mutations showing tradeoffs between reproduction within and survival outside of a host. We selected for individual mutations under fluctuating selective pressures for a ssDNA microvirid bacteriophage by alternating selection for increased growth rate with selection on biophysical properties of the phage capsid in high-temperature or low-pH conditions. Tradeoffs were prevalent when selection acted on a single trait, but payoffs resulted when multiple traits were selected for simultaneously. We employed a molecular-dynamics simulation method to determine the mechanisms underlying beneficial effects for three heat-shock mutations. All three mutations significantly enhanced the affinities of protein-protein interfacial bindings, thereby improving capsid stability. The ancestral residues at the mutation sites did not contribute to protein-protein interfacial binding, indicating that these sites acquired a new function. Computational models, such as those used here, may be used in future work as a predictive tool for mutational effects on protein or viral stability.

Understanding epistasis and gene networks in complex traits: An analysis of aggression in a model system

John Shorter, Wen Huang, Trudy Mackay

3A_206-Genetic Architecture
Monday, June 23, 2014 9:00 AM-9:15 AM

Most animals display aggressive behavior to secure food resources, protect against predators and facilitate access to mating partners. Inappropriate or excessive aggression has detrimental consequences for an individual, which can lead to lower fitness. Aggressive behavior is genetically complex, influenced by many genes as well as interactions with the environment. However, the genetic pathways affecting variation in aggressive behavior are evolutionarily conserved, enabling general inferences to be drawn from genetic analysis using model systems. We investigated the natural genetic variation of aggression using the Drosopihla melanogaster Genetic Reference Panel (DGRP), a collection of 205 inbred lines with fully sequenced genomes. We performed a genome wide association study (GWAS) and identified 74 genetic variants associated with variation in aggression. Additionally, we performed an independent experiment to replicate causal candidate variants by creating an advanced intercross population (AIP) from 6 lines representing the extremes of the DGRP. We measured aggressive behavior of 3,000 individuals after 10 generations of random mating from the AIP and performed extreme quantitative trait mapping. We observed that alleles significantly associated with aggression in the AIP replicated the allelic effect on aggression from the 6 extreme DGRP lines. Additionally, we generated a network of epistatic interactions using a model that tests for pairwise marker interactions across the DGRP. This analysis revealed that genes from these two populations are highly interconnected at the network level even though there is very little overlap of genes from the GWAS in the DGRP and AIP. Overall, these results show that our AIP replicated the allelic effects of aggression and that gene networks must be investigated when comparing a complex trait with epistatic interactions across two populations.

Opposing genotype-by-environment interactions and the maintenance of a genetic color polymorphism in a livebearing fish

Zachary Culumber, Molly Schumer, Scott Monks

3A_206-Genetic Architecture
Monday, June 23, 2014 9:15 AM-9:30 AM
Genetic variation persists within populations despite the eroding forces of natural and sexual selection. While environmental heterogeneity offers a potential solution to this evolutionary problem, examples in non-model systems are sparse and we have yet to fully understand functional mechanisms of intra-population processes. Livebearing fishes of the genus Xiphophorus are among the most variable species in terms of genetically-controlled color and pattern polymorphisms. The variable platyfish, X. variatus, exhibits polymorphism at a single locus with up to six, allelic tailspot patterns within single populations. Here we studied the effects and interaction of two environmental variables, temperature and food level, on two fitness-related traits in two genotypes of X. variatus. There was a significant genotype-by-environment (GxE) interaction with food stress on upper thermal limits (UTL), in which the wildtype genotype had a lower UTLs under normal food conditions but had higher UTLs than the other genotype under food stress. There was also a GxE interaction with thermal stress on energetic state. Wildtype fish gained more body mass than the other genotype at 25 °C but lost significantly more body mass under thermal stress at 34 °C. Wildtype fish therefore outperformed in UTLs during food stress, but underperformed in energetic state during thermal stress. The relative performance of the two genotypes was reversed between stress and non-stress conditions for the two environmental variables and each environmental variable affected performance in a different trait. Furthermore, data on body condition of adult males from multiple collections in natural populations was consistent with our laboratory experiment; wildtype males had poorer condition relative to other genotypes following periods of greater thermal stress. The findings demonstrate how the relative fitness of genotypes is not only dependent upon the environmental context but upon the trait being measured. The ability to withstand stressful temperatures is central to organismal survival and of particular importance given the stress-intensifying effects of global climate change. Energetic state (i.e., body condition) is important not only from a survival perspective due to associations with immune function, for example, but plays a role in mate choice in livebearing fishes. Better male body condition is associated with female preference, male courtship behavior, and reduced offspring-investment costs to females. The effects of heterogeneity in environmental variables such as temperature therefore can have simultaneous consequences for natural and sexual selection in the context of maintaining polymorphism.

Comparative quantitative genetics of the pelvis in four species of rodents: Evolution of the genetic and phenotypic covariance structure

Carl Saltzberg, Lee Walton, Angel Spotorno, Laura Walker, Scott Steppan

3A_206-Genetic Architecture
Monday, June 23, 2014 9:30 AM-9:45 AM
Quantitative genetics has been demonstrated to be a powerful tool for understanding how populations will evolve over microevolutionary timescales. Its application in understanding macroevolutionary patterns is debated as assumptions must be made about the long term stability of the underlying genetic and phenotypic variances and covariance's contained in the G and P matrix respectively. If these matrices are stable or change predictably then comparative quantitative genetics would be a way to bridge microevolutionary processes with macroevolutionary patterns. We conducted full-sib breeding programs to estimate G and P matrices for eight pelvic traits in two species of sigmodontine rodents from South America, the leaf-eared mice Phyllotis xanthopygus and P. darwinii. To expand the phylogenetic breadth of this study we compared G and P in Phyllotis to the two species reported for the same traits in Kohn and Atchley (1998): Mus norvegicus and Rattus rattus (Murinae). Using a phylogenetic comparative framework we tested the degree of divergence among all G and P matrices. We discuss the evolutionary stability of these over macroevolutionary timescales, and the correlation of matrix divergence with time.

Comparative methods for evaluating the evolutionary history of function-valued traits: a case study of salt tolerance in wild Helianthus (sunflowers)

Eric Goolsby

3A_301A-Phylogenetic Methods
Monday, June 23, 2014 8:30 AM-8:45 AM
Phylogenetic comparative methods such as ancestral state reconstruction provide methods for testing hypotheses of trait evolution, while methods such as phylogenetically independent contrasts (PICs) and phylogenetic generalized least squares (PGLS) allow for tests of correlated trait evolution. Although intraspecific differences due to measurement error, sampling error, or natural variation can be incorporated into error structures, these models generally operate under the assumption that individual species possess a fixed mean for any given trait. These assumptions are violated when environmentally-induced plasticity generates large trait shifts within species, which may result in the observation of substantial intraspecific variation.

However, uniform environments fail to capture the full extent of trait combinations possible within a species; instead, only a snapshot of possible trait combinations is identified, which is potentially problematic when making evolutionary inferences on putatively adaptively plastic traits. Categorical environmental manipulations, such as "low" and "high" treatments, offer an improved range of intraspecific trait plasticity, but problems are likely to arise if the slope, strength, or shape of reaction norms or plastically induced shifts in correlated traits differs across species. Application of continuous environmental gradients to all species of interest offers the opportunity to more fully assess the relationship between environment and plastically varying traits and shifts in correlated traits within species, and how the nature of such relationships vary across species. However, methods for analyzing function-valued traits in a phylogenetic context are few, providing little motivation for researchers to conduct studies of the magnitude that would produce the large amount of data necessary to make such inferences.

Here, these issues are explored using wild 34 wild Helianthus species exposed to a gradient of 9 different salt treatments (from 0 to 400 mM NaCl). Helianthus species are native to very diverse habitats across North America, including serpentine soils, salt marshes, shifting sand dunes, prairies, flood plains, and coastal soils. The evolutionary history of salt tolerance and correlated functional trait evolution in Helianthus is assessed using both traditional phylogenetic comparative methods and recently developed methods for evaluating function-valued evolutionary processes, and the strengths and weaknesses of each method are discussed.

Use of principal component analysis in species delimitation leads to (precise?) underestimation of species numbers

Iván Jiménez, Dilys Vela, Felipe Zapata

3A_301A-Phylogenetic Methods
Monday, June 23, 2014 8:45 AM-9:00 AM

Many species are delimited on the basis of discontinuities (i.e., gaps) in patterns of morphological variation. Recently developed Gaussian clustering methods are being increasingly used to discover these morphological gaps objectively. Systematists commonly perform Gaussian clustering after reducing the dimensionality of multivariate morphological space using ordination techniques such as principal component analysis (PCA). Based on statistical principles and biological reasoning, we predicted that this use of PCA leads to underestimation of species numbers, because the main axes of variation defined through PCA are likely unrelated to the morphological dimensions along which morphologically distinct species can be detected. We further predicted that the use of PCA increases the precision (i.e., repeatability) of estimates of species numbers, because it reduces the number of parameters involved in species delimitation. We tested these predictions using computer simulation experiments in which two morphologically distinct species were sampled to obtain morphological measurements that were analyzed with Gaussian clustering. We used three experimental treatments previous to Gaussian clustering: (1) reduction of dimensionality of morphological space using PCA, (2) reduction of dimensionality of morphological space using PCA based on robust covariance estimates, and (3) no reduction of dimensionality. As expected, estimates of the number of species based on reduced morphological space (experimental treatments 1 and 2) were more negatively biased than those based on the original unreduced morphological space (experimental treatment 3). However, contrary to predictions, estimates of the number of species based on reduced morphological space were not more precise (repeatable) than those based on unreduced morphological space. These results question the common use of PCA in species delimitation studies.

Metrics for comparing the fit of time trees to the fossil record

Julia Clarke, Clint Boyd

3A_301A-Phylogenetic Methods
Monday, June 23, 2014 9:00 AM-9:15 AM

Approaches quantifying the relative congruence, or incongruence, of molecular divergence estimates of clade age and the fossil record have been limited. Previously proposed methods are largely node specific, assessing incongruence at particular nodes for which both fossil data and molecular divergence estimates are available. These existing metrics, and other methods that quantify incongruence across topologies including entirely extinct clades, have so far not taken into account uncertainty surrounding both the divergence estimates and the ages of fossils. They have also treated molecular divergence estimates younger than previously assessed fossil minimum estimates of clade age as if they were the same as cases in which they were older. However, these cases are not the same. Recovered divergence dates younger than compared oldest known occurrences require prior hypotheses regarding the phylogenetic position of the compared fossil record and standard assumptions about the relative timing of morphological and molecular change to be incorrect. Older molecular dates, by contrast, are consistent with an incomplete fossil record and do not require prior assessments of the fossil record to be unreliable in some way.

Here, we compare previous approaches and introduce two new descriptive metrics. Both metrics incorporate information on uncertainty by utilizing the 95% confidence intervals for estimated divergence dates and data on stratigraphic uncertainty for the compared fossils. Metric scores are maximized when these ranges are overlapping. MDI discriminates between situations where molecular estimates are younger or older than known fossils reporting both absolute fit values and a number score for incompatible nodes. DIG range (divergence implied gap range) allows quantification of the minimum increase in implied missing fossil record induced by enforcing a given set of molecular-based estimates. These metrics are used together to describe the relationship between time trees and a set of fossil data, which we recommend be phylogenetically-vetted and referred on the basis of apomorphy. Differences from previously proposed metrics and the utility of MDI and DIG range are illustrated in three empirical case studies from angiosperms, ostracods, and birds. These case studies also illustrate the ways in which MDI and DIG range may be used to assess time trees resultant from analyses varying in calibration regime, divergence dating approach or molecular sequence data analyzed.

Non-null effects of a null range: Exploring parameter estimation in the dispersal-extinction-cladogenesis model

Kathryn Massana, Jeremy Beaulieu, Brian O'Meara, Nicholas Matzke

3A_301A-Phylogenetic Methods
Monday, June 23, 2014 9:15 AM-9:30 AM

Parametric models in historical biogeography that integrate geographic ranges and phylogenies have shown to be extremely informative in understanding the geographic range evolution of taxa. One such approach is the dispersal-extinction-cladogenesis (DEC) model, which has been widely used in empirical analyses of the evolution of geographic range using discrete area states. However, local extinction rates are difficult to estimate well in this model. We explore the cause of this as well as a potential solution.

Molecular species delimitation methods recover most song delimited cicada species in the European Cicadetta montana complex

Elizabeth Wade, Thomas Hertach, Chris Simon

3A_301A-Phylogenetic Methods
Monday, June 23, 2014 9:30 AM-9:45 AM

Molecular species delimitation is increasingly being used to discover and inform species level diversity and a number of methods have been developed. Here we compared two molecular species delimitation methods (BPP and GMYC) with song-delimited species in the Cicadetta montana cryptic species complex (Hemiptera: Cicadidae) which is found throughout Europe. Recent bioacoustics studies of male calling songs (pre-mating reproductive barriers) have revealed cryptic species diversity not previously recognized with morphological methods. Maximum likelihood and Bayesian phylogenetic analyses were used to analyze the mitochondrial genes COI and COII and the nuclear genes EF1α and period for twelve European Cicadetta species as well as the closely related monotypic genus Euboeana. Overall, the two molecular species delimitation methods used in this study were largely congruent. Used together, they were able to recover most song-delimited species and revealed additional cryptic species diversity.

Open Tree of Life version 1.0: a comprehensive and easily-updated tree of life

Karen Cranston

3A_301B-Methodology
Monday, June 23, 2014 8:30 AM-8:45 AM

Open Tree of Life has made considerable progress on assembling an online, comprehensive and dynamic tree of life. We report on the release of version 1.0 in terms of completeness, coverage and conflict, on methods for visualizing and accessing OpenTree data and on challenges to keeping this tree up-to-date with published knowledge. The content and structure of the synthetic Open Tree of Life depends not on phylogenetic knowledge, but on digital availability and curation of that knowledge. There is, therefore, a conflict between a synthetic tree that accurately represents our collective wisdom about the tree of life and one that strictly summarizes digitally available and well-curated phylogenies. There are simple data publication strategies that would greatly increase the usability of published phylogenies for Open Tree and other projects and reduce the downstream curation burden. We present curation tools to collaboratively annotate phylogenetic data and how novel database types enable synthesis and analysis of these data.

Bayesian estimation of phylogenetic information content and its implications for site-stripping

Paul Lewis, Ming-Hui Chen, Lynn Kuo, Louise Lewis, Karolina Fucikova

3A_301B-Methodology
Monday, June 23, 2014 8:45 AM-9:00 AM

We present Bayesian statistical methodology for estimating phylogenetic information content, and for identifying conflicting signal when present. The Kullback-Leibler (KL) divergence between prior and posterior, also known as the relative entropy of the posterior with respect to the prior, measures the amount of information about the model parameters contained in the data. Bounds for the minimum and maximum information content may be constructed using conditional clade estimates of tree topology posterior probabilities introduced recently by Larget. Conflicting phylogenetic information between data subsets is manifested as a decrease in information in combined compared to separate data sets. The ability to accurately measure information content has many applications in phylogenetics, providing, for example, a meaningful measure of saturation and an objective way to sort subsets of a partitioned data set (genes in a genomic alignment, morphology vs. molecules, codon positions, etc.) from most to least informative. As an example application, we compare two methods (Conditional Predictive Ordinates, CPO, and Observed Variability, OV) for identifying the noisiest sites in an alignment, and discuss the implications of using either OV or CPO for site-stripping.

Estimating Evolutionary Parameters and Full Length Haplotypes Simultaneously Using Short-Read Sequences Derived from Genetically Variable Populations

Steven Wu, Jeet Sukumaran, Yuantong Ding, Allen Rodrigo

3A_301B-Methodology
Monday, June 23, 2014 9:00 AM-9:15 AM

The advancement in next generation sequencing technologies allows researchers to obtain large amounts of genetic and genomic data in relative short periods of time, and at a fraction of the cost of conventional Sanger sequencing. Nevertheless, the evolutionary analysis of short read sequences generated from next generation sequencing remains challenging. We present a Bayesian method to derive posterior distributions of evolutionary parameters using next generation sequences obtained from a mixed sample of homologous sequences. The new method treats full length haplotypes as unknown parameters and calculates the joint posterior probability of the haplotypes, evolutionary parameters and genealogy, given the short read sequences. We apply a Markov chain Monte Carlo (MCMC) technique to recover this posterior distribution. Preliminary results show that the estimation of the evolutionary parameters of interest is comparable to results obtained using full length sequence alignments.

Phylogenetic comparative biology and morphometrics collide: PIC, PGLS, and the challenge of high-dimensional data

Dean C. Adams

3A_301B-Methodology
Monday, June 23, 2014 9:15 AM-9:30 AM

Studies of evolutionary correlations commonly utilize phylogenetically independent contrasts or phylogenetic generalized least squares to assess trait covariation in a phylogenetic context. However, while these methods are appropriate for evaluating trends in one or a few traits, they are incapable of assessing patterns in highly-multivariate data, as the large number of variables relative to sample size prohibits the algebra from being completed. This posesserious limitations for comparative biologists, who must either simplify how they quantify phenotypic traits, or alter the biological hypotheses they wish to examine. In this article, I propose a new statistical procedure for performing ANOVA and regression models in a phylogenetic context that can accommodate high-dimensional datasets. The approach is derived from the statistical equivalency between methods based on covariance matrices and those based on distance matrices, and uses a permutation procedure to assess significance. Using simulations, I show that under Brownian motion the method displays appropriate Type I error rates and statistical power, whereas standard approaches have decreasing power as data dimensionality increases. As such, the new procedure provides a useful means of assessing trait covariation across a set of taxa related by a phylogeny, enabling macroevolutionary biologists to test hypotheses of adaptation and phenotypic change in high-dimensional datasets.Studies of evolutionary correlations commonly utilize phylogenetically independent contrasts or phylogenetic generalized least squares to assess trait covariation in a phylogenetic context. However, while these methods are appropriate for evaluating trends in one or a few traits, they are incapable of assessing patterns in highly-multivariate data, as the large number of variables relative to sample size prohibits the algebra from being completed. This posesserious limitations for comparative biologists, who must either simplify how they quantify phenotypic traits, or alter the biological hypotheses they wish to examine. In this article, I propose a new statistical procedure for performing ANOVA and regression models in a phylogenetic context that can accommodate high-dimensional datasets. The approach is derived from the statistical equivalency between methods based on covariance matrices and those based on distance matrices, and uses a permutation procedure to assess significance. Using simulations, I show that under Brownian motion the method displays appropriate Type I error rates and statistical power, whereas standard approaches have decreasing power as data dimensionality increases. As such, the new procedure provides a useful means of assessing trait covariation across a set of taxa related by a phylogeny, enabling macroevolutionary biologists to test hypotheses of adaptation and phenotypic change in high-dimensional datasets.

Using networks of topologies and bipartitions to explore, quantify, and summarize phylogenetic tree space

Jeremy Brown, *Guifang Zhou, Wen Huang, Jeremy Ash, Melissa Marchand, Kyle Gallivan*

3A_301B-Methodology
Monday, June 23, 2014 9:30 AM-9:45 AM

Phylogenetic trees are now routinely inferred from enormous genome-scale data sets, revealing extensive variation in phylogenetic signal both within and between individual genes. However, approaches that quantitatively characterize the full scope of phylogenetic information from such data sets do not yet exist. Richer, quantitative characterizations of tree set distributions are needed. Here, we propose a set of complementary approaches based primarily on network analyses to explore, quantify, and summarize the phylogenetic information in massive sets of trees, to clarify the extent of phylogenetic concordance and conflict across genomes, and to test hypotheses regarding the biological causes of variation in phylogenetic signal. We employ two distinct types of networks. The first type uses topologies as vertices and topological (dis)similarity as edges. The second uses bipartitions as vertices and the degree of covariance in bipartition presence/absence as edges. We discuss how such networks are constructed and highlight some of the ways that they can be employed to answer a variety of questions about both evolutionary pattern and process.

The environmental determinants of natural selection

Christina Caruso, *Ryan Martin, Nina Sletvold, Joel Kingsolver, Michael Wade, Kate Augustine, Stephanie Carlson, Andrew Maccoll, Adam Siepielski*

3A_302A-Selection and Fitness
Monday, June 23, 2014 8:30 AM-8:45 AM

Although >6000 estimates of phenotypic selection have been published, the environmental factors that cause this selection have rarely been identified, making it difficult to predict how populations will respond to environmental change. One approach to identifying the causes of selection is to experimentally manipulate an environmental factor and compare estimates of selection between treatments. If the strength or direction of selection on a trait differs between treatments, then we can infer that the manipulated environmental factor is a cause of selection on that trait. But estimates of phenotypic selection from experimental studies, unlike estimates of selection from natural populations, have yet to be compiled and synthesized.

We compiled a database of estimates of selection from >140 experimental studies published between 1991 and 2013. We used this database to test two hypotheses as to why different environmental factors will be more or less likely to alter the strength of selection, as well as whether the strength of selection measured in experimental studies is comparable to selection in natural populations. We found that the strength of directional selection did not vary among environmental factors, which is not consistent with the hypothesis that the biotic environment exerts stronger selection than the abiotic environment. We also found that there was no relationship between the magnitude of change in mean fitness between treatments and the magnitude of change in directional selection between these treatments, which does not support the hypothesis that environmental factors that have a large effect on mean fitness will exert stronger selection than factors that have a small effect on mean fitness. However, estimates of directional selection from experimental studies were comparable to estimates of selection in the wild, supporting the use of experiments to identify the causes of natural selection.

Measuring pollinator-mediated selection with various fitness components: A review and a lesson from Linum pubescens

Yuval Sapir

3A_302A-Selection and Fitness
Monday, June 23, 2014 8:45 AM-9:00 AM

Pollinator-mediated selection has been postulated to drive floral trait evolution. Animal pollinators react to floral trait value differentially. This shapes the fitness function and provides inference of pollinator-mediated selection in floral evolution. Fitness can be measured in various ways, and a review in 2003 (Geber & Griffen, 2003) tabulated the various ways of measuring fitness in selection studies in plants. Since this decade-old review, many studies accumulated, and here we focus on studies that measured pollinator-mediated selection. We ask the following question: 1) Are fitness components measured as diverse as before 2003? 2) Is the fitness component chosen affects the extent of selection? And 3) is there interaction between the extent of pollinator-mediated selection and the fitness component chosen?

To assess the effect of various fitness components on inferring pollinator-mediated selection we measured four fitness components in the annual distylous plant Linum pubescens, and estimated selection on floral size and color, and on style morph. Three fitness components (number of fruits, number of seeds and their mass) were highly correlated, while the fourth component, fruit-set, had lower correlation to the other three. While floral color and style morph did not show selection, regardless the fitness component used, floral size was under positive linear selection using number of fruits, number of seeds and seeds mass. We discuss these results as related to the possible mechanism that create selection through pollinator behavior.

Fluctuating selection in the field explains natural variation in Arabidopsis thaliana glucosinolate plant defense

Rachel Kerwin

3A_302A-Selection and Fitness
Monday, June 23, 2014 9:00 AM-9:15 AM

High levels of standing phenotypic variation have been observed for many natural plant and animal populations, and researchers have long been interested in elucidating the genetic sources of this variation as well as the evolutionary forces that act to maintain this diversity. Wild populations experience complex fluctuating biotic environmental conditions, such as pathogen and insect pressures that vary temporally and spatially. Fluctuating biotic pressures generate fluctuating selective forces that have the potential to maintain natural variation within a species. Fluctuating selection is difficult to discriminate from balancing and other non-linear selection on a purely genetic basis and thus requires direct field trials. To test for the potential role of fluctuating selection in maintaining genetic diversity, we used single gene mutants to create a structured polymorphic Arabidopsis population in Columbia (Col-0) accession that represents a subset of natural genetic variation in the defensive GSL of Arabidopsis thaliana and conducted an empirical multi-year field study at two sites. This study showed that that variation in naturally polymorphic GSL genes significantly effects fitness in the field in a manner that is highly temporally and spatially variable. These changes were such that each location and year had a different optimal set of genotypes. Additionally, the fluctuating fitness of GSL genotypes within the structured population correlates with frequency of GSL profiles found among natural Arabidopsis accessions. This supports the idea that fluctuating selection is responsible for maintaining the natural GSL variation observed in this species.

"Fitness" has at least three incommensurable dimensions: growth, efficiency, and competitiveness

Joanna Masel

3A_302A-Selection and Fitness
Monday, June 23, 2014 9:15 AM-9:30 AM

Evolutionary biology "fitness" can be defined either in relative terms, normalized to the competition, or against an external standard. Many binary distinctions have been made between different kinds of fitness: not only absolute vs. relative fitness, but also r- vs. K-selection, natural vs. sexual selection, density-dependent vs. independent, selection on individuals vs. groups, and hard vs. soft selection. I propose a new formulation of the concept of biological fitness, with three rather than two incommensurable fitness dimensions, subsuming these prior distinctions and resolving past problems with them. Competitiveness is normalized and unitless, while growth and efficiency are both absolute, with time and resource units respectively.

Fitness functions and distributions: the shape of things to come

Frank Shaw, Ruth Shaw

3A_302A-Selection and Fitness
Monday, June 23, 2014 9:30 AM-9:45 AM

Fisher's Fundamental Theorem predicts fitness change from the additive genetic variance for fitness. We explore the characteristics of the distribution of additive genetic fitness effects under the standard Gaussian fitness function on a normally distributed trait, and extend this to fitness functions induced simultaneously by more than one fitness component, such as survival and fecundity.

Avian evolutionary history in the southern Neotropics: complex and varied patterns of diversification

Dario Lijtmaer, Cecilia Kopuchian, Ana Barreira, Pilar Benites, Kevin Kerr, Kazuya Naoki

3A_302B-Avian Evolution
Monday, June 23, 2014 8:30 AM-8:45 AM

Even though the study of the evolutionary history of the Neotropics has dramatically increased in the last few years, most work has been done in the Amazonian basin, the Atlantic forest and the northern part of the Andes mountains. By contrast, the southern cone of South America has barely been studied in this regard. This region is particularly interesting because of its high latitude, the occurrence of a diverse array of environments (including the highest peaks of the Andes mountains and the southernmost part of the Yungas and Atlantic Forest regions) and the presence of areas with some of the highest rates of avian diversification worldwide. We used citochrome c oxidase I (COI) sequences (DNA barcodes) from 3,425 specimens belonging to 730 species of Argentinean and Bolivian birds to analyze the patterns of diversification in this region and assess the role of various diversifying factors. Comparison with birds of the Nearctic and lower latitudes of the Neotropics evidenced that diversification patterns in southern South America are complex, consistent with the influence of glacial cycles as well as other factors more typical of the Neotropical realm. Comparisons among different areas of southern South America showed that species endemic to Patagonia and the Andes mountains are younger and less variable than more widely distributed species, and even more so than the northern, more tropical species. This pattern is consistent with a more prominent role of glacial cycles in the Andes and Patagonia and a more stable environment in the northern areas of this region. Finally, seven percent of the species showed high intraspecific variation, usually including deeply divergent lineages. The study of these cases with various algorithms permitted an initial assessment of the presence of evolutionary independent lineages. Further analyses including other molecular markers, morphology and vocalizations will indicate whether these taxa include overlooked species, allowing a better understanding of avian diversity in this region.

Assembly of the New World oscine passerine fauna

F. Keith Barker

3A_302B-Avian Evolution
Monday, June 23, 2014 8:45 AM-9:00 AM

Diversification of lineages is often analyzed at a global scale, which may prevent identification of locally successful lineages that have not diversified impressively from a global perspective. On the other hand, analyzing among-lineage patterns of diversification on geographically relevant scales is complicated by dispersal, especially in a group with high dispersal potential such as birds. I take a regional perspective on global diversification dynamics of oscine passerines, by inferring interhemispheric (Old World-New World) interchanges, estimating the timing of these dispersal events, and comparing post-dispersal net diversification of dispersing lineages. Most lineages arriving in the New World have diversified on a trajectory consistent with a constant-rates birth-death process with a relatively high extinction fraction. By contrast, several relatively old North American lineages have not diversified at all, and one widely-distributed lineage—the Emberizoidea—has diversified at a rate far exceeding comparably-aged New World lineages. These analyses are a crude step toward placing avian diversity into a more realistic geographic context. Even so, they offer significant insights into the evolution of avian diversity, suggesting that more fine-grained analyses enabled by more complete and robust phylogenies will offer even better.

A reappraisal of the productivity hypothesis for North American bird assemblages

LuAnna Dobson

3A_302B-Avian Evolution
Monday, June 23, 2014 9:00 AM-9:15 AM

~~Plant biomass/productivity and the species richness of birds are associated across a range of spatial scales. Species-energy theory is generally assumed to explain these correlations. If true, bird richness should also track productivity temporally, and there should be spatial and temporal relationships between bird abundance and both productivity and bird richness. Using summer Normalized Difference Vegetation Index (NDVI) from 1982 – 2006 and the North American Breeding Bird Survey, we evaluated the response of avian richness and abundance to temporal changes in plant biomass/production. We found positive spatial relationships all 25 years. However, richness and NDVI were temporally positively associated at 1,579 survey sites and negatively associated at 1,627 sites (mean r2 = 0.09). Further, total abundance and NDVI were unrelated spatially (r2s spanning

---

Rapid diversification and secondary sympatry in an island bird lineage (Aves: Todiramphus)

Michael Andersen, *Robert Moyle*

3A_302B-Avian Evolution
Monday, June 23, 2014 9:15 AM-9:30 AM

Todiramphus chloris (Aves: Alcedinidae) is the most widely distributed of the “great speciators” in the Pacific. Nearly 50 described subspecies of this kingfisher are distributed from the Red Sea to Polynesia, a distance of > 19,000 km. We reconstructed a molecular phylogeny of this enigmatic avian radiation from six genes and 157 individuals that spanned the entire Pacific distribution from the Marquesas to Singapore. The resulting phylogeny offers strong support that T. chloris radiated rapidly over an immense region of the Pacific. Genetic distances across the phylogeny were remarkably low. Molecular dating suggests that this radiation underwent extensive range expansion and diversification less than 1 Ma, with a diversification rate among the most rapid known of all birds. Incredibly, within the short timeframe of diversification, several instances of sympatry have accumulated in this group on Australia, as well as far-flung oceanic islands, including Palau, Vanuatu, and the Solomon Islands. In each case of sympatry, significant eco-morphological and behavioral differences exist, suggesting that pre-mating isolating mechanisms were achieved rapidly during diversification, perhaps as fast as any bird lineage studied to date. Our analyses found good node support across the entire phylogeny, despite shallow internode distances. We revealed several complex radiations within the ingroup, as well as numerous novel relationships, which require major taxonomic revision throughout the entire species complex. Of the 22 species in the genus Todiramphus, ten were embedded within or closely related to T. chloris, including five species that radiated in the remote islands of Eastern Polynesian and one (T. sanctus) that maintains some migratory populations. Complex biogeographic patterns were inferred from the topology. A major phylogeographic break in the eastern Solomon Islands separates a Northern Melanesian clade from Polynesian taxa. Otherwise, the biogeographic origin of the T. chloris complex was equivocal, likely owing to the radiation's rapid origin. This study makes a significant contribution to the study of rapid diversification and subsequent assembly of sympatric species on island systems, and to the systematics of a classically polytypic avian species complex in the Pacific.

Early burst in ecological radiation of birds

Jonathan Mitchell

3A_302B-Avian Evolution
Monday, June 23, 2014 9:30 AM-9:45 AM
Birds represent the most diverse clade of tetrapods, and in the modern world they span across three orders of magnitude in body mass and occupy niches on every continent. When this diversity evolved has been a long standing question, due to both uncertainty in the higher-level phylogenetics of birds, and their meagre fossil record. To help address this question, I made 22 skeletal measurements across 604 extant genera (1375 specimens) as well as 336 fossil specimens. The extinct taxa are derived primarily from three exceptional deposits: stem birds (pygostylians) from the 125Ma Jehol deposits from China, and crown birds from the 52Ma Green River deposits from North America and the 47Ma Messel pits from Germany. I found correlations between ecology in morphology in extant birds, and used those correlations to predict ecology in the fossil taxa, and tested those predictions against preserved gut contents in 18 fossil genera and found the extant ecomorphological correlations predicted gut contents significantly better than random (p

Predator-induced facultative group formation in Chlamydomonas depends on life history traits and the groups can be chimaeric.

Santosh Sathe, Pierre Durand

3A_302C-Evolutionary Transitions
Monday, June 23, 2014 8:30 AM-8:45 AM
The evolution of multicellularity is a major transition in evolution. While the advantages of multicellularity, for example those related to increased size and division of labour could be responsible for its maintenance, the selective pressures and the role of kinship for its origin are not clear. A group of unicellular individuals staying or coming together with little or no division of labour can be a first step towards multicellularity and predation pressure might have played a dominant role at this stage. Using an established model system (the volvocales) the response of the unicellular Chlamydomonas to predation pressure was studied. In addition, the correlation between life history traits like cell size or swimming speed and the ability to form groups as well as the kin structure of groups were examined.

Experimental data revealed that unicellular Chlamydomonas cells can defend themselves by coming together to form groups when co-cultured in the presence of a protozoan predator, Peranema trichophorum. Group formation is facultative. It is induced only in the presence of predators or their culture filtrate and cells in the group revert to a unicellular stage once the selection is removed. Group formation is costly as the groups sink to the bottom and some cells die. Life history traits are important in group formation; smaller and less motile cells form groups more readily. Interestingly, groups were genetically heterogeneous suggesting that in these early stages of the transition to multicellularity, life history traits rather than genetic relatedness played a dominant role.

Scaffolding the origin of multicellular evolvability

William Ratcliff, Johnathon Fankhauser, David Rogers, Duncan Greig, Michael Travisano

3A_302C-Evolutionary Transitions
Monday, June 23, 2014 8:45 AM-9:00 AM
A hallmark of major transitions in evolution is the emergence of evolvability in new biological structures. The origin of evolvability presents a conundrum: how can evolvability arise by natural selection? Here we address this problem by demonstrating that even the simplest of multicellular body plans can have an inherent capacity for higher-level adaptation. Disrupting the transcription factor ACE2 in Saccharomyces cerevisiae prevents cellular separation, generating multicellular 'snowflake' yeast. Snowflake yeast clusters exhibit three traits that are criteria for multicellular evolvability: they reproduce via multicellular propagules, they possess heritable variation for traits that affect fitness, and they pass through a unicellular genetic bottleneck during development (limiting within-cluster genetic conflict). This work highlights the critical importance of physical scaffolding during major evolutionary transitions.

The evolution of multicellularity as a key innovation for adaptive radiation in experimental microcosms

Maria Rebolleda Gomez, William Ratcliff, Johnathon Fankhauser, Michael Travisano

3A_302C-Evolutionary Transitions
Monday, June 23, 2014 9:00 AM-9:15 AM
Multicellularity is thought to play a critical role in the evolution of biological complexity, facilitating diversification by opening up new ecological opportunities. However, there is still debate on the importance of this transition driving diversification, as well as, the mechanistic ink between the evolution of multicellularity and increased rates of diversification. We examined a process of adaptive radiation following the evolution of multicellularity in the unicellular yeast Sacharomyces cerevisiae. At least two lineages with distinct multicellular life histories evolved and coexisted in 9 out of 10 replicate populations. We found that the origin of novel multicellular life histories was a critical factor, increasing the complexity of the environment. The large clusters of cells altered the fluid dynamics of the environment and the evolution of different life-stages allowed for exploitation of different niches. To understand the mechanism underlying this diversification, we looked at the evolutionary history of a single population in detail, and observed the rapid evolution of different multicellular life history strategies along a trade-off between growth and survival. Moreover, we found that disparate multicellular life histories were capable of stable coexistence. The evolution of multicellularity profoundly changed Earth's ecological and evolutionary dynamics.

Here we show that multicellularity can directly spur the evolution of not only increased biological complexity, but also its diversity.

The evolution of life cycle gene expression in the Volvocine algae: toward a molecular understanding of multicellular evolution

Tara Marriage, Bradley Olson

3A_302C-Evolutionary Transitions
Monday, June 23, 2014 9:15 AM-9:30 AM

Multicellularity is a major evolutionary transition that has occurred at least twenty-five independent times in eukaryotes. However, the molecular genetic basis of this transition in any taxa is not well understood. The Volvocine algae are a model system to study the evolution of multicellularity because they consist of a recently evolved (approximately 200 million years ago) monophyletic group of organisms that morphologically span from unicellular (Chlamydomonas reinhardtii) to multicellular with germa and soma differentiation (Volvox carteri). The colonial multicellular alga, Gonium pectorale, is a sister species to C. reinhardtii, and is an exemplary species to study the transition from unicellularity to colonial multicellularity. C. reinhardtii and G. pectorale grow and divide similarly; however when G. pectorale cells under go multiple fission (multiple rounds of mitotic divisions), the daughter cells remain attached to each other, whereas in C. reinhardtii, the daughter cells separate. This, along with other experimental evidence, suggests that the colonial multicellular phenotype of G. pectorale is under cell-cycle regulation. In this experiment, we used RNA-Seq analysis to investigate changes in gene expression across the 24-hour cell cycle of G. pectorale. We performed two independent RNA-Seq experiments: a broad scale experiment where RNA samples were pooled into 4 biologically relevant time points, and a finer scale experiment where RNA samples were pooled every two hours, again across the 24-hour cell cycle. RNA samples underwent Illumina library preparation and HiSeq sequencing. We then used the Tuxedo suite of software for differential gene expression analysis. Genes involved in cell-cycle regulation, cell wall organization and fission were significantly differentially expressed. We will confirm our results with functional characterization of strong multicellular candidate genes.

An inside-out origin of the eukaryotic cell

David Baum, Buzz Baum

3A_302C-Evolutionary Transitions
Monday, June 23, 2014 9:30 AM-9:45 AM

All existing evolutionary models for the origin of the eukaryotic cell have assumed that the nucleus and endomembrane system arose within the cytoplasm of a prokaryotic cell. Here we challenge this paradigm by proposing that an ancestral prokaryote, equivalent to the modern day nucleus, constructed an external membranous compartment, homologous to the modern eukaryotic cytoplasm. Our model begins with the extrusion of stable membrane-bound blebs that served to facilitate material exchange with ectosymbiotic proteobacteria that represent progenitors of mitochondria. Blebs were stabilized through the association of nuclear pore proteins within the bleb neck and attached to the outer cell wall by progenitors of LINC complexes. The space between adjacent blebs gave rise to the endoplasmic reticulum (ER), with subsequent bleb fusion events yielding a plasma membrane. Strikingly, this model explains previously enigmatic aspects of eukaryotic cell biology, including ER continuity, the close association between mitochondria and ER, the site of N-glycosylation in the lumen of nuclear proximal ER, and the ability of nuclei in syncytia to control their local cytoplasm. Moreover, our model is consistent with recent phylogenetic analyses supporting "eocytes" as sister to Eukarya, and the presence of bacterial lipids in eukaryotes. Thus, the inside-out model not only provides a new, more-plausible explanation of eukaryotic evolution, but also provides a new predictive framework by which to better understand the dynamic organization of modern eukaryotic cells.

Method to identify small-scale gene transpositions in rearranged genomes.

Mira Han

3A_303-Phylogenomics
Monday, June 23, 2014 8:30 AM-8:45 AM

Duplications and transpositions leading to gene rearrangements are frequent in eukaryotic genomes. These regions of rearrangements are readily identified through comparative genomics. But inferring the ancestral state of the genome, and the history of transposition events are still a challenge. Different algorithms have been developed to infer the phylogeny using gene order data and various distance models based on the rearrangement events. As an alternative to those approaches, I show that we can infer small-scale gene transposition events by mapping the gene positions onto the known phylogeny. The location of extant genes are mapped to a common map defined by conserved segments across species. Using a parsimonious reconstruction of gene locations, gene transpositions are identified within rearranged genomes. I applied the method to six primate genomes, and identified the genes that have transposed along the branches of the primate phylogeny. Since the method can be applied to species groups with moderate rearrangements, it will be useful in identifying gene transpositions among a wide range of taxa.

Caught in the Crossfire: Genes tangled up in host-mediated transposable element defense

Alexandra Erwin, Mauricio Galdos, Justin Blumenstiel

3A_303-Phylogenomics
Monday, June 23, 2014 8:45 AM-9:00 AM

Host genome defense against transposable elements (TEs) is complicated by off-target silencing effects. TEs that are epigenetically silenced by Piwi-interacting RNA (piRNA) can spread their silencing state to nearby genes as well as nucleate flanking non-TE sequences as new sources of piRNA. Host control of TEs can thus come at the cost of compromising local gene expression. Previous studies have found that maternal provisioning of piRNAs that target TEs is critical for maintaining TE repression across generations. In light of these studies, we are investigating the influence of maternal genic piRNA inheritance on patterns of gene expression in offspring. Results from the analysis of strains that contribute to a hybrid dysgenic syndrome in Drosophila virilis reveal differences in genic piRNA targeting, which allows for the analysis of how transgenerational genic piRNA pools influence gene expression in progeny. We find that differentially expressed genic piRNAs have variable effects on gene expression in future generations. In addition, the loci which are the targets of piRNA silencing in parents vary in the degree to which they produce piRNA in the next generation. Finally, global TE derepression seems to affect abundance of genic off-target effects. Thus, these small RNAs involved in germline TE defense can potentially influence gene expression variation in natural populations.

Ancient duplication of vomeronasal receptor class 1 (V1R) genes in lemurs

Anne Yoder, Peter Larsen, Mario dos Reis, Lauren Chan, Christopher Campbell, Joseph Bielawski

3A_303-Phylogenomics
Monday, June 23, 2014 9:00 AM-9:15 AM

Vomeronasal receptor genes have frequently been invoked as integral to the establishment and maintenance of species boundaries among mammals due to the elaborate one-to-one correspondence between semiochemical signals and neuronal sensory inputs. We report the most extensive sample of vomeronasal receptor class 1 (V1R) sequences ever generated for a diverse yet phylogenetically coherent group of mammals, the tooth-combed primates (suborder Strepsirrhini). Phylogenetic analysis confirms that we have intensively sampled from a single V1R subfamily, apparently unique to the strepsirrhine primates. We designate this subfamily as V1Rstrep. The subfamily retains extensive repertoires of gene copies that descend from an ancestral gene duplication that appears to have occurred prior to the diversification of all lemuriform primates excluding the basal genus Daubentonia (the aye-aye). Comparison of the two clades reveals different amino acid compositions corresponding to the predicted ligand-binding site and thus potentially to altered functional profiles between the two. In agreement with previous studies of the mouse lemur (genus, Microcebus), the majority of V1Rstrep gene copies appear to be intact and under strong positive selection, particularly within transmembrane regions. Finally, despite the surprisingly high number of gene copies identified by both Sanger and PacBio CCS methodologies, it is nonetheless probable that V1R diversity remains underestimated in these non-model primates.

Whole Genome Sequence of the Behaviorally Polymorphic White-Throated Sparrow 1: Mapping Genes for Socio-genomics

Elaina Tuttle, Marisa Korody, Teri Lear, Rusty Gonser, Marlys Houck, Oliver Ryder, Michael Romanov, Christopher Balakrishnan, Alan Bergland, Wesley Warren

3A_303-Phylogenomics
Monday, June 23, 2014 9:15 AM-9:30 AM

Chromosomal inversions are thought to lead to adaptation and speciation as they reduce recombination thereby protecting favorable genetic linkages. If this is the case, it is predicted that beneficial combinations of genes associated with fitness be located within chromosomal inversions. Here, we use whole genome sequencing and mapping with bacterial artificial chromosomes (BAC) to understand how gene arrangement leads to the morphological, behavioral, and physiological differences exhibited by two morphs of the white-throated sparrow (Zonotrichia albicollis). In this species, both sexes occur as white or tan morphs that have adopted alternative life-history strategies. Morph is determined by the presence or absence of a large rearrangement, which limits recombination of the second autosome. We have amassed 25 years of detailed data on this species making it possible to identify the genetic, epigenetic, and environmental bases of behavior. To begin these analyses we generated a high-quality 1Gb reference genome with N50 contig length of 104kb and scaffold length of 4.9Mb. We then used high-resolution BAC mapping to anchor the genome, and in doing so we were able to identify the breakpoint in this chromosome as well as several other smaller rearrangements of gene order. Despite considerable synteny in avian genomes, evolutionary analyses indicate minimums of 11 rearrangements between white and tan morphs, 35 rearrangements between chicken and sparrow, and 26 rearrangements between zebra finch and sparrow. Morphs of the white-throated sparrow provide a unique opportunity to study intraspecific genomic differences, which have resulted from two separate, yet linked evolutionary trajectories - such results can transform our understanding of the evolution of genomes as well as highlight the importance of inversions as drivers of evolution.

Whole Genome Sequence of the Behaviorally Polymorphic White-Throated Sparrow 2: Population Genomics

Christopher Balakrishnan, Alan Bergland, Rusty Gonser, Wesley Warren, Daniel Newhouse, Elaina Tuttle

3A_303-Phylogenomics
Monday, June 23, 2014 9:30 AM-9:45 AM

Chromosomal inversions are thought to contribute to adaptation and speciation as they reduce recombination, protecting favorable combinations of alleles. White-throated sparrows Zonotrichia albicollis are a remarkable species in which a major intraspecific structural polymorphism in the genome is perfectly associated with a suite of behavioral and morphological characteristics. This polymorphism, in combination with disassortative mating, leads to the stable maintenance of two “morphs” within the species. Among the behavioral traits that vary predictably by morph are key aspects of behavior including levels of aggression and parental care in both sexes. The unique features of this system have made white-throated sparrows a model system for the study of social behavior. With this is mind, we sequenced and assembled to the complete genome of the white-throated sparrow. Doing so, in combination with pooled whole genome resequencing (poolseq), enabled us to resolve the evolutionary and demographic history of the inversion. As expected, we find a bimodal distribution of Fst across the genome, with regions encompassing the inversion displaying high Fst (0.3) between morphs. We also find that the white morphs show essentially perfect linkage disequilbrium across the inversion. Analyses of allele frequency spectra suggest that the “white” form of the chromosome represents a large partial sweep with little recombination between the derived and ancestral chromosomes. Comparison with transcriptomic data from two songbird outgroups indicates that within the inversion, that the tan morph more closely resembles the ancestral form, suggesting a transition from a more highly parental, less aggressive form to a more territorial form represented by the white morph.

Climate variability may limit evolutionary adaptation to climate change in montane and alpine butterflies

Joel Kingsolver, Lauren Buckley

3A_305A-Climate and Evolutionary Change
Monday, June 23, 2014 8:30 AM-8:45 AM
Evolutionary potential will be important for the many organisms with limited ability to track long-term climate change via movement. We integrate biophysical, demographic and evolutionary models with climate data to explore selection and evolution of wing melanin on the posterior ventral hindwings in montane and alpine Colias butterflies in the Rocky Mountains. Higher levels of wing melanin increase the absorption of radiation and can dramatically increase body temperatures. The fitness surface (fitness as a function of wing melanin) has a single peak as a result of two opposing factors: wing melanin increases activity times and reproductive success in cool conditions, but can reduce egg production and adult survival due to short-term overheating. Mean summer temperatures have increased at both montane and alpine sites over the past 60 years, but with substantial variation among years. As a result the location of the fitness peak varies between years, producing temporal variation in the magnitude and direction of selection, especially at montane sites. Recent and future climate warming are predicted to cause evolutionary reductions in mean wing melanin, but the evolutionary responses of montane and alpine butterflies may be strongly limited by seasonal and annual variability in temperature and cloudiness in these regions.

Physiological adaptation of thermal sensitivity of Colias larvae in response to climate change

Jessica Higgins, Heidi MacLean, Joel Kingsolver, Lauren Buckley

3A_305A-Climate and Evolutionary Change
Monday, June 23, 2014 8:45 AM-9:00 AM
Understanding how local adaptation affects a population’s ability to respond to novel thermal regimes is increasingly important given recent climate change.We studied the temperature dependence (thermal performance curves, TPCs) of larval feeding rate for two populations each of Colias eurytheme and Colias eriphyle in North America that occur over a range of elevations and climates. Using historical data for two of the populations, we assessed changes over time in both climatic (Tair) conditions and TPCs for larval feeding. Populations at lower elevations with longer growing seasons had broader TPCs for larval feeding. In contrast, higher elevation populations with shorter growing seasons had higher optimal and maximal temperatures for feeding. Overall mean air temperatures during the growing season showed little change at the two sites, but the frequency of high air temperatures (>28°C) has increased markedly at both sites over the past 40 years. This climatic shift was associated with increased rates of larval feeding at higher temperatures (>28°C) in both populations. These results suggest that recent climate warming has led to physiological shifts in the TPCs for larval feeding in this system, implicating larval thermal adaptation as an important response that may ameliorate the fitness consequences of rapid climate change in insects.

Modeling and detecting biological responses to climate changeweather variability using first-principles of physiology and estimates of food resource

Catherine Graham, Susan Wethington, Donald Powers, Pieter Beck, Scott Goetz

3A_305A-Climate and Evolutionary Change
Monday, June 23, 2014 9:00 AM-9:15 AM
Predicting how species will respond to climate change and weather variability is critical if we are to mitigate the effects of these environmental changes. However, to date the vast majority of predictive models use statistical correlative methods to estimate how species geographic ranges might shift in response to climate changes. While these approaches provide valuable insight into how species might respond to climate change, they generally rely on long-term climate and do not uncover the mechanisms that influence species responses. Recent attempts to develop process-based models are starting to provide alternative ways to deal with the complex problem of predicting how species will respond to climate change. We add to this research agenda by developing a physiologically-informed modeling approach which uses fine-temporal scale remote sensing and weather data and long-term monitoring data to evaluate what factors influence behavioral and physiological responses of the Broad-tailed Hummingbird (Selasphorus platycercus). In doing so, we develop a mechanistic approach that can be applied to other organisms to explore how they might respond to climate change.

Genomics of adaptation to altitude in Mus musculus

Felipe Martins, Ke Bi, Sara M. Keeble, Jeffrey M. Good, Michael Nachman

3A_305A-Climate and Evolutionary Change
Monday, June 23, 2014 9:15 AM-9:30 AM
Organisms living at high altitudes are presented with physiologically and metabolically challenging conditions due to the reduction in barometric pressure and oxygen availability. Hypoxia can be detrimental to survival, and a powerful homeostasis system has evolved in animals to cope with fluctuations in oxygen concentration. Besides the plastic physiological response displayed by many organisms, there is strong evidence for genetic adaptation to altitude in humans and other vertebrates. We studied the genomic basis of adaptation to high elevation in the house mouse, Mus musculus, a species that has been recently introduced to high altitude. We collected mice from five populations along an altitudinal transect in Ecuador, from 0 to 3000 meters elevation. We sequenced 50 complete exomes representing 10 unrelated individuals from each of five localities. Associations between genotype and environmental variables were identified using a variety of approaches that attempt to control for the correlated histories of populations, including Bayenv2, LFMM and SPA. Using these approaches, the identified candidate genes mostly differed from those previously implicated in adaptation to high elevation in

humans. Nonetheless, the identified genes include VLDL, which is part of the cellular response to hypoxia, as well as SGPP2 and APC which are related to lung function. Other identified genes are linked to muscle development (TAF3, TMEM2, VSP13a) and adipose tissues (BRD8, Phb2). Changes at these genes may underlie adaptation to hypoxia, but might also reflect adaptation to the extreme temperature fluctuations at high altitudes.

Target Enrichment of Ultraconserved Elements in Sky Island Frogs of the Brazilian Atlantic Rainforest

Marcio Pie, Marcos Ricardo Bornschein, Luiz Fernando Ribeiro, Brant Faircloth, John McCormack

3A_305A-Climate and Evolutionary Change
Monday, June 23, 2014 9:30 AM-9:45 AM

The Brazilian Atlantic Rainforest (BAR) is characterized by a remarkable degree of diversity and endemism, particularly in montane areas. In particular, recent studies have suggested that these areas might have served as climatic refugia during the climatic oscillations of the Quaternary, yet studies to date have mostly focused on few species and loci, this limiting the power to distinguish alternative diversification scenarios. In this study we investigate two co-distributed anuran genera - Brachycephalus (Brachycephalidae) and Melanophryniscus (Bufonidae) - showing highly restricted populations limited to montane cloud forests in the southern BAR. Genetic variation among populations was assessed using target enrichment of ultraconserved elements, thus providing a highly robust assessment of both species phylogenetic relationships and the level of intrapopulation variability. Our results are consistent with the existence of many highly restricted (and still underscribed) species, some of which limited to a single mountaintop. Moreover, the timing of diversification of both genera is consistent with a common scenario of a climatic shift “trapping” populations into cloud forests, followed by a relative climatic stability that maintained their isolation. The implications of these discoveries to the conservation of microendemic montane species are discussed.

The Trojan Female Technique – A novel approach for pest population control

Neil Gemmell

3A_305B-Invasion and Evolution
Monday, June 23, 2014 8:30 AM-8:45 AM

Humankind’s ongoing battle with pest species spans millennia. Pests cause or carry disease, damage or consume food crops and other resources, and drive global environmental change. Conventional approaches to pest management usually involve lethal control, but such approaches are costly, of varying efficiency, and often have ethical issues. Thus, pest management via control of reproductive output is increasingly considered an optimal solution. One of the most successful such ‘fertility control’ strategies developed to date is the sterile male technique (SMT), in which large numbers of sterile males are released into a population each generation. However, this approach is time-consuming, labour-intensive and costly. We use mathematical models to test a new twist on the SMT, utilising maternally inherited mitochondrial (mtDNA) mutations that affect male, but not female reproductive fitness. ‘Trojan Females’ carrying such mutations, and their female descendants, produce ‘sterile-male’-equivalents under natural conditions over multiple generations. We find that the Trojan Female Technique (TFT) has the potential to be a novel humane approach for pest control. Single large releases and relatively few small repeat releases of Trojan Females both provided effective and persistent control within relatively few generations. Although greatest efficacy was predicted for high turnover species, the additive nature of multiple releases made the TFT applicable to the full range of life histories modelled. The extensive conservation of mtDNA among eukaryotes suggests this approach could have broad utility for pest control.

Baker’s General Purpose Genotype: Are highly tolerant weeds also the most fit?

Lindsay Chaney, Regina Baucom

3A_305B-Invasion and Evolution
Monday, June 23, 2014 8:45 AM-9:00 AM

As defined by Baker (1965), the ‘general purpose genotype’ (GPG) refers to a weed with a wide range of climatic and edaphic tolerances. It has been hypothesized that plasticity in fitness and fitness-related traits may underlie the GPG’s ability to enter new areas and thus become an invasive. One idea in particular that has been examined is that of ‘fitness homeostasis,’ or the ability to maintain fitness across new or damaging environments. Interestingly, the plant defense literature has been discussing ‘tolerance’ in the same vein for many years. Here we ulitize data from a large data set with 12 different weeds and/or invasive species planted in a variety of enviroments to investigate tolerance, as defined by the evolutionary ecology literature, both intra-specifically and in context of the GPG. Explicitly, we investigate the relationship between fitness and tolerance and tolerance and trait plasticity across many plant species to understand how to best describe the GPG.

Comparative QTL mapping, population genetics, and the parallel evolution of weedy rice

Xinshuai Qi, Kenneth Olsen

3A_305B-Invasion and Evolution
Monday, June 23, 2014 9:00 AM-9:15 AM

Agricultural weeds related to crops are especially challenging to agriculture. Understanding the origin and evolutionary history of these weeds is not only essential for weed control, but also of great interest to evolutionary biologists. In recent years, a worldwide crop mimic, weedy rice (Oryza sativa L., also called red rice), has infested rice fields and caused major reductions in crop yield. In the US, there are two major weedy rice strains, straw hull (SH) and black hull awned (BHA), that have been identified. Genetic surveys have demonstrated that they were derived from two Asian domesticated rice varieties: indica and aus. However, it is still unclear whether this parallel evolution of weediness has occurred through shared genetic mechanisms or not. Another question is the extent to which weedy rice populations found in world regions with wild Oryza species, such as Southeast Asia, have been influenced by genetic introgression from the wild populations. Here we first used GBS-derived SNPs to construct genetic maps of two

F5 recombinant inbred line populations, derived from crosses between each US weed form and indica rice. With dense SNPs across the rice genome, we were able to create two fine scale linkage maps, and identified 53 weedy rice QTLs. The mapping results showed that the similar phenotypic traits in the two US weedy rice strains are primarily controlled by different genetic mechanisms. We then did a parallel population genetic study focusing on the comparative weedy rice origins between the US, South Korea and Southeast Asia. STRUCTURE and PCoA analyses suggest that weedy rice populations in Cambodia, Thailand, Vietnam and Indonesia has a genetic admixture of crop and wild rice, which is different from the US, South Korea and Malaysian weedy rice. Our studies demonstrate multiple, parallel origins of weedy rice. This knowledge of weed origins is essential for future weedy rice control strategies.

The origin of south Asian red rice and weed competitiveness

Zhongyun Huang

3A_305B-Invasion and Evolution
Monday, June 23, 2014 9:15 AM-9:30 AM

Red rice (Oryza sativa) is an aggressive conspecific weed of cultivated rice, detrimental to rice agriculture systems worldwide. Previous research has suggested that the genetic background of red rice varies in different parts of the world. To account for this, various mechanisms for the origin of red rice have been proposed, including de-domestication from local crops, evolution from local wild rice, and hybridization between cultivars and wild rice. Red rice accessions collected from various places of the world may have evolved to have similar phenotypes making them successful weeds. The evolution of similar weedy traits from different ancestors or mechanisms makes red rice an ideal system to study parallel evolution. Previous assessments of US red rice show that there are two distinct populations, the BHA and the SH, with genetic resemblance to aus and indica cultivars respectively. To-date, there has been limited study of red rice populations that occur in South Asia, which is likely the center of domestication of the indica lineage of cultivated rice and also an area with high Oryza diversity. We characterized a panel of 186 accessions that includes South Asian weeds, US weeds, local wild rice, local cultivars of indica, aus and japonica varieties, and other Oryza outgroup species using Genotyping by Sequencing (GBS). Principle Component Analysis (PCA) and STRUCTURE analyses suggest that (1) there are multiple genetically differentiated groups in South Asian, with aus and some other local wild Oryza species contributing to South Asian red rice origins; (2) US weeds resemble subgroups of South Asian red rice but may have descended directly from Asian cultivars. We subsequently assessed red rice seed morphology (awn, hull color and seed color) from multiple genetically differentiated groups and their potential cultivar ancestors. Morphology traits assessment suggests that (1) there is a correlation between phenotype and genetic origins; (2) red rice is very different from its cultivated ancestors in terms of seed “weedy” traits. To investigate the possibility of selection leading to “weedy” trait occurrence, we applied Fst outlier tests to red rice subgroups and their cultivar ancestors. Loci that may be under selection or linked to loci under selection were detected from aus-resembling red rice subgroup. Current efforts to understand the growth performance of red rice varieties and the physiological traits that contribute to weed competitiveness will be discussed.

Clonal genotype influences behavior and response to predators in invasive New Zealand mud snails (Potamopyrgus antipodarum)

Edward Levri, T.J. Clark, Brittany Smith, Sarah Landis

3A_305B-Invasion and Evolution
Monday, June 23, 2014 9:30 AM-9:45 AM

The success of introduced species is determined by traits under selection that influence their invasion success. Behavior can be an important determinant of the success of a non-native species. In the New Zealand mud snail (Potamopyrgus antipodarum), behavior has been shown to be influential in predator avoidance, and behavior likely plays a role in dispersal. We investigated differences in behavior between different asexual clones of this species and compared introduced clones characterized by various levels of invasive ability and New Zealand native clones with respect to rheotactic, geotactic, photokinetic, and dispersal behaviors. We also examined the influence of predator detection on these behaviors. There was a significant difference in behaviors between clonal genotypes in each of the behaviors evaluated. Interestingly, the most invasive clone (US1) behaved most differently from the other clones demonstrating differences to other clones in all behaviors including a greater propensity to disperse. Differences between clones in their behavioral responses to the detection of fish predators were also found. These results indicate that there is a genotypic effect on behaviors in this freshwater snail, and this variation may help to explain why some clones are more invasive than others.

Shade avoidance and Brassica rapa leaf development: Bayesian modeling and QTL analysis allows for predicting phenotypes from genotypes

Robert Baker, Leong Wen Fung, Marcus Brock, Matthew Rubin, Stephen Welch, Cynthia Weinig

3A_306A-Trait Evolution
Monday, June 23, 2014 8:30 AM-8:45 AM

Leaves perform the crucial task of photosynthesis; therefor we examined the morphological development of leaves throughout ontogeny in an experimental segregating population of B.rapa (RILs). RILs were grown in crowded and uncrowded conditions over multiple years, and leaf length and width data were collected throughout ontogeny. We generated Bayesian models of leaf development and use parameters of these models in quantitative-genetic analyses to demonstrate that crowding affects leaf development, and that developmental patterns are correlated with photosynthetic rate, plant architecture as measured by spectroradiometric readings, circadian rhythms, and fitness. To explore the g*e interactions, model parameters describing leaf development were mapped to a high-density linkage map of B. rapa. In addition to uncovering significant g*e, this study highlights the importance of an ontogentic approach for understanding the genetic and environmental components of leaf development, because different QTL underlie growth rate and final leaf size. When predicting phenotypes based on genotypes, final measures of leaf size do not reveal important aspects of leaf morphology, especially growth dynamics during early development when leaf-based photosynthesis is particularly critical for carbon assimilation.

Evolution of leaf defenses in relation to environment and leaf economics across the genus Helianthus

Chase Mason, Lisa Donovan

3A_306A-Trait Evolution
Monday, June 23, 2014 8:45 AM-9:00 AM

Leaf defenses are physical or chemical traits that act to prevent herbivory. Because plant growth is ultimately limited by resource availability, plants are known to balance resource allocation to growth and defense in response to the environment, where species from low resource environments typically have slower growth and higher defense, and species from higher resource environments typically have faster growth and lower defense. Variation in growth rate strategies is well-described by the concept of the leaf economics spectrum, though to date this paradigm has largely ignored leaf defenses. This is curious, as many common traits considered defensive are either directly or indirectly involved in leaf economics, as defenses directly influence leaf lifespan and the initial leaf carbon and nitrogen investment. Unlike LES traits, leaf defenses have not been found to form a unified global axis of variation; rather, many different defense trait combinations can be employed to achieve a similar goal of reducing herbivory. While no evidence has been found for global syndromes of leaf defense across broad collections of plant families, it has been proposed that trade-offs could exist at lower levels of organization, such as within diverse genera. This study uses a phylogenetic comparative approach to investigate leaf defenses across wild sunflowers (the genus Helianthus) to explore the potential for evolutionary trade-offs between physical and chemical defenses, latitudinal and environmental gradients in defenses, and the relationship between leaf defenses and the leaf economic spectrum. Focal defense traits include leaf thickness, toughness, trichome density, tannin activity, lipid content, ash content, and leaf dry matter content.

A within-species comparative method reveals reproductive character displacement to a geographic mosaic of interspecific interactions

Deren Eaton, Richard Ree

3A_306A-Trait Evolution
Monday, June 23, 2014 9:00 AM-9:15 AM

The geographic mosaic theory of coevolution posits that variation within species results from differences in selection across the landscape. A common goal when investigating within-species variation is to detect correlated differences between phenotype and local environmental variables, but a confounding factor is that geographically proximate populations can exhibit similar phenotypes for two reasons: (i) parallel adaptations to similar environments, or (ii) because common ancestry or gene-flow causes them to be similar. Using genomic RADseq data I applied a migration-matrix based within-species comparative method to account for migration among populations in a widespread and variable species, Pedicularis cranolopha. We find that variation within P. cranolopha covaries with its local biotic environment composed of a mosaic of congeners across its range. Experimental crosses were performed to confirm the functional significance of floral differences within P. cranolopha, showing that interspecific interactions in this highly diverse plant group promote intraspecific divergences with the potential to promote speciation.

Fins as highly integrated building blocks promoting fish morphological disparity

Olivier Larouche, Richard Cloutier, Miriam L. Zelditch

3A_306A-Trait Evolution
Monday, June 23, 2014 9:15 AM-9:30 AM

Among fishes, actinopterygians have achieved a phenomenal ecological and evolutionary success: this group includes approximately 30 000 living species as well as an abundant fossil record. No less impressive is the extent of morphological disparity that can be observed among them, notably in terms of fin configurations, which includes position, size and shape. The diversity of fin morphologies might have been facilitated by a modular organization. As such, fins could constitute highly integrated sub-units that behave quasi-independently during ontogeny or evolution, making these structures evolvable and therefore explaining the observed patterns of morphological disparity. Several morphological (e.g., dorsal-anal fin positioning module), developmental (e.g., dorsal-anal and pectoral-pelvic patterning modules) and functional modules have already been proposed for median and paired fins. Using geometric morphometrics, we investigate the positional modularity of fins by analyzing patterns of morphological integration. More precisely, the aim is to establish which subsets of fins are quasi-independent and which are most highly integrated in terms of their positioning on the fish’s body. We have focused on two cyprinid species: the zebrafish (Danio rerio), a commonly used model organism, and the northern redbelly dace (Chrosomus eos), for which specimens come from a single lacustrine population. Several hypotheses of modularity were tested, including those based on functional demands, topological relationships, or previous results from a broad-scaled phylogenetic analysis focusing on the correlated presence/absence of fins. Hypotheses were evaluated using a combination of methods (e.g., minimum deviance method, matrix correlations, graphical modeling). Preliminary results suggest that if parts of the body and fins are constrained to belong to a single module, the best fitting models for both D. rerio and C. eos are those that predict that dorsal, anal and caudal fins constitute an integrated unit. In these preferred models, the paired fins are variably associated with either the head region or with the other median fins. This commonality suggests that patterns of integration and modularity are not species-specific but are rather phylogenetically conserved. Removing the constraints on the models, however, reveals that these integrated units preserve significant associations to other regions of the fish’s body.

The evolutionary origin and development of adipose fins, exploring novelty in vertebrate appendages

Thomas Stewart, Melina Hale

3A_306A-Trait Evolution
Monday, June 23, 2014 9:30 AM-9:45 AM

Characterizing the anatomy and development of evolutionary novelties is essential to understanding their origin. Adipose fins are appendages found in over six thousand species of actinopterygian, or ray-finned, fishes. These fins are positioned on the dorsal midline posterior to the dorsal fin and usually lack associated musculature and skeleton. This apparently rudimentary anatomy and their small size have led to hypotheses that adipose fins are non-functional and potentially vestigial. Hypotheses of adipose fin origin were revisited by applying models of ancestral state reconstruction to newly published phylogeny of actinopterygian fishes. These analyses find support for adipose fins having evolved repeatedly. This result is consistent with the known distribution of adipose fins in the fossil record. As convergent morphologies, we argue that adipose fins are likely adaptive, although their function remains untested. To begin exploring the developmental and genetic basis of these fins, we describe adipose fin ontogeny in Corydoras aeneus (Callichthyidae), a South American armored catfish. Antibody staining is used to characterize adipose fin neuroanatomy. In C. aeneus, adipose fin development involves the retention and elaboration of a larval structure, the median fin fold (MFF). During adipose fin development, mesenchyme migrates into the MFF and condenses to form an ossified adipose fin spine. This ossification begins halfway along the proximo-distal axis of the MFF and then extends both proximally and distally until it reaches the body wall, at which point adipose fin nerves are apparent. These nerves originate from dorsal rami of the spinal cord and possibly also from the recurrent ramus of the facial nerve. In adults, a primary adipose fin nerve runs along the proximo-distal axis of the fin, posterior to the fin spine. This primary nerve repeatedly ramifies, extending projections along the antero-posterior axis of the fin, which terminate as free nerve endings. This anatomy suggests that the adipose fins of C. aeneus have sensory potential, consistent with the hypothesis that they function as flow sensors. Additionally, we compare adipose fin development in C. aeneus to what is known of other species and also of other fin systems.

The role of selection in the rapid evolution of reproductive genes: are we using the correct null hypothesis?

Amy Dapper, *Michael Wade*

3A_306B-Sexual Selection
Monday, June 23, 2014 8:30 AM-8:45 AM

Male reproductive genes tend to have elevated levels of divergence among species, a pattern frequently attributed to strong sexual selection acting on these genes within species. We model the expected level of polymorphism and divergence for sperm protein genes evolving by post-copulatory, pre-zygotic fertility competition. We find that, in theory, both the equilibrium level of polymorphism at mutation-selection balance, as well as the expected level of divergence between species, are functions of the harmonic mean number of mates per female: the greater the harmonic mean number of mates, the stronger the intensity of male-male sperm competition. We compare the theoretically expected levels of polymorphism and divergence of sperm competition genes with the observed levels of polymorphism and divergence in 17 Drosophila melanogaster male reproductive protein genes. We find that the observed levels of elevated sequence variation for male reproductive genes are better explained by relaxed selection than by any of the adaptive hypotheses proposed to date. We argue that tests of specific adaptive hypotheses require more robust theoretical predictions and we propose such a method for discriminating among alternative hypotheses.

Sexual selection and sperm competition in a widespread dung fly, Sepsis punctum (Diptera: Sepsidae)

Nalini Puniamoorthy, *Scott Pitnick*

3A_306B-Sexual Selection
Monday, June 23, 2014 8:45 AM-9:00 AM

Post-copulatory sexual selection and sperm competition have been suggested to drive reproductive trait divergence and speciation in various animal groups. Theory predicts that males have limited resources to invest in reproduction, which they must allocate to mate acquisition as well as insemination and competing for fertilizations. Because adaptations to both episodes of selection may be costly, trade-offs are predicted to arise between traits that influence pairing success and those that enhance fertilization success. In recent work, we demonstrate a geographic reversal in sexual size dimorphism (SSD) in the widespread dung fly Sepsis punctum (Diptera: Sepsidae), where males are larger than females in Europe (EU) and females are larger in North America (NA). We find higher female (re-)mating rates among EU populations, where larger males acquire more matings and face a high risk of sperm competition. Consequently EU males have not only evolved larger testes and steeper hyper-allometry with body size but also longer sperm. In sharp contrast, NA populations display much reduced, if any, effect of body size on those traits, with males producing sperm that is almost half the length in EU. Instead, NA males have a distinctive abdominal courtship display that is completely absent in EU and varies in intensity between eastern and western populations. Finally, a phylo-geographic approach using mitochondrial and microsatellites markers recovers distinct clusters that show clear isolation-by-distance within the continents. Hence, the spatial differentiation in genetic structure, the associated changes in behavior and SSD, coupled with varying intensities of sperm competition, suggest a shift in mating systems and incipient speciation in this species.

Partitioning additive and nonadditive genetic effects on offspring quality in a broadcast spawning marine invertebrate

David Aguirre

3A_306B-Sexual Selection
Monday, June 23, 2014 9:00 AM-9:15 AM

In sexual selection, females can choose to mate with either males of higher genetic quality, or more genetically compatible males. Choice for both male quality and male compatibility increase female reproductive success by increasing the genetic quality of her offspring. Studies on broadcast spawning species have shown that species recognition happens at the level of gametes – eggs can recognize sperm of the same species, and it appears that this gamete-level choice also occurs within species. Some male × female combinations of gametes result in higher fertilization success than others, but whether this reflects female choice for male quality or genetic compatibility remains unknown. Here, we used a diallel breeding design to partition additive genetic (i.e. genetic quality) and nonadditive genetic (i.e. genetic compatibility) effects on the association between fertilization success and offspring quality in the broadcast spawning ascidian Ciona intestinalis. We found that genetic quality effects were weaker than genetic compatibility effects. In addition, eigenanalysis of the additive genetic and nonadditive genetic covariance matrices indicated that the dimensionality of genetic quality effects was less than the dimensionality of genetic compatibility effects. Last, rotating the genetic space to align with the axis maximising associations between fertilization success and offspring quality revealed differing effects of genetic quality and genetic compatibility on offspring – genetic quality effects at fertilization were most strongly associated with increases in larval survival, whereas genetic compatibility effects at fertilization were most strongly associated with increases in juvenile survival. Overall, our results suggest that gametes that are more compatible at fertilization result in higher performing offspring. Furthermore, we provide evidence that mate-choice can occur in the ancestral reproductive strategy of broadcast spawning.

Shifting lines in the sand: determinants of spatiotemporally dynamic opportunities for sexual selection in a polygynous mammal

Jeff Manning, Philip McLoughlin

3A_306B-Sexual Selection
Monday, June 23, 2014 9:15 AM-9:30 AM

Opportunities for sexual selection in animal populations involve sex ratio, competition for limited resources and mates, and the presence of non-mating males. Although these factors can vary spatially and temporally within a population, we know little about how this variability may manifest itself in opportunities for selection. We quantified spatially explicit local densities, adult sex ratios, opportunities for selection associated with harem and mate acquisition, and harem dispersion among males over 5 breeding seasons in a 300-year-old feral horse population on Sable Island, Canada. Density and distance from a limiting resource (freshwater) showed pronounced interactive effects with weather (drought conditions) in determining spatiotemporal variability in sex ratios, and effects of non-mating males were also evident. Density of non-mating males explained much of the spatial variability in the opportunity for selection associated with acquiring a harem beyond that explained by sex ratio, whereas distance from water best explained mate acquisition. Distance from water also contributed substantially to harem dispersion, and interacted with drought conditions to drive a spatiotemporally shifting boundary of under-dispersion in harems (i.e., opportunities for male selection) across the island. Understanding how sex ratio and opportunity for selection vary spatially according to environmental conditions and in accordance with inter-annual weather is critical for predicting how sexual selection may respond to changes in resource availability and climate change.

The evolutionary importance of male and mutual mate choice

Ingo Schlupp

3A_306B-Sexual Selection
Monday, June 23, 2014 9:30 AM-9:45 AM

Male mate choice is increasingly recognized as important. I will look at the role of male mate choice in an extreme system, where male choice has a very important role. I will place this example in a broad context and suggest approaches and methods to advance the field.

Comparative transcriptomics identifies the gene repertoires underlying functional differentiation of spider silk glands

Nadia Ayoub, Thomas Clarke, Jessica Garb, Cheryl Hayashi

3A_306C-Transcriptomes and Adaptation
Monday, June 23, 2014 8:30 AM-8:45 AM

Spiders (Araneae) are exceptional among silk producing arthropods for the diversity of silk types and functions found within and among species. Araneoids, a mega-diverse clade of spiders that spin orb-webs, sheet-webs, and cobwebs, possess up to seven specialized abdominal gland types that each produce silk fibers or glues with distinctive mechanical properties that correspond to a particular function. Some silks have multiple functions, such as the fiber produced by the major ampullate glands, which forms the dragline as well as the frame and radii of the orb-web. Other silks are devoted to a single purpose, such as the fibers from the tubuliform glands that are used only to protect eggs. Almost all molecular studies of spider silks have focused on members of the gene family that encode the fibers' primary structural proteins – spidroins. Each of the spidroin paralogs characterized thus far appears to have gland-specific expression. For instance, major ampullate silk is composed of two spidroins encoded by MaSp1 and MaSp2, and the egg case silk is primarily composed of the spidroin expressed in the tubuliform glands, TuSp1. Recently, high throughput sequencing of genes expressed in the silk glands of the Western black widow, Latrodectus hesperus, identified ~650 transcripts that were significantly more abundant in silk glands than other tissues, suggesting a far more complex silk protein system than previously recognized. Here we describe gene expression patterns of all seven of the functionally differentiated silk gland types in three species of cob-web weaving spiders including the Western black widow. GO term analysis of differentially expressed transcripts identified similar functions enriched in each of the differentiated gland types in all three species, including oxidation-reduction, extracellular exportation, and lipases. Intriguingly, the identity of these transcripts in each of the individual gland types is unique – e.g. different paralogs are expressed in each of the gland types within a single species. Thus, silk glands types share basic functions, with functional differentiation achieved through the evolution of gland-specific expression of paralogs.

Spider Transcriptomes Identify Ancient Large-Scale Gene Duplication Event and its Role in Silk Gland Evolution

Thomas Clarke, Nadia Ayoub, Jessica Garb, Robert Haney, Cheryl Hayashi

3A_306C-Transcriptomes and Adaptation
Monday, June 23, 2014 8:45 AM-9:00 AM

Spiders (Order Araneae) evolved silk production more than 392 million years ago. Since that time the silk producing glands have diversified into numerous morphologically distinct types that each produce task-specific fibers composed of unique proteins that derive from a single gene family. Large-scale gene duplication events are thought to contribute to the evolution of such novel tissues and functional diversity. While a large-scale duplication event has been hypothesized to have occurred within spiders, its age and influence on the evolution on the silk glands is not known. Using high-throughput sequencing of RNAs expressed in 12 tissues of three cobweb weaving spider species, we de novo assembled transcriptomes and identified numerous paralog pairs of similar age, supporting an ancient Large-Scale Spider Duplication event (LSSD). We compared these paralogous transcripts to orthologs from previously published partial transcriptomes from seven other spider species, and estimated the age of duplication events relative to spider speciation events. The distribution of the number of synonymous substitutions per synonymous site (dS) for duplication events was similar to the distribution of dS for the divergence of the two spider suborders, Araneomorphae and Mygalomorphae (~300 mya). Transcripts expressed exclusively (or at significantly higher levels than other tissues) within the silk glands were more likely to have a paralog dating to the ancient duplication event compared to generally expressed transcripts. Additionally the silk-specific transcripts show elevated amino acid replacement rates compared to generally expressed transcripts, in part due to relaxed selection on paralog pairs relative to single copy genes. However, the elevated amino acid replacement rates in silk-specific transcripts compared to their generally expressed counterparts does subsist even when correcting for gene family size. We propose that the LSSD post-dates the origin of silk glands in spiders, but contributed to the diversification of silk glands through the co-option of multiple genes for silk gland-specific expression.

Natural selection maintains high diversity in candidate genes underlying local adaptation to climate: evidence from whole-transcriptome sequencing

Paul Gugger, Shawn Cokus, Juan Manuel Peñaloza Ramírez, Victoria Sork

3A_306C-Transcriptomes and Adaptation
Monday, June 23, 2014 9:00 AM-9:15 AM

Understanding the genetic basis of the local adaptation of populations to different environments is a major goal of evolutionary biology. Two ways to identify genetic loci important in local adaptation are 1) identifying single-nucleotide polymorphisms (SNPs) that are extremely correlated with climate and 2) identifying genes that are differentially expressed by different populations under climate stress. We applied these approaches to populations of valley oak (Quercus lobata), an ecologically important California oak whose distribution has long been stable within a heterogeneous landscape, offering opportunity for local adaptation. To this end, we assembled a 73-Mb reference transcriptome composed of at least 12,000 complete transcripts and confidently called genotypes at over 200,000 SNPs for 22 valley oak individuals from throughout its natural distribution. Using a linear mixed modeling approach (EMMAX) that accounts for background population genetic structure (i.e. kinship), we identified dozens of SNPs from dozens of genes that are extremely associated with climate variables. We then performed a greenhouse experiment exposing 12 seedlings from 4 climatically different sample sites to drought stress and measuring changes in gene expression before and after. We found thousands of differentially expressed genes. Genes with SNPs strongly associated with climate in natural populations were significantly overrepresented in the list of differentially expressed genes in the greenhouse experiment, providing strong evidence for their role in adaptation to local climate. These candidate genes had significantly higher nucleotide diversity and polymorphism rates than non-candidate genes, suggesting that spatially/environmentally varying natural selection maintains diversity in genes important in local adaptation to climate.

The genomics of adaptation and divergence in a wild sunflower

Brook T. Moyers, Loren H. Rieseberg

3A_306C-Transcriptomes and Adaptation
Monday, June 23, 2014 9:15 AM-9:30 AM

Helianthus argophyllus is a wild sunflower that exhibits striking phenotypic variation across its small native range in south Texas. Populations growing on the coast include some individuals who flower early, in mid-Summer, and grow only about a meter tall, while other individuals flower in early Fall and can reach heights of over four meters. Populations growing inland are almost uniformly tall and late flowering. In a common garden, late flowering plants produced more flowers, potentially due to their longer growing season, but our 2011 field study of natural selection in wild populations shows strong evidence for directional selection on early flowering, especially in coastal populations. A comparison of flowering time and height QST values to nuclear SNP FST values supports this hypothesis of divergent selection. We then investigated the genetic architecture of adaptation and divergence in this system, using transcriptome data to identify outlier loci and peaks of genomic divergence between inland and coastal populations. Candidate genes for salt tolerance are associated with peaks of genomic divergence, which is sensible given the saline habitats of coastal populations. However, we found no genes related to flowering time among the outlier loci or underlying the divergence peaks, suggesting that selection on another trait may be acting pleiotropically on flowering time, or that the key differences may be in non-coding regulatory sequence.

Facultative endohyphal bacterial symbionts alter phenotypes of fungal endophyte hosts

Kayla Arendt, David Baltrus, A Elizabeth Arnold

3A_402-Symbiosis
Monday, June 23, 2014 8:30 AM-8:45 AM

Plant-associated fungi provide important ecosystem services as pathogens, mycorrhizae, endophytes, and saprotrophs. Endophytic fungi colonize healthy, living plant tissues in all biomes, often providing protection from pathogens, herbivores, and other environmental stressors. Saprotrophic fungi are the primary decomposers of senescent plant materials, cycling nutrients by breaking down cellulose and lignin. Many fungi play more than one of these roles throughout their life cycles, with functional switches in ecological modes driven in part by interactions with additional microbes. Recently diverse endophytic fungi were found to harbor endohyphal bacteria (EHB), which live within apparently healthy, viable fungal cells. Differences in suites of EHB between closely related fungal endophytes suggest horizontal transfer of these symbionts in nature. This relationship appears facultative for both partners, as bacteria can grow freely under laboratory conditions and we have successfully cured fungi of their EHB. Furthermore, we have developed re-association techniques to examine phenotypic changes associated with bacterial symbiosis under laboratory conditions.

We found that the presence and identity of EHB significantly influenced the success of plant infection by fungal endophytes, and that these effects display some host-specificity. Relative to axenic controls, fungal cultures infected with EHB grew significantly more rapidly on senescent tissue of their native host, and more effectively degraded senescent foliage. In vitro assays revealed that EHB can significantly alter cellulase activity and ligninase production of their fungal hosts. Because EHB can have drastic effects on fungal phenotypes and plant-fungal symbioses, and can be horizontally acquired, we suggest that they can influence plant-fungal interactions, resultant ecosystem services, and the functional diversification of plant-associated fungi, especially with regard to the saprotroph-endophyte continuum.

Asymmetric host resources affect mycorrrhizal responses to host relatedness

Amanda File, John Klironomos, Susan Dudley

3A_402-Symbiosis
Monday, June 23, 2014 8:45 AM-9:00 AM

Mycorrhizal colonization of soil and plant roots has been demonstrated to depend upon the relatedness of the group of plants, i.e. whether they are siblings or strangers. However, the symmetry or asymmetry of resources available to each plant may also have important implications on the symbiosis. Since mycorrhizal hyphae connect neighbouring plants, an individual with less to give to the fungal partner could act as a freeloader and effectively cheat by paying less carbon while still reaping benefits from its neighbour's contributions to the fungus. But kin selection should favour a well-supported fungal partner even when siblings are experiencing asymmetric resource availability. Here we show that fungal responses to the relatedness of a pair of Plantago lanceolata plants depends on whether one plant, neither plant, or both plants are shaded. In particular, when shading was asymmetric, sibling pairs had greater fungal colonization than stranger pairs. These results indicate that siblings will cooperate to help their shaded neighbour but strangers will not. Thus plants can show altruism to relatives by maintaining a strong fungal network.

An Investigation of Bacterial and Fungal Symbionts of the Planthoppers (Hemiptera: Fulgoroidea)

Julie Urban, Jason Cryan

3A_402-Symbiosis
Monday, June 23, 2014 9:00 AM-9:15 AM

Planthoppers (Hemiptera: Fulgoroidea) are a diverse superfamily of phytophagous insects with more than 14,000 species in 21 families described worldwide. Planthoppers, and other lineages within the hemipteran suborder Auchenorrhyncha, are unusual in that they appear to house a variety of multi-species assemblages of endosymbionts -- a condition that has been described as a "hunger for symbionts." Although these symbiotic associations have been examined in other auchenorrhynchan lineages, planthopper symbionts have remained largely unexplored and uncharacterized. Using capillary-sequencing as well as metagenomics deep sequencing of regions of 16S and 18S rDNA, we surveyed exemplars of 18 planthopper families to identify planthopper-associated bacteria and fungi. We present these results in the context of our reconstructed planthopper phylogeny, allowing us to interpret symbiont co-occurrences, losses, and replacements in light of known evolutionary patterns of host plant usage.

Disentangling the coevolutionary histories of animal gut microbiota

Jon Sanders, Nathaniel Bresnick, Aaron Behr, Corrie Moreau, Daniel Kronauer, Naomi Pierce

3A_402-Symbiosis
Monday, June 23, 2014 9:15 AM-9:30 AM

To what extent does coevolutionary history shape commensal microbial communities? Partner fidelity, linking fitness outcomes among partners, is thought to be an important stabilizer in mutualisms; over long enough timescales, it may result in codiversification, as is frequently observed in the vertically transmitted endosymbionts of insects. But can historical partner fidelity operate effectively on complex extracellular communities, in the face of competition from exogenous microbes and greater opportunity for horizontal transmission?

Here, using two ant genera as test cases, we introduce methods to explore whether individual lineages of gut bacteria have codiversified with their animal hosts. Beginning with a host genus (Polyrhachis) known to harbor the codiversifying endosymbiont Blochmannia, we demonstrate that 16S rRNA amplicon sequence data can reveal expected patterns of codiversification with both specificity and some sensitivity. Extending this analysis to an ant genus known to harbor a dense and specific bacterial gut community (Cephalotes), we recover patterns of codiversification across a taxonomically diverse subset of the microbiota. We then use shotgun metagenomic sequencing to verify and elaborate these findings, estimating well-supported multi-gene phylogenies for the some of the most abundant microbial taxa. Finally, we demonstrate the general utility of these tools by identifying candidate codiversified bacterial lineages in published comparative metagenomic datasets for mammals in general and hominids specifically. We show that putatively codiversified bacterial lineages recovered from these datasets are also present in human microbiota -- though at significantly different abundances in some groups of humans than in others.

Our results suggest that partner fidelity can be sufficiently strong to link the fates of host and gut microbe over millions of years of evolution. As additional comparative microbiome data become available, the techniques presented here will become a powerful tool for exploring broad trends in the evolution of host-associated microbial communities.

Where are all old fungal ectomycorrhizal lineages?

Martin Ryberg

3A_402-Symbiosis
Monday, June 23, 2014 9:30 AM-9:45 AM
Ectomycorrhiza (ECM) is a root associated symbiosis between fungi and, mostly woody, plants where the fungi get energy rich carbon compounds from the plant in exchange for nutrients such as nitrogen. Many stand forming trees, especially in the boreal region, depend on ECM for their nutrient supply. ECM fungi are one of the most diverse fungal guilds, both regarding number of species and number of separate evolutionary lineages. There are still many questions about the evolution of fungal ECM lineages that needs to be answered to understand this diversity, among those their ages. Pinaceae is the putatively oldest ECM plant lineage. It most likely originated in the Jurassic or Early Cretaceous. Many major ECM angiosperm plant groups are younger with origins in the Late Cretaceous. Halling (2001), logically, proposed that ECM fungi also evolved in the Jurassic with a boost in diversity in the Late Cretaceous. However, Bruns at al. (1998) observed that many ECM clades reside on shallow nodes, indicating young ages, and they consequently suggested that ECM fungi diversified more recently together with the expanding ECM dominated temperate forest after the mid-Eocene climatic optimum. Recent studies estimating the age of fungal ECM lineages using molecular clocks tend to give relatively young ages with origins in the Late Cretaceous or Paleogene. Here I will review the evidences for the different hypotheses and discuss different explanations to why we do not observe older ECM lineages. I will also present some preliminary results from a dated phylogeny of the Agaricomycotina, the subphylum that contain >90% of the known fungal ECM species.

Reproductive isolation and the causes of speciation rate variation in nature

Dan Rabosky

3A_BalC-ASN Solicited Symposium: Beyond reproductive isolation: microevolutionary controls on macroevolutionary speciation dynamics
Monday, June 23, 2014 8:15 AM-8:45 AM
Species richness varies dramatically across the Tree of Life: some groups of organisms contain tremendous numbers of species, yet many other groups are species poor. At least some of this variation can be attributed to differential rates of species formation. I will explore the relationship between intrinsic reproductive isolation and speciation rates as measured at macroevolutionary scales. I will also describe several challenges in developing a hierarchical theory of speciation that can account for macroevolutionary speciation dynamics in terms of population-level processes.

Geographic range size and speciation

Kaustuv Roy, Emma Goldberg, Danwei Huang

3A_BalC-ASN Solicited Symposium: Beyond reproductive isolation: microevolutionary controls on macroevolutionary speciation dynamics
Monday, June 23, 2014 8:45 AM-9:15 AM
Geographic range size is known to influence macroevolutionary dynamics through its effects on extinction and species durations. In contrast, the relationship between range size and speciation rate still remains poorly explored. While many authors, starting with Darwin, have postulated a positive relationship between geographic range size and speciation, others suggest a negative association. Empirical analyses of this relationship are still relatively scarce and comparisons across studies are hampered by substantial differences in data and methodologies used.

Testing whether range size positively or negatively correlates with speciation dynamics is not straightforward since range size, unlike most traits, is not only an emergent, species-level trait but is also known to change over the lifespan of a species. Thus the present day range size of a species is likely to be a poor proxy for events earlier in its history. Furthermore, paleontological data suggest at least two distinct models of how range size evolves over the lifespan of a species.

In this talk we will use simulations in conjunction with paleontological and phylogenetic data to investigate how geographic range size influences speciation dynamics. In particular, we will explore how contrasting models of range size evolution affect our ability to reconstruct the influence of range size on past speciation events.

Zen and the art of speciation

Erica Rosenblum

3A_BalC-ASN Solicited Symposium: Beyond reproductive isolation: microevolutionary controls on macroevolutionary speciation dynamics
Monday, June 23, 2014 9:15 AM-9:45 AM
It often appears difficult to reconcile speciation rates inferred from studies spanning different time scales. Speciation rates derived from studies of young evolutionary radiations are often much faster than those derived from studies over deeper time scales. However, the concept of "ephemeral speciation" can help bridge this gap. In the ephemeral speciation model, speciation is common and rapid but species rarely persist. We will look at the past history and present role of the ephemeral speciation concept in evolutionary biology. We will also discuss how evolutionary factors operating at the population level can affect speciation rates over deeper time scales.

Coevolution of Complexity as Seen by a Digital Host's Adaptive Landscape

Luis Zaman

3B_201-Evolution of Complexity
Monday, June 23, 2014 10:15 AM-10:30 AM

The world is populated by incredibly diverse and complex organisms, yet probably had only a single simple origin. While evolution often results in more complex organisms, complex traits are not necessarily adaptive. How can we reconcile the evolutionary process, which does not intrinsically produce complexity, with the overwhelmingly complex organisms all around us? One hypothesis is that arms races driven by antagonistic coevolution produce complexity as increasing defenses and counter-defenses evolve. We find evidence for this hypothesis using coevolving digital organisms, where parasites steal processing power from their hosts. But, instead of trait escalation, we find that a diverse community of interacting hosts and parasites is necessary for complexity to evolve. We demonstrate that these community effects actually deform the host's fitness landscape in a way that favors the evolution of increased complexity. These results highlight the importance of biotic interactions in evolution, and provide a hypothesis about how coevolution could drive complexity. In addition to direct selection for complex traits, we also find that hosts end up in a more evolvable region of the genetic landscape when they coevolved with parasites.

Extending the concept of diversity partitioning to characterize phenotypic complexity

Zachary Marion, James Fordyce, Ben Fitzpatrick

3B_201-Evolution of Complexity
Monday, June 23, 2014 10:30 AM-10:45 AM

Many if not most phenotypes can be considered complex traits, consisting of multiple subsidiary parts that function and evolve as integrated units. These trait complexes vary qualitatively in their individual components (e.g., chemical compounds, cell types, genes expressed) and quantitatively in the counts, concentrations, or amounts of those components. As trait complexity increases, so does the challenge of measuring and analyzing that complexity in intuitive yet biologically meaningful ways that capture both qualitative and quantitative aspects of the variation. Ecologists have long formalized community complexity in terms of well-known diversity indices. We extend that conceptual framework to describe phenotypic complexity as the diversity—or effective number—of distinct subsidiary traits making up an individual's phenotype. Then, using a hierarchical framework, we illustrate how the total phenotypic diversity within a particular level (e.g., individual, species, life-history strategy) can be partitioned into within-group (i.e., α diversity, average effective number of subsidiary traits in a replicate) and between-group components (β diversity, effective number of completely dissimilar trait combinations). We then demonstrate the utility of our method with an example from the evolutionary ecology of chemical defense to illustrate biologically significant differences in complexity and diversity that standard analyses would not reveal. Our unified, hierarchical view of complexity and diversity shows how analytical methods developed in population genetics and community ecology can be used to characterize complex phenotypes, and helps place questions about the ecology and evolution of complexity in a population/community context.

The evolution of placentae; complex trait evolution can be constrained by ancient features of an organism's genome

Oliver Griffith, Matthew Brandley, Katherine Belov, Michael Thompson

3B_201-Evolution of Complexity
Monday, June 23, 2014 10:45 AM-11:00 AM

Understanding how complexity has evolved in multicellular organisms has been a pursuit of science since Darwin published on the origin of species in 1859. Convergent evolution provides a unique opportunity to study the evolution of complex structures in slowly evolving organisms because of replication of the evolutionary process, and can allow scientists to draw conclusions about evolutionary processes that may otherwise be limited to studies utilising rapidly evolving microorganisms. A fascinating example of convergence is the evolution of placentae in amniotes (mammals, birds and reptiles), which has occurred frequently, most notably in the eutherian mammals, which ultimately gave rise to humans. Placentae are complex organs that facilitate maternal-embryo interactions in live bearing animals. We identified genes important for placental functions in the southern grass skink (Pseudemoia entrecasteauxii) using transcriptome sequencing. To identify if there was redundancy or constraint in the genes available for the evolution of complex traits we tested if there was convergent or divergent use of amino acid transport protein genes in P. entrecasteauxii and human placenta. Both linneages have evolved the complex funciton of placental protein transport by using the same non-randomly selected amino acid transport protein genes, suggesting that the genome has retained constraints on the way its genes can be utilised for the evolution of novel traits that arose more than 300 million years ago.

Ribozyme plasticity and molecular trade-offs can account for increasing complexity and network stability at the origin of life.

Nisha Dhar, Marco Weinberg, Richard Michod, Pierre Durand

3B_201-Evolution of Complexity
Monday, June 23, 2014 11:00 AM-11:15 AM

In the RNA-world hypothesis large ribozymes capable of enzymatic functions like polymerization and recombination were essential for life to begin. However, a knowledge of how complex ribozymes emerged from simple oligomers (

Horizontal transfer and size evolution in yeast mitochondrial genomes

Weilong Hao

3B_201-Evolution of Complexity
Monday, June 23, 2014 11:15 AM-11:30 AM

Mitochondrial (mt)DNA recombination not only takes place within species, but also takes place between different species, which is often referred as horizontal gene transfer (HGT). HGT in mtDNA has not been systematically studied in yeast. Based on our previous findings that recurrent mtDNA recombination has occurred in various intronic regions of the 21S rRNA between Saccharomyces cerevisiae and a subset of Torulaspora strains, we took a whole genome sequencing approach and sequenced the mtDNAs of eight Torulaspora strains in four species pairs. Our results observed horizontal transfer in a majority of mitochondrial introns, which opens the door to questions on whether mtDNA HGT is indeed frequent in yeast, but has largely been overlooked. We also observed evidence of small-scale horizontal transfer in the protein coding regions, raising the question on whether HGT plays a significant role in altering mitochondrial protein coding capacity in yeast. Furthermore, there is a significant genome size variation among these yeast mitochondrial genomes, which would serve an excellent model system to study the evolution of genome complexity. In recent years, the mutation burden (MB) hypothesis has emerged as a potentially unifying explanatory framework arguing for a central role for nonadaptive processes such as mutation and drift in the evolution of genome size and complexity. Among these variable, but also closely related, mitochondrial genomes, we will discuss the possible evolutionary processes that introns, AT-rich sequences, and GC-clusters act together to drive the evolution of yeast mitochondrial complexity.

Structure of geno- and phenotypic variation in a radiation of island amphibians

Simon Maddock

3B_206-Evolution on Islands
Monday, June 23, 2014 10:15 AM-10:30 AM

The Seychelles archipelago, partially a microcontinent, is unique among isolated island systems because of the occurrence of (possibly ancient) radiations of amphibians that have been separated from mainland relatives for at least 65 million years. One of these radiations contains six nominal species in three genera of a relatively unknown order (Gymnophiona), the limbless caecilians. The Seychelles species are unique in comprising the only island radiation of caecilians worldwide, and for a small group they have notable morphological and ecological diversity. However, little previous work has been carried out and the group's internal phylogenetic relationships have defied resolution. As with other amphibians, caecilians are considered intolerant to saltwater, yet all but one Seychelles species occurs on more than one island, raising questions about within- and among-island variation (and gene flow) and potential cryptic taxonomic diversity. Based on extensive fieldwork (> 1,000 person days), we have identified new island records for some species. Analyses of multilocus molecular and external and cranial morphological data indicate that intraspecific variation is not similarly spatially structured in all species, and that differences do not wholly match predictions from ecology. Phylogenetic analyses provide support for at least one previously unidentified species and a possible case of convergent dwarfism within Seychelles caecilians.

The phylogeography of Peromyscus maniculatus across the northern California Channel Islands

Paul Durst, *V. Louise Roth*

3B_206-Evolution on Islands
Monday, June 23, 2014 10:30 AM-10:45 AM

The California Channel Islands, off the coast of Southern Caliornia, host a unique flora and fauna highlighted by a large number of noteworthy endemic species such as (now extinct) pygmy mammoths, the giant coreopsis and the island fox. Among resident species, the deer mouse, Peromyscus maniculatus, is the only mammal found on every island and each island has its own morphologically distinct subspecies; yet the pattern and timing of the colonization and diversification of deer mice across the Channel Islands remains poorly understood. To shed light on the phylogeography of P. maniculatus across the northern Channel Islands, we collected samples from all five of the islands in Channel Islands National Park along with two mainland sites and we sequenced a 394 base pair region of the mitochondrial control region as well as 5 microsatellite loci. Classical population genetics parameters, phylogenetic analyses, and a statistical parsimony haplotype network for the control region point to significant differentiation between island and mainland populations. Shared haplotypes between the islands and one but not the other of the two mainland sites suggest a potential origin for the island populations. The microsatellite loci revealed a great deal of genetic diversity, and Cluster and Migrate analyses suggest a complicated colonization history influenced by male-biased dispersal between islands.

Resolving the complex evolutionary history of a Philippine songbird with genome-wide markers

Peter Hosner

3B_206-Evolution on Islands
Monday, June 23, 2014 10:45 AM-11:00 AM

Inferring historical relationships between lineages of organisms can be a major challenge, especially when different data sources conflict. In the yellow-bellied whistler (Pachycephala philippinensis), a polytypic bird species found in the Philippine archipelago, phylogenetic inference based on mitochondrial DNA resulted in puzzling relationships that contradicted subspecies boundaries (based on plumage variation) and prevailing biogeographic hypotheses. To infer population structure, topology, and population sizes in whistlers, we selected 40 individuals from 12 islands (including all ten mitochondrial clades and seven described subspecies) for genomic sequencing. We used a genotype by sequencing approach, which recovered 15,000 high coverage loci. Assessments of population structure suggest discordance between mitochondrial and genomic DNA. Individuals from central Mindanao Island share mtDNA with western Mindanao, but share their genomic DNA with Eastern Mindanao. The topology of the population genomic species tree is also discordant with the mitochondrial genealogy. The genomic species tree supports a colonization scenario shaped by Pleistocene aggregate island boundaries, whereas the mitochondrial tree supports a stepping-stone colonization model. Estimates of effective population size are strongly correlated with island size. Distinctive populations inhabiting small, peripheral islands are recently derived from large-island populations, suggesting rapid phenotypic change on small islands and stasis on large islands.

Ecological Correlates of Body Size Change in Island Populations of Wild House Mice

Lauren Brooks, Bret Payseur, John Orrock

3B_206-Evolution on Islands
Monday, June 23, 2014 11:00 AM-11:15 AM

The "Island Rule" states that small mammals evolve larger body sizes on islands whereas large mammals reduce their sizes. The search for evolutionary and ecological mechanisms behind this phenomenon has focused on patterns observed across species. Although this approach has been useful, it necessarily conflates many factors that could influence patterns of body size. We evaluate the ecological correlates of body size in a widespread mammal, House mice (Mus musculus), which have a nearly global geographic range, including many islands. This wide distribution of mice on islands with variable biotic and abiotic environments creates a valuable resource to understand how natural selection shapes body size change in populations with limited gene flow. To identify factors responsible for body size evolution over shorter timescales, we analyzed published body masses for island populations from a single house mouse subspecies, Mus musculus domesticus. Across 43 islands, we compared body mass to a series of abiotic and biotic variables: geographic location, island area, island perimeter, temperature, irradiance, human population size and density, avian predators, mammalian predators, and mammalian competitors. Using multiple linear regression, analysis of covariance, and Bayesian model averaging, we found that mice had a significantly lower body mass on islands with three or more avian predator species and on islands with at least one mammalian predator species. Collectively, several abiotic variables, including temperature range and irradiance explained a moderate amount of the body weight variation seen from island to island. These environmental correlates suggest that the interplay of predators, resource availability, and energetic demands are critical contributing factors to the evolution of body size for this species on islands. In addition to informing the possible sources of selection behind the "Island rule" often observed in insular species, these results highlight how studying species with cosmopolitan distributions can inform our understanding of broad patterns of evolution and also illustrate the capacity for significant biogeographic variation.

Estimating how contemporary taxa will evolve in the future to understand how island communities were assembled in the past

Jeremy Beaulieu, Brian O'Meara

3B_206-Evolution on Islands
Monday, June 23, 2014 11:15 AM-11:30 AM

The ocean surrounding isolated islands forms a significant barrier to their successful colonization. Certain traits may assist dispersal to these islands, but getting there is this is only half the battle: organisms must also cope with the potentially novel environments in which they may find themselves. Nevertheless, it is clear that successful colonization of oceanic islands can result in dramatic and rapid radiations, both in terms of producing new species as well as in the novel physical phenotypes that often result. The most general explanation for these radiations is one of ecological opportunity, where species that disperse to a new island habitat with few competitors are thought to rapidly radiate to fill empty niches. Another possibility, however, is that only a peculiar subset of species actually possess the capability to radiate in this manner, and the process of dispersing and surviving filters only these species from a larger pool of potential immigrants. In other words, from a given pool of candidate species are the winners a random draw or is there something about their potential to evolve that allows them to succeed? Here we develop a set of novel techniques for quantifying and summarizing the evolutionary potential of contemporary species and test whether a species,Äô inherent ability to evolve is an important component of the successful colonization of remote oceanic islands. We focus our attention on the species of the Hawaiian Islands, which are well-known for exhibiting a tremendous amount of variation in phenotype as an apparent consequence of movements onto these islands. Our findings suggest that the inherent evolutionary potential of a species has played a critical role in the process of arriving and thriving on the Hawaiian Islands. Our study also highlights that when looking at which organisms thrive in a newly available set of niches, we should look at their underlying, intrinsic rate of innovation as well as their more obvious phenotypic states. In this way, evolutionary potential represents an important new measure about nature that may help explain global distribution of species, which taxa survived past extinction pulses, and those that are predisposed to thrive in the current one.

AVAToL microbial phenomics: An ontology and natural language processing tools to facilitate trait evolution studies for the archaeal domain of life

Carrine Blank, Hsin-Hui Wu, Hong Cui, Lisa Moore, Gordon Burleigh, Jing Liu

3B_301B-Methodology
Monday, June 23, 2014 10:15 AM-10:30 AM

The study of the evolution of traits (phenomics) in any group has been cumbersome due to the time-consuming step of manually compiling traits from the taxonomic literature to create character matrices. Nevertheless, such studies of character evolution in the cyanobacteria and archaeal domain of life have led to fundamental new insights into the evolutionary history of prokaryotes, which in turn have influenced biogeochemical cycles through deep time.

We report here two new tools that are being created to automate the construction of large character matrices for prokaryotic taxa. The first is a natural language processing tool (MicroPIE, or MICRObial Phenomics Information Extractor). This program is an extension of CharaParser, which was developed for extracting character information from more formally structured taxonomic descriptions of eukaryotes. MicroPIE uses existing parsers, machine-learning tools, and a library of microbial-specific terms derived from ~1000 taxonomic descriptions from the Archaea, Bacteroidetes, Cyanobacteria, and Mollicutes. MicroPIE extracts both discrete and continuous characters in the context of the sentence, exporting the marked up character information into a spreadsheet file. This file is provided to a tool called MatrixConversion, which converts the spreadsheet file into a discrete character matrix that can be analyzed using a number of existing phylogenetic software packages.

We also report here the development of MicrO, an ontology of terms found in prokaryotic taxonomic descriptions. MicrO was constructed from the library of microbial-specific terms, organized using a formal logical framework. It also incorporates microbial-specific terms from a number of other ontologies, including ChEBI (CHemical Entities of Biological Interest), GO (Gene Ontology), PATO (Phenotypic Quality Ontology) and NCBI Taxonomy. The purpose of the ontology is to assist in character identification and extraction using MicroPIE, facilitate the identification of trait synonyms used in prokaryotic taxonomic descriptions, and to populate character matrices with higher-level character states.

We demonstrate the usefulness of MicroPIE to extract character information from taxonomic descriptions from the archaeal domain of life and compare these matrices to those constructed manually. Finally, we use ancestral state reconstruction (using Mesquite) to infer the evolution of character states along a phylogenomic tree constructed from a phylogenetic analysis of 100 concatenated proteins and ribosomal RNA genes.

Billion year old rate shifts in microbial evolution

Josef Uyeda, Carrine Blank, Lisa Moore, Luke Harmon

3B_301B-Methodology
Monday, June 23, 2014 10:30 AM-10:45 AM

Phylogenetic comparative methods are increasingly being applied to large-scale phylogenies to give novel insights into the history of life. Here we apply these methods to extend our knowledge into deep time by studying trait evolution across microbial phylogenies that span billion-year timescales. We examine patterns of trait evolution and covariation across the phylogenies of archaea and cyanobacteria. Furthermore, we employ methods that estimate the location of shifts in evolutionary rates across a suite of metabolic, ecological and morphological traits. We then test whether estimated rate shifts in trait evolution correspond to major events in the history of earth, such as the Great and Secondary Oxygenation events. Our preliminary findings identify broad concordance for rate shifts in traits that overlap these geologic events.

Our work represents a collaboration between the Next-Generation Phenomics and Arbor working groups as part of the NSF Assembling, Analyzing and Visualizing the Tree of Life (AVAToL) program. Phylogenomic trees were calculated using Bayesian analyses of large concatenated alignments of protein and ribosomal RNA genes from prokaryotic genomes, where the branch lengths were scaled to time using penalized likelihood in r8s. Character matrices were created manually as part of the AVAToL Phenomics project. These matrices are being used to test the ability of MicroPIE (a natural language processing algorithm being developed by the AVAToL Phenomics team) to automatically construct character matrices from prokaryotic taxonomic descriptions. The AVAToL Arbor team is also using these trees and character matrices as a test case for the development of the Arbor software package, which is a scalable, web-services based platform for conducting phylogenetic comparative analyses. We demonstrate how these software tools enable the collection of large-scale phenomic datasets that can then be flexibly and reproducibly analyzed on phylogenetic trees to test evolutionary hypotheses.

Transformation of Taxonomic Literature to a Taxon-Character Matrix for Phylogenetics

Carmen Lorena Endara, Gordon Burleigh, Hong Cui, Jing Liu, Nathalie Nagalingum

3B_301B-Methodology
Monday, June 23, 2014 10:45 AM-11:00 AM

Taxonomic literature contains valuable phenomic data for taxa that often is not included in phylogenetic reconstructions. The goal of this project is to develop tools that will facilitate the extraction of phenomic data from species descriptions, and convert the information into taxon/character matrices for phylogenetic analyses.

The complete process can be divided in four steps and is achieved using three programs. In the first step, phenomic information is extracted from taxonomic descriptions using CharaParser. Next, the terms that are not recognized are manually classified by the user in the “Ontology Term Organizer Program” (OTO-http://biosemantics.arizona.edu/ONTNEW/). The function of this step is to provide the parsing program with additional information about problematic words. The dataset is then re-analyzed using CharaParser and the resulting file is converted into a taxon-character matrix using the MatrixMaker software. The MatrixMaker interface facilitates the evaluation of character state homology for each character, and it provides tools to enable the characters to be converted into a discrete character matrix, for use in phylogenetic analyses.

We tested the performance of this process using descriptions of the Cycadales (Cycads). The Cycad dataset consisted of generic and species descriptions extracted from the Cycad pages (http://plantnet.rbgsyd.nsw.gov.au/PlantNet/cycad/), and it encompassed 300 terminal species. We obtained 647 characters using this process; and 27.20% of them (176 characters) included information from four or more terminals and more than one character state. Overall, 38.51% (67) of these characters are discrete, 31.61% (55) are numerical continuous characters, and 29.9% (52) were characters with non-homologous states that could not be used. We used the remaining 122 characters to reconstruct a morphology only-based phylogeny and also a combined molecular-morphological supermatrix analysis. Although there was limited support for analyses using morphology alone, the combined analysis provided a credible, comprehensive phylogeny of cycads.

aTRAM - automated Target Restricted Assembly Method: A fast method for assembling genes from massively parallel sequence data

Julie Allen, Daisie Huang, Quentin Cronk, Kevin Johnson

3B_301B-Methodology
Monday, June 23, 2014 11:00 AM-11:15 AM
New sequencing technologies have rapidly increased the amount of genetic data obtained in a single run. These datasets present a large computational challenge for biologists, and software is needed to reduce computational time to sort through and obtain necessary genes. Here we describe software that will rapidly assemble individual genes from massively paralleled sequencing without a complete genome assembly: aTRAM, automated Target Restricted Assembly Method. aTRAM uses a query sequence and BLAST to target matching short genomic reads, identifies their paired ends, and assembles them using a de novo assembler. These contigs are then used as the query in an iterative procedure to recover the full locus. An example 36 GB dataset was run through aTRAM and queried for 1,534 genes, taking on average 55 seconds per gene. Our results indicate that genes assembled by aTRAM were as, or more, complete than those assembled from a reference based or de novo assembly. These results suggest that this software can reduce the computational time necessary to assemble gene space data from short read sequencing methods.

Assembling genes without genomes: phylogenomic exploration within the family Salicaceae

Daisie Huang, Julie Allen, Quentin Cronk, Kevin Johnson, Carl Douglas

3B_301B-Methodology
Monday, June 23, 2014 11:15 AM-11:30 AM
For many comparative questions of gene evolution, sequencing millions of short reads has become much faster and easier, while at the same time, full genome assembly of multiple target species is still time consuming and not necessarily feasible on many taxa. However, depending on the question, targeted assembly of paralogs or putative homologs across phylogenetic space may be sufficient to address these questions. aTRAM, or automated Target-Restricted Assembly Method, is a new tool that can direct de novo assembly at only genes or regions of interest. This method can be used to efficiently assemble only the regions needed to address specific evolutionary questions, without additional library preparation or sample enrichment before sequencing.

We report progress on a Salix eriocephala gene-space assembly generated via aTRAM using the Populus trichocarpa reference genome. We also report progress on multilocus phylogenies across the Salicaceae, using loci generated by aTRAM. These results suggest that aTRAM can be used to address questions both broadly across phylogenetic space as well as deeply within genomic space

---

Ecological genomics of incipient speciation in Mimulus aurantiacus

Matt Streisfeld, Sean Stankowski

3B_302A-Speciation
Monday, June 23, 2014 10:15 AM-10:30 AM
Identifying the ecological genomic mechanisms contributing to the formation of new species is essential for understanding the origins of biodiversity. Despite a long focus on the geography of speciation, it is now recognized that a period of contact may be common during the divergence of many species. Recent speciation-with-gene-flow models have demonstrated that evolutionary factors preventing the break-up of favorable allelic combinations can allow reproductive isolation to evolve despite gene flow. However, the genomic changes responsible for this incipient species formation are poorly understood. Moreover, connecting these genomic changes to trait differences and ecologically-based divergent selection under natural conditions remains a major, ongoing challenge for speciation-with-gene-flow research.

In this study, we unite novel population genomic techniques with classical ecological genetics to evaluate the evolutionary processes underlying the early stages of divergence in the genus Mimulus. In a classic example of incipient speciation, two ecotypes of Mimulus aurantiacus remain partially isolated due to differences in pollinator behavior and habitat use. However, where the two ranges overlap, incomplete isolation results in a natural hybrid zone that allows gene flow between the ecotypes. To identify the genomic changes that led to the evolution of these isolating barriers, we analyzed patterns of clinal variation and population structure for signatures of divergent selection at over 60,000 SNP markers. The results indicate extreme heterogeneity among loci in the magnitude and direction of introgression across the hybrid zone, providing unprecedented detail into the evolutionary mechanisms and genome architecture that gave rise to ecotypic divergence in this group.

Phenotypic and ecological divergence between closely-related and reproductively isolated sympatric species of Mimulus

Katherine Toll, John Willis

3B_302A-Speciation
Monday, June 23, 2014 10:30 AM-10:45 AM
The evolution of ecological differences and reproductive isolation are necessary for secondary sympatry and stable coexistence of closely related species. Without reproductive isolation, incipient species will hybridize and fuse back together into a single species, and without ecological differences competitive exclusion will result in local extinction. Little is known about the ecological trait differences that allow species to coexist and their genetic basis. Species that presently co-occur may have evolved ecological differences while physically separated, or they may have evolved differences in the same area through selection to minimize hybridization or competition.

Mimulus guttatus, a western North American wildflower, and its sister species Mimulus nudatus co-occur on serpentine soils in northern California but live in distinct microhabitats that differ in the onset of summer drought. These species are a classic system for investigating the ecology and genetics of reproductive isolation. Pollinator constancy causes partial prezygotic isolation, but seed lethality is the primary barrier to hybridization between them. M. nudatus grows on serpentine slopes that dry out early in the spring, while M. guttatus inhabits ephemeral streams where drought imposed death is later than in the M. nudatus habitat. These habitats can be very close to one another, within a scale of several meters, so habitat partitioning is on the scale of dispersal and gene flow.

Sympatric and allopatric populations of each species were grown in common gardens to quantify ecologically important trait differences. These phenotypic differences are hypothesized to enable coexistence by contributing to niche differentiation and minimizing interspecific competition. Sympatric populations of M. nudatus have narrower leaves and smaller flowers than M. guttatus. Sympatric populations of M. nudatus also exhibit rapid development characteristic of plants that inhabit marginal habitats; they germinate later, but flower earlier than sympatric populations of M. guttatus. We have also identified several QTL underlying differences in leaf shape, critical photoperiod and bolting. Future work will determine how these loci contribute to microhabitat differentiation and species interactions.

Patterns of introgression between sympatric Mimulus species divergent for flowering phenology and mating system

Amanda Kenney, *Andrea Sweigart*

3B_302A-Speciation
Monday, June 23, 2014 10:45 AM-11:00 AM

Naturally hybridizing species present an opportunity to investigate the evolutionary processes that contribute to speciation. What are the genetic mechanisms and ecological factors that maintain species in sympatry? What proportion of the genome contributes to local adaptation and/or reproductive isolation? We begin to explore these key questions in two closely related species of Mimulus that differ in flowering phenology and mating system: M. nasutus is highly selfing and flowers rapidly under the relatively short day length of early spring, whereas M. guttatus is predominantly outcrossing and remains vegetative until the days become longer. When populations are sympatric, these phenotypic and ecological differences have profound effects on reproductive isolation between species. In this study, we characterize flowering phenology and genomic variation between M. nasutus and M. guttatus within a focal sympatric population. We document ongoing, asymmetrical gene flow from M. nasutus into M. guttatus, with a spectrum of admixture from early-generation hybrids to late-generation hybrids and mostly ‘pure’ M. guttatus individuals. Associations between microhabitat, phenology and genomic composition indicate that recent hybrids occur in intermediate environments and have intermediate flowering times between M. nasutus and M. guttatus. Lastly, to address whether particular genomic regions contribute to the maintenance of species divergence, we quantify patterns of introgression across the genome. These results represent a detailed view of how ecological divergence and gene flow may contribute to patterns of introgression between Mimulus species.

Correlated selection by pollinators generates strong premating isolation across a hybrid zone

Sean Stankowski, *Matt Streisfeld, James Sobel*

3B_302A-Speciation
Monday, June 23, 2014 11:00 AM-11:15 AM

A primary goal of speciation research is to understand how ecological differences generate reproductive isolation despite gene flow. One obstacle is that most species pairs have evolved strong intrinsic reproductive barriers that can obscure the traits that were important in promoting early divergence and isolation. Moreover, it is often difficult to establish the evolutionary genetic mechanisms responsible for maintaining particular combinations of traits that together are necessary for effective reproductive isolation. It has been suggested that studying speciation at an earlier stage of divergence--when isolation is not yet complete--may overcome these limitations.

Differentiated ecotypes of Mimulus aurantiacus in southern California provide an excellent opportunity to address these questions. Although they are distinguished primarily based on flower color—red in the west and yellow in the east—several additional floral and ecophysiological traits vary between them. Consistent with these differences, ecogeographic and pollinator isolation are strong, and intrinsic barriers are weak. Nevertheless, reproductive isolation is incomplete, and the ecotypes hybridize in nature, allowing for gene flow. Taking advantage of this natural, ecological hybrid zone, we used clinal analysis and classical genetic approaches to (1) identify the traits involved in generating reproductive isolation in this system, and (2) to demonstrate that correlational selection is responsible for maintaining particular floral trait combinations that contribute to pollinator isolation.

Despite many ecophysiological traits displaying clinal variation, floral traits consistently showed narrower clines, indicating they experienced stronger divergent selection and contribute more to isolation. Moreover, even though many of these floral traits are controlled by independent genetic factors, correlations between them persist in the hybrid zone in the face of gene flow. Taken together, these results not only suggest that pollinators are selecting for divergent floral trait combinations that results in pre-mating isolation, but they also demonstrate the power of natural hybrid zones for the study of speciation.

Genomic discord at different stages of divergence with gene flow in six lineages of Holarctic ducks

Jeffrey Peters, *Kevin McCracken, Kevin Winker*

3B_302A-Speciation
Monday, June 23, 2014 11:15 AM-11:30 AM

Divergence with gene flow may be an important mode of speciation for Holarctic taxa that have experienced opportunities for intercontinental gene flow during cycles of range expansions and contractions throughout the Quaternary. To test this hypothesis we sequenced 21 independent loci for six lineages of Holarctic ducks (genus Anas) in a replicated study design, taxonomically spanning population-to-species level divergences among the six pairwise comparisons. We predicted (1) genetic differentiation between Eurasia and North America, (2) evidence of intercontinental gene flow, and (3) heterogeneous patterns of genomic differentiation among loci. Divergence between Eurasia and North America has occurred in mtDNA for five of the six lineages, and in 2–11 nuclear loci (nuDNA) for four lineages.

Coalescent analyses revealed significant evidence of intercontinental gene flow in all cases. Finally, mtDNA differentiation was stronger than expected given background levels of nuDNA divergence in four lineages, and three nuDNA loci (CHD1Z, LDHB, & CRYAB) were significant outliers for divergence among three lineages, suggesting that selection has affected these loci in parallel among some lineages. Although male-biased gene flow likely contributed to mito-nuclear discordance, the observed heterogeneity within nuDNA suggests a prominent role of divergence with gene flow for Holarctic ducks. Our results show that the Holarctic is rich in opportunities to study evolutionary processes shaping divergence and gene flow across a continuum of speciation stages.

Estimating gene flow directionality and demography of western Atlantic Syngnathidae with population genomic RADseq data

J.T. Boehm, John Robinson, Nathan Putman, Michael Hickerson

3B_302B-Phylogeography
Monday, June 23, 2014 10:15 AM-10:30 AM

Powerful ocean currents and historical climatic fluctuations play a significant role in the diversification and population connectivity of coastal fishes. However, the impact of these abiotic forces cannot be decoupled from life history traits, including early stages of larval development or adult biology traits such as swimming capacity and zonation preference. One often over looked trait is the ability of species to raft on floating mats of vegetation, specifically Sargassum spp, shown to be a significant determinate for successful long distance dispersal in the Atlantic. Seahorses (Hippocampus) and pipefish (Syngnathus) are direct developers and relatively poor swimmers, though some species exhibit substantial connectivity across regional distributions, partially attributed to their rafting ability. Rafting is passive and therefore gene flow between populations is predicted to follow directional ocean currents, whereas climactic driven changes in available habitat could result in a history of divergence and genomic admixture that is incongruent with oceanic currents. To test the relative contribution of these two processes, we use RADseq from five co-distributed species of western Atlantic Syngnathids and estimate gene flow directionality and magnitude between regional populations.

Keywords: population genomics, RADseq, gene flow, ocean currents, fishes, seahorse and pipefish (Syngnathidae)

Comparative Phylogeography of Lizards from the Brazilian Cerrado

Fabricius Domingos, Guarino Colli, Alan Lemmon, Emily Lemmon, Luciano Beheregaray

3B_302B-Phylogeography
Monday, June 23, 2014 10:30 AM-10:45 AM

Cerrado, the Brazilian Savanna, is the second largest biome of South America and one of the world's 25 biodiversity hotspots. The squamate levels of endemism in this biome are higher than any other vertebrate group, with 42% of Cerrado's lizard species being endemic. Recent studies suggest a major role of ancient vicariant processes in shaping the biogeographic history of the region. However, there is still a great debate considering the evolutionary origins and diversification patterns of the Cerrado herpetofauna. We investigated biogeographic history in the Brazilian Cerrado using co-distributed lizards as a research subject. We used species distribution modelling (past and present), Sanger-sequencing and Next-Generation sequencing (anchored phylogenomics) to reconstruct the phylogeographic history of three Cerrado lizards: Gymnodactylus amarali (Phyllodactylidae), Micrablepharus atticolus (Gymnophtalmidae), and Tropidurus itambere (Tropiduridae). Using a hypothesis testing framework that combined paleoclimatic and coalescent-based methods we retrieved evolutionary patterns consistent with the geological history of the Cerrado. Results indicate a number of divergent clades within the three species that possibly relate to cryptic speciation, whereas phylogeographic patterns appear linked to the tectonic uplift of the Central Brazilian Plateau.

Using the multi-species allele frequency spectrum (msAFS) for next-generation comparative phylogeography

Alexander Xue, Michael Hickerson

3B_302B-Phylogeography
Monday, June 23, 2014 10:45 AM-11:00 AM

Comparative phylogeography involves reconstructing the history of biological communities with population-level genetic data collected from assemblages of species that presently co-occur spatially. One of the long-standing objectives of this discipline is to test hypotheses of shared demographic histories that may arise from climate shifts that might affect whole communities in order to gain understanding of large-scale processes underlying regional patterns of biodiversity and community assembly. However, most studies to date have been limited to using mtDNA and a handful of nuclear loci. Now, next-generation sequencing allows the potential to overcome this limitation to gain community-scale inference at unprecedented resolution, yet aggregate data sets of such size bring analytical challenges.

The allele frequency spectrum (AFS) has become a powerful way of characterizing population genomic data for demographic inference, and here we expand this into the multi-species allele frequency spectrum (msAFS). This study describes how the msAFS is constructed over an arbitrary number of co-occurring populations and subsequently investigates how it behaves under different simulated co-expansion scenarios for 5 to 100 species with 25,000 SNPs from each species. By compressing the super-matrix into the first two axes of a principle component analysis, we demonstrate that various alternative multi-species histories can be discriminated with the msAFS. In addition, we utilized RAD-tag data from three lake populations and two oceanic populations of the three-spine stickleback (Gasterosteus aculeatus) to assess the applicability of the msAFS with empirical data.

The msAFS will be suitable for using within a hierarchical modeling framework, allowing selection of co-expansion models and hyperparameter estimation (i.e. the variability of species-specific parameters). This study is the first to explore methods for the analysis of multi-species population genomic-scale data, and as

RAD-seq protocols become routine for obtaining large-scale SNP data from non-model taxa, the msAFS opens the door for more powerful community-level demographic inference for next-generation comparative phylogeographic studies.

Keywords: comparative phylogeography, population genomics, allele/site frequency spectrum, co-expansion, hierarchical modeling

---

Assessing GIS estuarine habitat predictions with a new statistical approach for genetic signatures of postglacial recolonization

Greer Dolby, David Jacobs

3B_302B-Phylogeography
Monday, June 23, 2014 11:00 AM-11:15 AM

Much work has centered on understanding the impact of Pleistocene glacial cycles on patterns of genetic diversity and ranges of modern species. Here we address such questions comparatively across three fishes in the estuaries of southern and Baja California where slope and bathymetry exert primary control over habitat formation through time. We present GIS-based habitat models since the Last Glacial Maximum (LGM) at a millennial time scale and identify lowstand refuges, which are supported by diversity indices and mismatch distributions in mtDNA. Using discriminant function analysis on highly polymorphic microsatellite datasets we determine suites of species-specific refugial alleles and calculate the frequencies of these in a geographically explicit framework in all individuals at intervening, nonrefugial sites.

Results indicate dramatically reduced habitat at lowstand (120-140 mbsl) with two identified refuges. Habitat increases precipitously after 15 ka, peaking between 12 - 9 ka, as supported by prior archeological and anthropological work and declines ca. 7 ka to present. Using AICc to evaluate regression models applied to the discriminant allele analysis suggests that genetic mixing does not follow an isolation by distance null model, but rather supports habitat origination time as revealed by habitat models as a foremost player in moderating gene flow since the LGM in these three fishes.

Do ecological communities co-diversify? An investigation into the Sarracenia alata pitcher plant system

Jordan Satler, Bryan Carstens

3B_302B-Phylogeography
Monday, June 23, 2014 11:15 AM-11:30 AM

Investigations into communities of co-distributed species is of central importance for understanding biogeographic regions, as congruent patterns across multiple species provide strong evidence for a shared response to the presence of historical events that have shaped both genetic and species diversity. Examining such communities with ecological relations in this framework is expected to provide greater insight, as levels of congruence among phylogeographic patterns can allow us to disentangle the effect of how historical processes have helped shape community level structure and interactions. Although many studies have been performed in a comparative phylogeographic framework (i.e., analyzing species individually, then comparing across species for congruent patterns), fewer studies have explicitly estimated the evolutionary history of a community itself, where simultaneous analysis of the species is used to recover a community-level signal. Both approaches have merit, and we explore their use in an investigation into the Sarracenia alata (F. Sarraceniaceae) pitcher plant system. The carnivorous pitcher plant S. alata is found along the gulf coast of the southeastern US, and contains a disjunct distribution separated by the Mississippi River/Atchafalaya Basin. Recent work has recovered phylogeographic structure congruent with the major rivers in the region, suggesting that these rivers have structured genetic diversity within the plant. Here we explore the arthropod community ecologically associated with S. alata, and test for simultaneous divergence across the Mississippi River/Atchafalaya Basin, a known biogeographic barrier.

Impact of ascertainment bias on phylogenetics of foodborne pathogen outbreaks

Emily Jane McTavish, Marc Allard, Ruth E Timme

3B_302C-Phylogenetics and Population Genetics
Monday, June 23, 2014 10:15 AM-10:30 AM

Whole genome phylogenetics is increasingly being utilized in the regulatory environment for identifying the contamination source of foodborne pathogens. However, these types of clonal outbreak phylogenies often have extremely recent divergence times, relying on only a few mutations for phylogenetic reconstruction. This makes them particularly vulnerable to sequencing errors or biases in single nucleotide polymorphism (SNP) calls. In this study we use an empirical dataset of a recent Salmonella outbreak in concert with simulated data to compare SNP calling methods and their impact on accurately reconstructing the phylogeny of bacterial pathogen outbreaks.

Impacts of Individual Loci on Species Tree Inference: An Empirical Example from Slender Salamanders (Batrachoseps)

Elizabeth Jockusch, Iñigo Martínez-Solano, Elizabeth Timpe

3B_302C-Phylogenetics and Population Genetics
Monday, June 23, 2014 10:30 AM-10:45 AM

Species tree methods are now widely used to infer the relationships among species from multi-locus datasets. Many methods have been developed, which differ in how gene trees are used to infer the species tree. While these methods all perform well on simulated data, less is known about what impacts their performance on empirical data. We used a dataset including five nuclear genes and one mitochondrial gene for 22 species of Batrachoseps to compare the effects of method of analysis, within-species sampling and gene sampling on species tree inferences. For this dataset, the choice of inference method had the largest effect on the species tree topology. Exclusion of individual loci had large effects in *BEAST and STEM, but not in MP-EST. Different loci carried the greatest weight in these different methods, suggesting that the causes of their disproportionate effects differ. Even though substantial information was present in the nuclear loci, the mitochondrial gene dominated the *BEAST species tree. If loci with disproportionate impacts also violate the assumption of these species tree methods that all discordance is due to incomplete lineage sorting, then analyses may be positively misled. The potential for this problem is expected to be especially pervasive with animal mitochondrial loci, which are both typically far more variable than nuclear loci and highly subject to introgression. Within-species sampling was also important, as shown by differences in tree topology across 100 subsampled datasets. *BEAST showed high levels of variation in nodal support across these subsamples (ranging from

Using transcriptomes for functional phylogenomic studies: promises and pitfalls

Ya Yang, Stephen Smith

3B_302C-Phylogenetics and Population Genetics
Monday, June 23, 2014 10:45 AM-11:00 AM

Transcriptome sequencing provides a new path for cost-effective genome-scale functional analysis in non-model species. Homolog and ortholog sets from housekeeping genes are rich resources for reconstructing phylogeny and mapping genome-wide molecular rate shifts and genome duplications. In addition, the large number of homologs obtained from these data sets provide a rich resource for investigating candidate genes that may have contributed to adaptive changes. We discuss key methodological issues and misconceptions involving homology and orthology inference, evaluation of gene tree conflicts, and detection of shift in dN/dS ratios.

Performance and utility of Single Nucleotide Polymorphisms (SNPs) in fine scale population study

Eugenia Lo, Mariangela Bonizzoni, Anthony James, Elizabeth Hemming, Yaw Afrane, Andrew Githeko

3B_302C-Phylogenetics and Population Genetics
Monday, June 23, 2014 11:00 AM-11:15 AM

In the era of high-throughput generation of genomic data, genome-wide Single Nucleotide Polymorphisms (SNPs) have been increasingly popular in population studies of model and nonmodel organisms. The rapid growth of SNP data in public databases and the advent and accessibility of cost-effective, multiplexing platforms provide powerful opportunities to select and apply SNPs on various scales of study. While SNPs have been shown to be useful in revealing population structure with broad-scale samples (i.e., at the continental or regional levels), it remains unclear whether they provide resolving power to microgeographical samples, and whether different types (e.g., nonsynonymous and silent) and numbers of SNPs yield different clustering results. This study evaluated the performance of SNP markers and their utility compared to microsatellites in a fine-scale population study using Plasmodium parasite samples collected from Western Kenya. Nonsynonymous and silent SNPs were found to indicate different levels of genetic variability and signature. A small subset of 'quality' SNPs outperformed a larger number of SNPs and provided the best resolving power to fine-scale samples, even when compared to microsatellites. A cautionary, sophisticated assessment and selection of SNP markers is needed for fine-scale population studies to capture and reveal population signals. This process entails knowledge of SNP loci and testing population samples in depth. Our study highlights the importance of SNPs selection and identifies a set of loci useful in tracing Plasmodium spread on a fine scale and potentially in broader areas. In addition, we provide an overview and caveat of contemporary SNP typing platforms with the aim to facilitate decision-making between budget and scale of study.

Influence of mating system on genome evolution in Caenorhabditis

Janna Fierst, John Willis, Rose Reynolds, Timothy Ahearne, Cristel Thomas, Wei Wang, Kristin Sikkink, Asher Cutter, Patrick Phillips

3B_302C-Phylogenetics and Population Genetics
Monday, June 23, 2014 4:15 PM-4:30 PM

Self fertilization is predicted to reduce levels of standing genetic variation at neutral loci by one half. More importantly, however, self fertilization reduces the effective recombination rate, which should dramatically increase the opportunity for linkage disequilibrium, thus making the genomes from self-fertilizing species more susceptible to selective sweeps and/or background selection. In turn, these effects should have important consequences for distribution of genomic variation and the evolution of genomic structure. Nematodes of the genus Caenorhabditis display mating system variation in which selfing hermaphrodites have evolved independently from an outcrossing male-female ancestor. Using a combination of next generation sequencing and genetic mapping approaches, we have assembled the genome of C. remanei, a close outcrossing relative of the selfing C. elegans model system. We can compare these genomes, together with that from C. briggsae, which has also independently evolved hermaphrodites, to gain insights into how the evolution of self fertilization influences genome structure, including the evolution of gene families and the evolution of genome size.

Investigation of gene expression variation within the Yellowstone National Park gray wolf population using RNA-Seq

Pauline Charruau, Rachel Johnston, Amanda Lea, Noah Snyder-Mackler, Dan Stahler, Bridgett vonHoldt

3B_303-Gene Expression
Monday, June 23, 2014 10:15 AM-10:30 AM

Modification of gene expression levels can serve as a first line response to sudden environmental and social changes, yet with potential consequences on individuals' fitness. With the advent of high throughput sequencing technology, it is now possible to examine gene expression variation for thousands of genes, in known individuals from natural populations. Wild gray wolves (Canis lupus) live in social packs and their position as a top predator makes them more sensitive to ecosystem disturbances. Furthermore, the gray wolf is a model species for studying population-wide gene expression in a natural context, as its closest relative, the domestic dog (C. l. familiaris), has a well-annotated genome. Here, we conducted an exploratory analysis of RNA-seq-based gene expression data from 27 wild gray wolves in Yellowstone National Park, USA. In this project we aimed to: i) assess genome-wide gene expression variation in an easily accessible tissue, such as whole blood; and ii) identify molecular pathways and individual genes for which expression is associated with important environmental or demographic factors, specifically social rank, age, and sex. Our preliminary results indicate a strong effect of traits associated with age on gene expression patterns, with a significant enrichment of immune pathways. This project will help to define the nature and limits of gene expression response in wolves and evaluate of the potential of RNA-sequencing as a tool for conservation.

Using NGS to investigate differentially expressed genes and SNPs between closely related tephritid fruit flies, Anastrepha fraterculus and A. obliqua

Carlos Congrains, Victor Rezende, Iderval Sobrinho Jr, Samira Chahad-Ehlers, Reinaldo de Brito

3B_303-Gene Expression
Monday, June 23, 2014 10:30 AM-10:45 AM

Anastrepha fraterculus and A. obliqua are closely related South American fruit flies (Tephritidae: Diptera) that infest several different hosts and are morphologically similar, which renders their identification difficult. Previous studies have failed to identify genetic markers that separate the species due to their recent divergence. In this work, we generated multiple Next Generation Sequencing (NGS) cDNA libraries of A. obliqua and A. fraterculus and studied patterns of expression and single nucleotide polymorphisms (SNPs) seeking transcripts that may be involved with species differences, which would help us discriminate these species. We generated cDNA libraries from total RNA extracted from fly heads and reproductive tissues pooled from mature virgin and post-mating males and females, as well as from post-ovipositing females, with replicas, totaling 20 libraries per species. We generated close to 300 million reads, after trimming and filtering for quality on SeqyClean. We used a combination of Trinity and Velvet to assemble these data, after normalization, which led to about 180,000 contigs with N50 of 2012 and an average length of 1,225 bp. Over 46,000 contigs had more than 1,000 bp and almost 23,000 had more than 2,000 bp. We annotated these contigs using BLAST2go and used SAMtools and Bowtie2 to align each species reads back onto the total assembly. Our analyses found thousands of differentially expressed genes across the different reproductive stages studied. Our combined analyses identified over 100,000 intraspecific SNPs, twice as many that were only polymorphic in A. fraterculus when compared to A. obliqua and about 8,000 SNPs that segregate in both species. We focused on 389 contigs that had at least one fixed interspecific difference between the species and investigated for patterns of positive selection on these transcripts that resulted in 12 potentially interesting genes that express in the head and 15 reproductive genes that may be involved with species differences, among them serine proteases, odorant-binding proteins as well as some uncharacterized proteins. These results provide us with a set of candidate genes that are potentially important to understand the evolution of genetic differences between A. obliqua and A. fraterculus

---

Association mapping reveals the evolutionary forces maintaining genetic variation for gene expression.

Emily Josephs, Young Wha Lee, John Stinchcombe, Stephen Wright

3B_303-Gene Expression
Monday, June 23, 2014 10:45 AM-11:00 AM

The genetic variation in phenotypic traits may be maintained by two processes: mutation-selection balance and balancing selection. These processes are expected to have different effects on the allele frequencies of loci influencing phenotypic traits, making it possible to use experimentally-determined genetic architecture to investigate the maintenance of variation. We took this approach using gene expression as a model trait. We measured expression and identified SNPs in 94 individuals collected from a large population of the outcrossing plant Capsella grandiflora using genome-wide next generation RNA and DNA sequencing. We then conducted an association mapping study to determine the local genetic variants associated with gene expression (eQTLs) and identified a large number of SNPs that were significantly associated with the expression of nearby genes. These eQTLs are present in the population at lower allele frequencies than those SNPs that were not associated, suggesting that mutation-selection balance largely drives genetic variation for gene expression.

Co-Option of an RNA-Binding Protein in the Translational Regulation of a Hypervariable Vertebrate Pheromone, Plethodontid Modulating Factor

Damien Wilburn, Richard (Rick) Feldhoff

3B_303-Gene Expression
Monday, June 23, 2014 11:00 AM-11:15 AM

For more than 100 million years, plethodontid salamanders have utilized a complex mixture of proteinaceous courtship pheromones to regulate reproductive behavior and mating success. One component, Plethodontid Modulating Factor (PMF), is a hypervariable pheromone related to the three-finger superfamily. The diversity of PMF isoforms varies among plethodontid salamanders, with some species, such as Plethodon shermani, expressing more than 30 distinct PMFs of ~30% average amino acid similarity. These complex isoform mixtures are the products of gene duplication and positive selection. However, despite rapid evolution of the coding regions, the untranslated regions (UTRs) are ~98% conserved and maintained by purifying selection. This form of disjunctive evolution was hypothesized to permit expansion of PMF's functional breadth while providing a mechanism to regulate simultaneous expression of the many isoforms. In order to identify possible regulatory proteins that bind the UTRs, transcriptome analyses were performed on developing P. shermani glands and analyzed for putative RNA binding proteins. From ~55,000 assembled contigs, the only major candidate identified was Cold Inducible RNA-Binding Protein (CIRBP). Binding and kinetics assays revealed that CIRBP cooperatively binds the PMF 3' UTR. Gene expression was negatively correlated between CIRBP and PMF (at both mRNA and protein levels). Thus, CIRBP was hypothesized to be a negative regulator of pheromone expression by influencing mRNA stability and/or rates of translation, and was postulated to be the proximate cause of purifying selection on the

PMF UTRs. As a “cold inducible” protein, CIRBP may play a critical role(s) in the translational regulation of PMF expression during pheromone gland development, and as global climate change alters seasonal temperatures, the regulation of this protein may have profound impacts on reproduction in these cold-blooded animals.

X-linked regulation in the Drosophila male germline

Emily Landeen

3B_303-Gene Expression
Monday, June 23, 2014 11:15 AM-11:30 AM

Heteromorphic sex chromosomes have evolved independently numerous times across taxa, often accompanied by the evolution of sex-chromosome specific regulation. Transgenic reporters driven by testis-specific promoters reveal an X-autosome difference in regulation: X-linked transgenes show significantly reduced expression compared to autosomal transgenes. We extend this analysis to endogenous genes to ask how testis-specific and non-specific gene expression changes for genes located on the X and autosomes. We compare endogenous X-autosome testis expression using small (2.5 Mb) X-autosome transpositions, and translocations. Testis and non-specific genes from transpositions show a significant increase in expression when moved to an autosome, but testis-specific genes show a significantly greater increase in expression compared to non-specific genes. We find that X-linked testis-specific expression increases over time, suggesting X-linked testis-specific promoters evolve in response to the severe suppressive environment of the X. We computationally identify and transgenically test a candidate regulatory motif that is overrepresented in the 5’ regulatory region of X-linked testis-specific genes, associated with increased X-linked testis-specific expression, and conserved across species. These findings are significant for understanding the evolution of sex chromosomes, gene expression in the male germline and X-autosome gene movement patterns.

The Genome Sequence of a Widespread Apex Predator, the Golden Eagle (Aquila chrysaetos)

Jacqueline Doyle, Yanzhu Ji, Bhagya Wijayawardena, J. Andrew DeWoody, Todd Katzner, Pete Bloom

3B_305A-Understanding Genomes
Monday, June 23, 2014 10:15 AM-10:30 AM

Biologists routinely use molecular markers to identify conservation units, to quantify genetic connectivity, to estimate population sizes, and to identify targets of selection. Many imperiled eagle populations require such efforts and would benefit from enhanced genomic resources. We sequenced, assembled, and annotated the first eagle genome using DNA from a male golden eagle (Aquila chrysaetos) captured in western North America. We constructed genomic libraries that were sequenced using Illumina technology and assembled the high-quality data to a depth of ~40x coverage. The genome assembly includes 2,552 scaffolds >10 Kb and 415 scaffolds >1.2 Mb. We identified repetitive regions spanning 92 Mb (~6% of the assembly), including LINES, SINES, LTR-RTs and DNA transposons. We annotated 16,571 genes that are involved in myriad biological processes, including such disparate traits as beak formation and color vision. Such work can inform management decisions for species of conservation concern. For example, conservationists have suggested that coating wind turbines with ultraviolet-reflective paint might prevent collisions between eagles and the man-made structures. However, sequencing genes associated with vision provides evidence that golden eagles have violet-tuned, rather than ultraviolet-tuned, vision. We have additionally identified >3,000 orthologs in the golden eagle, two species of falcon and 5 other non-raptor avian species. Identifying genes associated with vision, hearing, and olfaction that are under selection may provide insight to how raptors interact with their environment. Finally, the data reveal that several anonymous microsatellites commonly used for population studies are embedded within protein-coding genes and thus may not have evolved in a neutral fashion. Because the genome sequence includes ~800,000 novel polymorphisms, markers can now be chosen based on their proximity to functional genes involved in migration, carnivory, and other biological processes.

Capturing highly divergent regions in genomes: Next-Gen Sequencing and why “false positives” might be exactly what you are looking for.

Martine Zilversmit, Sebastian Gurevich, Gordon Bullen, Sethu Nair, Sittiporn Pattaradilokrat, Yanwei Qi

3B_305A-Understanding Genomes
Monday, June 23, 2014 10:30 AM-10:45 AM

Genome structure, in addition to natural selection, can have a strong influence on the patterns and mechanisms of molecular evolution. The reduced sequence complexity of A+T-biased genomes (such as those of the malaria parasites (Plasmodium yoelii (78% A+T) and P. falciparum (80% A+T)) affects rates of point mutation, recombination, and repeat expansions. These mechanistic changes, combined with short generation times and strong selective pressures, can produce and maintain high levels of genetic divergence among individuals. In addition, these factors make it challenging to use Next-Generation Sequencing data for comparative genomics because methods for detecting variation are not sensitive to low-complexity genome structure or regions of rapid evolution. Using an evolutionary approach, and four genomes of the rodent malaria parasite P. yoelii (three within the same species group, and one outside), we have developed methods to uncover hundreds of regions of extreme divergence that would have been discarded by standard methods as “false positives.” These regions can range in size from 10 to over 100 residues, and represent both large insertion/deletion events as well as regions without size differences that are highly divergent. Among genomes that normally range between 98.5% to 99.6% identity at the nucleotide-level (99% to almost 100% amino acid identity), these rapidly evolving regions average just 50% amino acid identity. Genes of all functional groups contain these regions, including surface antigens and cell-invasion ligands likely under strong selection, and enzymes and structural proteins that are not normally associated with high levels of diversity or divergence. This method, combined with modifications to the standard applications of open-source computational tools, allows us to capture a more complete picture of functional and overall sequence diversity in these parasite genomes.

Comparative genomics and transcriptomics of the New Zealand Giant Weta

Victoria Twort, Richard Newcomb, Howard Ross, Thomas Buckley

3B_305A-Understanding Genomes
Monday, June 23, 2014 10:45 AM-11:00 AM

Giant Weta are among the largest extant insects on earth, and are an iconic part of the New Zealand biota. However, a number of these species are highly endangered. The Poor Knights Giant Weta (Deinacrida fallai, Orthoptera) is one such species, and is restricted to a small offshore island. Despite widespread interest in this and related species, the current genomic resources are lacking. Our aim is to construct a comparative genomic dataset that will be used to investigate various aspects of molecular evolution and evolutionary relationships of this endemic New Zealand insect. Its genome is large; current estimates indicate that the genome is approximately 10 GB in size, which is larger than the only published Orthopteran genome, that of Locusta migratoria. Our current draft assembly for Weta has been obtained from a mixture of paired-end and mate pair libraries. In addition, a de novo transcriptome has been generated for this species from five different tissues using Trinity. The resulting unigenes are being used to identify transcripts of interest, including male reproductive proteins, glycolytic genes and odorant receptors, in order to study rates and patterns of evolution among species. RNA-seq data has also been generated for a number of Tree and other Giant Weta species, resulting in an average number of 128,912 contigs per species, and an average N50 of 1kb. The current data sets will be combined with Genotyping-By-Sequencing data to investigate various conservation genetics issues, in order to better inform current and future conservation efforts.

Understanding genome evolution in the dogwood genus Cornus L. (Cornaceae) from analyses of transcriptome sequences

Yan Yu, Jenny Xiang, Baohua Song, Paul Manos

3B_305A-Understanding Genomes
Monday, June 23, 2014 11:00 AM-11:15 AM

The pattern and rate of genome evolution is a central question in evolutionary biology. Genome and gene duplications are known to be major forces driving flowering plant evolution. However, in most non-model plants, the dynamics of genome evolution and the pattern of large-scale genome duplications (including polyploidization) still remain largely unknown. High through-put transcriptome sequence data obtained using next generation sequencing technology have enabled novel investigation of genome evolution using new bioinformatics and methodological tools and phylogeny-based comparative analyses among closely related species. Here we compare several de novo assembled transcriptomes representing four closely related dogwood species of the showy-bracted clade of Cornus and the outgroup genus Alangium. Through gene annotation and molecular evolutionary analyses of gene sequences, we aim to address the following questions: 1) Is there evidence of ancient polyploidy in any of these species? if so, when and where in the genus phylogeny did the genome duplication likely occur? 2) Is there evidence of rate shifts in molecular evolution following genome duplication, as expected from differential fates of duplicated genes, e.g., lost function, conserve the original function, or diverge and gain new function? 3) Is there a genome-wide acceleration of molecular evolution in the herbaceous lineage, as predicted by a possible shorter generation time and long branches in the molecular phylogeny of the genus? If so, what are the underlying evolutionary forces? 4) What causal factors may explain the differences in the pattern and rate of genome-wide molecular evolution among the dogwood species? Answering these questions will contribute to advancing our knowledge in genome evolution of non-model organisms.

Experimental evolution to domesticate a filamentous multicellular fungus yields diverse novel phenotypes

Alexis Powell, Hui Lin, Romas Kazlauskas, Michael Travisano

3B_305B-Experimental Evolution
Monday, June 23, 2014 10:15 AM-10:30 AM

Experimental evolution to domesticate a filamentous multicellular fungus yields diverse novel phenotypes

Alexis F. L. A. Powell1, Hui Lin1, Romas J. Kazlauskas1,2, and Michael Travisano1,3

1BioTechnology Institute; 2Department of Biochemistry, Molecular Biology, and Biophysics; and 3Department of Ecology, Evolution, and Behavior; University of Minnesota, St. Paul, MN 55108

Domesticated organisms exhibit many traits unknown in their wild ancestors. Plant and animal domestication is generally thought to be governed by strong artificial selection on a few high value traits, accompanied by release of many formerly functional traits from natural selection. Both sets of traits may evolve to unusual states that are hallmarks of domestication. By contrast, accounts of microbial domestication do not give attention to evolution of nonadaptive traits, and some studies have found that domesticated microbes do not show the genomic signatures of relaxation of selection or population bottlenecks that typify domesticated plants and animals. We used experimental evolution to domesticate the filamentous fungus Trichoderma citrinoviride by subjecting replicate populations to a culturing protocol with > 200 serial transfers designed to favor evolution of rapid growth in agitated liquid with suspended insoluble cellulose media, high production of extracellular cellulosic enzymes, and easy transferability via micropipette. Evolved populations were plated on malt extract agar media to study aspects of their aggregate growth and morphology. We found substantial phenotypic variation among lineages, including novel phenotypes not known from the wild-type ancestor. Our results suggest that the evolutionary consequences of domestication for this filamentous microbe are not unlike those seen in plants and animals. These results also suggest that other Trichoderma species, which exhibit little morphological variation despite occupying a wide range of habitats and employing different nutritional modes (saprotrophy and mycoparasitism), likely have latent potential for similar evolution but are ecologically constrained by factors not relevant in the domestic environment.

Genome-Wide Convergence with Repeated Evolution in Drosophila melanogaster.

Joseph Graves, Michael Rose, Lee Greer, Laurence Mueller, Larry Cabral, Molly Burke, Mark Phillips, Mira Han, Kate Hertweck

3B_305B-Experimental Evolution
Monday, June 23, 2014 10:30 AM-10:45 AM

~~High levels of diversified, sequence polymorphism across numerous sites genome-wide in populations under strong purifying or adaptive directional selection, are expected under a hypothesis of balancing selection at multiple individual loci. Since February of 1980, our research laboratory has developed outbred, moderate Ne populations of fruit flies with 5-fold replication under various selection regimes for life-history reproductive delay, vial and cage adaptation, and phenotypic assays of dietary and physiological characters. Each treatment has been maintained in stable environments for tens to hundreds of generations of various sustained selection conditions. These long-term experiments form an elegant, parallel-branch fly phylogeny, with known branching times, generation numbers, and well-characterized population censes. Populational genomic re-sequencing of representative lines of our phylogeny, has yielded surprising levels of genome-wide polymorphism across multiple lines, with scarcely any evidence for classical genetic sweeps. These lab populations, the largest of their kind for multicellular model organisms, encounter stable-environment, sustained selection unlike most natural populations. Yet, the lack of features expected under classic population genetic models suggest (1) that multi-locus, perhaps gene network-leveraged, balancing selection may be far more common than previously supposed, and (2) that there may be the need for new paradigmatic approaches to understanding genomic evolution in natural populations.

Adaptation of a freshwater alga to marine conditions in the laboratory

Josianne Lachapelle, Nick Colegrave, Graham Bell

3B_305B-Experimental Evolution
Monday, June 23, 2014 10:45 AM-11:00 AM

Experimental evolution is most often used to study adaptation to slightly modified ecological conditions. Rarely have we been able to study how populations manage to adapt to novel ecological conditions. We have taken a freshwater alga, Chlamydomonas reinhardtii, and propagated it over time in ever increasing concentrations of salt. These experimental lines can now grow in levels of salinity that are way beyond what was available to the ancestors. And in fact, the lines are now capable of growth in seawater. We show that both phenotypic plasticity and genetic adaptation play a role in extending the range of salinities that sustain growth. We also show that there is a significant amount of variation among the independent lines. Thus the transition from freshwater to marine conditions has occurred following more than one trajectory. Adaptation to novel ecological conditions can occur over relatively short timescales in the laboratory, enabling us to gain more insight into such macroevolutionary processes.

Inferring allele frequency trajectories of experimentally evolved Drosophila populations with Gaussian process models

Agnes Jonas, Hande Topa, Antti Honkela, Carolin Kosiol, Robert Kofler

3B_305B-Experimental Evolution
Monday, June 23, 2014 11:00 AM-11:15 AM

Recent advances in sequencing technologies have provided a new experimental approach: evolve and resequence (ER). Using ER experiments we can investigate the dynamics of allele frequency changes at the molecular level in great detail. We can now monitor genome-wide allele frequency (AF) trajectories at millions of single nucleotide polymorphisms (SNPs) for several replicate populations. The resulting time serial data enable us to identify candidate regions that are likely to evolve under selection. However, limited tools are available that can efficiently include all accessible information from the data, such as AF at intermediate time points, replicate experiments and sources of uncertainty coming from the sequencing.

We address these problems by developing a beta-binomial Gaussian process (BBGP) model for finding SNPs with significant frequency change over time that is consistent across replicates (codes are available at https://github.com/handetopa/BBGP). The beta-binomial model captures the uncertainty arising from finite sequencing depth and Gaussian processes provide a flexible way to model frequency trajectories of alleles. We show that for simulated data the GP-based methods outperform frequently used pairwise statistical tests for finding selected alleles in average precision. Our results demonstrate that GP models are well suited for analyzing genomic time series data because they can effectively utilize the available information, making good use of additional time points and replicates.

We present results from applying our approach on real data from Drosophila experimental evolution for temperature adaptation. Preliminary results suggest that the proposed method might be better suited to detect selection of small effect size or to model soft or incomplete sweeps.

Analysis of variance in fitness over 50,000 generations in an evolution experiment

Michael Wiser, Noah Ribeck, Richard Lenski

3B_305B-Experimental Evolution
Monday, June 23, 2014 11:15 AM-11:30 AM

How repeatable the process of evolution is remains a central question within the field of experimental evolution. The Long Term Evolution Experiment (LTEE) is an ongoing experiment, in which 12 populations of Escherichia coli have been evolving separately for more than 50,000 generations. We have previously shown how fitness has changed within these populations over this time period. In this talk, we will discuss how the among population variance in fitness has changed, and what this can tell us about the underlying fitness landscape these populations have been experiencing. Empirical data will be compared tosimulations, allowing us to test whether our theoretical model captures the reality of the system.

Impact of self-fertilization on fecundity, the timing of reproduction, and population genetic structure, in a marine ribbon worm (Nemertea)

Serena Caplins

3B_306A-Selfing and Outcrossing
Monday, June 23, 2014 10:15 AM-10:30 AM
Organisms capable of self-fertilization typically exhibit two evolutionary syndromes uniting high inbreeding depression with low levels of selfing, or low inbreeding depression and high levels of selfing. This study tests for inbreeding depression in an apparent self-compatible, hermaphroditic marine nemertean worm, Prosorhochmus americanus. Fecundity and timing to first reproduction were assessed in isolated and paired worms. Isolated worms produced significantly more offspring than paired worms and did not show inbreeding avoidance. The selfing rate of natural populations was evaluated using species-specific microsatellites and is consistent with preferential selfing (mean: 0.801), though some outcrossing appears to take place. Population genetic structure indicates populations are disjunct and characterized by low levels of gene flow. Our results reveal P. americanus exhibits an interesting suite of life-history traits, uniting high dispersal potential through self-fertilization and high fecundity, with the lack of a dispersive larval stage and low levels of gene flow.

Selfing allele favored by male function in experimental populations of Witheringia solanacea in Costa Rica

Judy Stone, Emily VanWyk, Jennifer Hale

3B_306A-Selfing and Outcrossing
Monday, June 23, 2014 10:30 AM-10:45 AM
The evolution of self-fertilization is one of the most commonly traversed transitions in flowering plants, with profound implications for population genetic structure and evolutionary potential. We investigated factors influencing this transition using Witheringia solanacea, a predominantly self-incompatible species within which self-compatible genotypes have been identified. We showed that self-compatibility in this species segregates with variation at the S-locus as inherited by plants in F1 and F2 generations. To examine reproductive assurance and the transmission advantage of selfing, we placed self-compatible and self-incompatible genotypes in genetically replicated gardens and monitored male and female reproductive success, as well as selfing rates of self-compatible plants. Self-compatibility did not lead to increased fruit or seed set, even under conditions of pollinator scarcity, and the realized selfing rate of self-compatible plants was less than 10%. Self-compatible plants had higher fruit abortion rates, consistent with previous evidence showing strong inbreeding depression at the embryonic stage. Although the selfing allele did not provide reproductive assurance under observed conditions, it also did not cause pollen discounting, so the transmission advantage of selfing should promote its spread. Given observed numbers of S-alleles and selfing rates, self-compatibility should spread even under conditions of exceedingly high initial inbreeding depression.

Bayesian Co-estimation of Selfing Rate and Locus-Specific Mutation Rates for a Partially Selfing Population

Benjamin Redelings, Marcy Uyenoyama

3B_306A-Selfing and Outcrossing
Monday, June 23, 2014 10:45 AM-11:00 AM
We present a novel Bayesian method for inferring the selfing rate and scaled mutation rates in a partially selfing population. We use the infinite-alleles model, and obtain the likelihood for diploid samples by extending the Ewens Sampling Formula to account for partial selfing. Our method allows inference from multi-locus data under a model that accounts for mutation-rate variation by allowing each locus to draw a mutation rate from a common distribution of mutation rates. This distribution is itself estimated from the data. We construct an MCMC algorithm and apply this model to an androdioecious population, jointly inferring the frequencies of males and hermaphrodites along with the selfing rate and other model parameters.

Global biogeography of mating system variation in seed plants

David Moeller, Ryan Briscoe Runquist, Annika Moe

3B_306A-Selfing and Outcrossing
Monday, June 23, 2014 11:00 AM-11:15 AM
Mating systems are among the most labile features of seed plants, with frequent evolutionary transitions across the spectrum from outcrossing to selfing. Previous work has shown strong associations between mating system variation and life history and vegetative growth form. Less is understood about the biogeography of mating system variation despite considerable speculation in the literature. For example, it has been argued that stronger biotic interactions at lower latitudes are associated with a higher frequency of outcrossers compared to high latitudes. Alternatively, it has been argued that latitudinal variation in the frequency of mating systems may simply arise as a by-product of geographic variation in the frequency of life history and growth form strategies. We examined the biogeography of mating system variation in seed plants using a global database of outcrossing rate estimates from 624 published studies of 492 taxa. We tested for an association between outcrossing rate and latitude, biome, life history, and growth form. We conducted analyses that accounted for phylogeny, in part, because we detected significant phylogenetic signal in our dataset. Consistent with previous analyses of a subset of this dataset, we found that life history and growth form were the strongest predictors of mating system variation. When examined alone, latitude was significantly associated with variation in outcrossing rates; however, this relationship was not apparent when phylogeny was taken into account. Similarly, when either life history or growth form was accounted for, we did not detect any geographic patterns to mating system variation. Our results are consistent with the hypothesis that biogeographic patterns of mating system variation are best explained by spatial patterns in the frequency of vegetative forms and life history strategies rather than by variation in biotic environments.

The evolution of selfing is accompanied by an increased frequency of effectively neutral and strongly deleterious mutations

Ramesh Arunkumar, Stephen Wright, Rob Ness, Spencer Barrett

3B_306A-Selfing and Outcrossing
Monday, June 23, 2014 11:15 AM-11:30 AM
The transition from outcrossing to selfing is predicted to reduce the genome-wide efficacy of selection because of the lower effective population size (Ne) that accompanies this change in mating system. In contrast, strongly recessive deleterious mutations exposed in more homozygous selfing backgrounds should be under stronger purifying selection. Here, we examine the distribution of fitness effects (DFE) and changes in the magnitude of effective selection coefficients (Nes) acting on mutations during the transition from outcrossing to selfing. Using forward simulations we investigated the ability of the DFE inference approach to detect the joint influence of mating system and the dominance of deleterious mutations on selection efficacy. We then investigated predictions from our simulations in the annual plant, Eichhornia paniculata, in which selfing has evolved on multiple occasions. We used range-wide sampling to generate whole transcriptome datasets and identified nonsynonymous and synonymous polymorphisms segregating in outcrossing and selfing populations. Based on both simulation and empirical results, we found that the transition to selfing was accompanied by a change in the DFE, with a larger fraction of sites that were effectively neutral (NesNe in selfers. Moreover, an increased proportion of sites in selfers were under stronger purifying selection (Nes>100), potentially because of the exposure of recessive deleterious mutations. We conclude that the transition to selfing in E. paniculata has been accompanied by the genome-wide influences of reduced Ne and stronger purifying selection against deleterious recessive mutations, an example of purging at the molecular level.

Getting into the cold: evolution of adaptations to freezing conditions in angiosperms

Amy Zanne, Jeremy Beaulieu, William Cornwell, David Tank

3B_306B-Climate and Evolution
Monday, June 23, 2014 10:15 AM-10:30 AM
Early angiosperms are thought to have been woody evergreen species restricted to warm habitats with few environmental stresses on their water-transporting vasculature; they have since expanded into almost every climate around the globe. As angiosperms spread, they needed to evolve traits that allowed them to survive in novel conditions such as freezing. In this expansion, stem and leaf construction are crucial as they determine how a plant experiences changing climates. To understand the evolutionary linkages between plant construction and freezing exposure, we assembled a large database of angiosperm growth habit, in conjunction with existing databases on leaf phenologies and water transporting conduit diameters, environmental exposure to freezing, and an unparalleled dated molecular phylogeny. We used likelihood based modeling to test for coordinated evolution between freezing exposure and leaf and stem traits. Climate exposure transition rates were strongly coordinated with leaf and stem trait states leading to different constructions in the presence of freezing. An evolutionary shift into freezing was coordinated with a shift to small conduits and/or a deciduous leaf phenology when species remained woody or a shift to an herbaceous habit. In most cases, angiosperms had already acquired the herbaceous habit or small conduits before moving into the cold while they acquired a deciduous leaf phenology after moving into the cold. The data reported here reflect that throughout the evolution of angiosperms, plant construction and freezing exposure have been intertwined allowing plants to either withstand or avoid seasonal freezing.

Historical responses of Antarctic penguins and seals to climate change

Jane Younger, Karen Miller, Barbara Wienecke, Mark Hindell, John van den Hoff

3B_306B-Climate and Evolution
Monday, June 23, 2014 10:30 AM-10:45 AM
It is estimated that 34% of Antarctic sea ice will be lost by 2100, greatly reducing the available habitat for predators that rely on sea ice for breeding and foraging, such as Emperor penguins and Weddell seals. In order to implement effective management plans for these animals we need a better understanding of the likely impacts of climate change. To address this need, we used genetic data to understand how populations have responded to past periods of climate change and their current adaptive capacity. The mitochondrial control region and cytochrome b were sequenced for 110 Weddell seals and 120 Emperor penguins from colonies across East Antarctica. Present day gene flow patterns for populations of seals and penguins were determined using FST to understand population structure and dispersal ability. We also used Extended Bayesian Skyline Plots in conjunction with a heterochronous dataset and molecular clock methods to investigate historical population trends and how these might be related to climate change. Despite their similar habitat requirements we found very different population structures for the two predators. In the case of Emperor penguins the entire 4000km of East Antarctica constitutes a single breeding population (overall FST = -0.00472; p = 0.553; pairwise FST amongst localities p > 0.05). In contrast, Weddell seals are significantly structured across the same spatial scale (overall FST = 0.12602; p = 0.000). This suggests that there are some barriers to dispersal for Weddell seals in this region, which may impede their ability to range shift under future climate change scenarios. In terms of demographic history we discovered that the East Antarctic Emperor penguin population has increased in abundance by a factor of four since the end of the Last Glacial Maximum, concurrent with rising air temperatures. Weddell seals show no concomitant increase, with the population remaining relatively stable throughout several climate fluctuations. This is intriguing given the apparently similar habitat niche for the two species. Overall these two ice-dependent predators show very different responses to climate change and will require different management strategies despite their similar habitat.

The combined effects of artificial warming, competition, and community composition on life history traits and patterns of natural selection

Susana Wadgymar, Benjamin Gilbert, Matthew Cumming, Caroline Tucker, Marc Cadotte, Arthur Weis

3B_306B-Climate and Evolution
Monday, June 23, 2014 10:45 AM-11:00 AM

Climate warming has influenced patterns of growth and phenology in many plant species. The adaptive nature of life history traits suggests that any warming-induced plasticity is likely to influence patterns of selection. However, competitive interactions can also influence the expression of these traits, and studies examining responses to climate change have not typically accounted for variation in the competitive environment. Selection for specific traits may be weaker or stronger in the presence of competitors, depending on common responses to warming cues. For example, selection for earlier flowering onset with warming may be dampened when a competitor species has an earlier phenology, or alternately be heightened when a competitor has a later phenology. This potential for competitive interactions to alter the selective regimes imposed by warming remains unexplored.

We manipulated competitive and thermal regimes for 3 competing weedy plant species: Sinapis arvensis (early flowering), Chamaecrista fasciculata (intermediate flowering) and Ambrosia artemisiifolia (late flowering). Each species was planted in high and low density monocultures as well as in polycultures that included all three species. These communities were then either artificially warmed via infrared heating or exposed to ambient temperatures. Seed production was measured for each individual and selection on flowering onset (a temperature-sensitive trait) and plant size (a trait representative of competitive ability) was estimated in each environment.

Artificial warming advanced flowering in the early and intermediate flowering species. Competition with non-conspecifics delayed flowering time for the intermediate and late flowering species, producing a response antagonistic to that of warming for the intermediate species. Intraspecific competition and high densities reduced plant size for the earliest species, while interspecific competition and high densities had the same effect for the intermediate and late flowering species. Elevated temperatures increased plant size only in the last species to flower. Directional selection for larger plant size was significant for all species in all treatments but was stronger in monoculture plots for early and late species whereas it was stronger in mixed culture plots for the intermediate species. Selection for flowering onset was consistently insignificant for the middle and late flowering species and was only positive for the early flowering species when grown in noncompetitive conditions.

These results suggest that the effects of increased temperature and competition on a species may depend on its position within the developmental sequence of a community. Specifically, species with intermediate flowering times face competition from early and later developing species, and this produces a constraint on selection for flowering onset. Over time, this may lead to altered competitive dynamics that can act synergistically with the direct effects of global warming.

Natural variants of the gene Crystallin are associated with differential seasonal adaptation in Drosophila melanogaster

Xiaqing Zhao, Subhash Rajpurohit, Alan Bergland, Ozlem Onder, Paul Schmidt

3B_306B-Climate and Evolution
Monday, June 23, 2014 11:00 AM-11:15 AM

The worldwide expansion of Drosophila melanogaster from tropical areas of Africa to temperate regions has required adaptation to the pronounced seasonality in temperate habitats. Diapause was shown to be a derived life history strategy that D. melanogaster take to increase overwintering survivorship, hence adapt to the temperate climate. It is a genetically determined syndrome cued by shortened photoperiod and/or reduced temperature that results in lifespan extension, delayed senescence, increased stress tolerance and reproductive quiescence. In natural populations of Drosophila melanogaster, the expression of diapause is highly variable. In our study of the transcriptomic and proteomic profiling of diapause and non-diapause populations, the gene Crystallin (Cry), which is known to be a structural constituent of eyes, came out as one of the most differentially expressed genes, with low expression in diapause populations as compared to non-diapause populations; this was consistent at both the mRNA and protein levels. In our search of seasonal genetic variants in natural populations, a SNP on the intronic region of Cry is found to oscillate in frequency among seasons consistently over 3 consecutive years, indicating that it is subject to strong, temporally variable selection. This SNP is trans-specific in D. melanogaster and D. simulans, thus is likely to be under balancing selection before the two lineages diverged. To investigate the functional significance of this SNP in Cry, we constructed pairs of out bred populations with the Drosophila Genome Reference Panel (DGRP) lines that are know to carry one or the other allele at this specific site, such that the only difference between the populations is their allele state on this SNP and the background is randomized. Another pairs of populations are constructed with a matched control SNP in the same way. Diapause incidence under long and short day conditions demonstrated that the summer-adapted allele is more responsive to photoperiod than the winter-adapted allele. Furthermore, the alternative alleles are also shown to affect a subset of other traits genetically correlated with diapause expression. These effects were also confirmed with complementation tests. Our result indicates that the two alleles in Cry may contribute to seasonal adaptation through differential perception of light. This study represents a comprehensive evaluation of seasonal adaptation, from genome wide screens to the functional validation of identified genes and SNPs.

Climate change, phylogeography and the future of genetic diversity

Katharine Marske, Mirnesa Rizvanovic

3B_306B-Climate and Evolution
Monday, June 23, 2014 11:15 AM-11:30 AM

One response available to species during periods of rapid climate change is to shift their distributions to track suitable climatic conditions. Predictive models of where species are likely to occur in the future have thus emerged as an important scientific and conservation tool, but deploying these models at the species level may fail to detect important intraspecific variation related to local environmental adaptation or that will provide the raw materials for future evolution. We estimated how much existing genetic diversity is likely to remain by the end of this century, and which aspects of a species' phylogeographic history this represents, for New Zealand forest beetles under different climate change scenarios. Each species' phylogeny was pruned to include just those haplotypes currently present in areas predicted by ecological niche models to remain climatically suitable. Trees resulting from these future haplotype pools were compared against a series of random draws from the full haplotype pool to determine whether genetic diversity will be lost in a random or nonrandom fashion. This provides the opportunity to calculate not just projected loss of genetic diversity (i.e, number of haplotypes and genetic distance), but the extent to which this loss obscures a species' evolutionary history.

The soft shoulder effect: spurious signatures of soft and partial selective sweeps result from linked hard sweeps

Daniel Schrider

3B_306C-Genetics of Adaptation
Monday, June 23, 2014 10:15 AM-10:30 AM
Characterizing the nature of the adaptive process at the genetic level is a central goal for population genetics. In particular, we know little about the sources of adaptive substitution. Historically, population geneticists have focused attention on the hard sweep model of adaptation in which a de novo beneficial mutation arises and rapidly fixes in a population (e.g. Maynard Smith and Haigh 1974). Recently more attention has been given to soft sweep models, in which alleles that were previously neutral, or nearly so, drift until such a time as the environment shifts and their selection coefficient changes to become beneficial (e.g. Hermisson and Pennings 2005). It remains an active and difficult problem however to tease apart the tell-tale signatures of hard vs. soft sweeps in genomic polymorphism data. Through extensive simulations of hard and soft sweep models, here we show that indeed the two might not be separable through the use of univariate summaries. In particular it seems that recombination in regions linked to, but distant from, sites of hard sweeps can create patterns of polymorphism that closely mirror what is expected to be found near soft sweeps. This problem of "soft shoulders" suggests that we currently have only a very limited ability to differentiate soft vs. hard sweep scenarios in molecular population genomics data, particularly when the targets of selection are not known a priori (e.g. genome-wide scans). Further we find a very similar shoulder effect confounds haplotype-based statistics that are aimed at detecting partial or ongoing selective sweeps.

Genomics of Variation in Nutrient Metabolism and Stress Resistance in Yeast

Dana Opulente, Christopher Morales, Isaak Heon, Kashyapa Bandaralage, Joshua S. Rest

3B_306C-Genetics of Adaptation
Monday, June 23, 2014 10:30 AM-10:45 AM
The genomic basis of adaptation to diverse environments is an outstanding question in evolution. Further, the extent that co-variation or tradeoffs among sets of traits, or among environmental parameters, shapes patterns of variation in poorly studied. We took advantage of the diverse habitats and variable ability to assimilate alternative nutrient sources in budding yeast, Saccharomyces cerevisiae, to identify patterns of co-variation and its possible genomic basis. We examined the growth of diverse strains of S. cerevisiae across environmental parameters (18 carbon and 3 nitrogen sources, and 2 different stressors) in a fractional factorial experiment. We show that there is significant variation in growth among strains across environmental and nutrient conditions, and significant interaction terms relating growth among carbon and nitrogen sources, and carbon sources and stressors. We took advantage of available genome sequence for a subset of these strains to examine the genetic basis of this growth variation. We find that both gene content and copy number variation play a role in the variation in environmental and nutrient responses we observe across strains.

Comparative analysis of preference and performance genes in the evolution of host specialization in Neodiprion sawflies

Kim Duong, Catherine Linnen

3B_306C-Genetics of Adaptation
Monday, June 23, 2014 10:45 AM-11:00 AM
Ecological specialization is crucial for the extensive biodiversity and overall abundance of phytophagous insects. Understanding the genetic architecture behind the evolution of specialist traits will enhance our understanding of host use adaptation and provide insights into species diversity. Previous research in Drosophila suggests that ecological specialization may evolve through widespread loss-of-function (LOF) mutations and pseudogenization in host preference genes, particularly those for chemosensory recognition and avoidance. Because of the lack of ecological knowledge in Drosophila, however, we do not know if these genetic patterns apply equally to the gain of novel hosts and the loss of ancestral hosts, or if they apply to host use phenotypes beyond chemosensation. To address this gap, I propose a genus-wide study of the ecologically well-characterized pine sawfly genus Neodiprion, with emphasis on the N. lecontei and N. pinetum clade and white pine (Pinus strobus) host use phenotype. I will compare genomic data to identify signs of LOF mutations and pseudogenization in chemosensory and detoxification genes and use RNA-seq to identify expression divergence in host-related genes. Genus-wide comparisons will allow for the identification of genetic patterns unique to the gain and or loss of specific host plants and also for the identification of loci repeatedly acted on during specialization. This research will determine how general the conclusions from Drosophila are for phytophagous insects, contribute critical data regarding host performance, make it possible to distinguish the genetics of host loss from host gain, and potentially identify predictable genetic underpinnings for the evolution of host plant specialization.

EDA signaling and phenotypic evolution of sculpins (Cottus) after admixture

Jie Cheng, Arne Nolte

3B_306C-Genetics of Adaptation
Monday, June 23, 2014 11:00 AM-11:15 AM

A hybrid lineage of sculpins (Cottus) resembles one of the ancestral species (C. perifretum) more than the other one (C. rhenanus) in phenotypic features. This contrasts with the expectation of hybrid intermediacy because most of the genome is thoroughly admixed. Thus, it is likely that phenotypic traits are subject to directional selection. Two of the concerned traits, the scale-like skin prickling and body shape, represent a common source of variation among a number of Cottus species. The Ectodysplasin (EDA) signaling pathway provides promising candidates to investigate the genetic basis of these traits because it is known to affect the development of dermal bones and scales in fishes. We identified and mapped Cottus EDA signaling pathway components and performed quantitative trait locus (QTL) mapping for prickling and body shape. A single genomic region that affects prickling in Cottus was detected. This region contains the EDA receptor (Edar) but none of the other EDA pathway genes. The same QTL region also shows effects on body shape. In situ hybridization experiments confirmed that Edar expression is associated with the development of prickling. A population genomic analysis of the admixed Cottus gene pool showed that Edar genomic ancestry is biased towards C. perifretum, which agrees with the phenotypic similarity of invasive Cottus with that species. Taken together, the data implies that the Edar allele inherited from C. perifretum strongly determines phenotypic variation of hybrid Cottus. EDA signaling constitutes a key adaptive trait in stickleback and our results suggest that the same pathway may contribute to conspicuous phenotypic variation in Cottus.

Building developmental mechanisms into genotype-phenotype predictions in changing environments

Daniel Runcie, Johanna Schmitt, Stephen Welch, Reena Sellamuthu, Martha Cooper

3B_306C-Genetics of Adaptation
Monday, June 23, 2014 11:15 AM-11:30 AM

A fundamental challenge in evolutionary biology is to understand the genetic basis of phenotypic differences among individuals. Here, we present a detailed mechanistic genotype – phenotype model of the timing of flowering in the annual plant Arabidopsis thaliana. Our model draws on physiology, genetics and gene networks to explain how environmental conditions throughout the entire developmental history of an organism shape its relationship between genotype and phenotype. We show how gene x environment interactions and epistasis among alleles are emergent properties of the developmental model. Finally, we demonstrate the power of our model by predicting flowering time phenotypes of novel genotypes in a recombinant inbred line panel in seasonal environments and validating these predictions against field data.

Nutritional contributions by gut symbionts ensures metabolic homeostasis in an insect host

Hassan Salem, Eugen Bauer, Martin Kaltenpoth

3B_402-Symbiosis
Monday, June 23, 2014 10:15 AM-10:30 AM

In many animals, symbiotic microorganisms play an important role for nutrition, but remarkably little is known about the host’s metabolic response to symbiont presence, despite the far-reaching implications for fundamental and applied sciences.

Within the Pyrrhocoridae insect family (Hemiptera), recent characterization of the microbial community revealed a consistent and conserved microbiota, with the notable co-occurance of two actinobacterial taxa (Coriobacterium glomerans and Gordonibacter spp.) throughout the M3 and M4 regions of the insect's mid-gut. Similar to many hemipterans, firebugs rely on egg smearing for the vertical transmission of their gut symbionts. This involves the deposition of symbiont-bearing droplets by adult females over newly laid eggs, and the subsequent oral uptake of the microbes by the hatched nymphs.

Across two species of firebugs (Pyrrhocoris apterus and Dysdercus fasciatus), we demonstrate that egg surface sterilization results in symbiont-deprived individuals (aposymbionts) that exhibit slower growth rates, higher mortality and lower reproductive success, suggesting an essential function for the actinobacterial symbionts. Additional findings from artificial diet experiments demonstrate that the symbionts contribute towards their host through the provisioning of B-vitamins; a condition further supported by the discovery of complete pathways for the biosynthesis of thiamine (B1), riboflavin (B2), nicotinamide (B3), pantothenate (B5) and folic acid (B9) in the sequenced genome of C. glomerans.

Additionally, comparative transcriptomic analyses of insect genes expressed in the mid-gut regions of firebugs revealed a differential up-regulation of genes involved in the import and processing of B-vitamins among aposymbionts relative to symbiont-bearing individuals. This is consistent with the regulatory mechanisms known for the B-vitamin metabolism, where specific transcriptional activators are preferentially expressed in the absence of their respective vitamin co-factors (i.e. in case of deficiency). Normal expression levels of these genes, however, can be restored in firebugs either through the artificial supplementation of B-vitamins into the insect's diet or reinfection with actinobacterial symbionts.

Collectively, our findings demonstrate that – despite an extracellular localization – beneficial gut microbes can be integral to an insect’s metabolic homeostasis, reminiscent of bacteriome-localized intracellular mutualists.

Geographical stability of endosymbiotic gut bacteria of the large pine weevil and their role in the detoxification of terpenes

Aileen Berasategui, Christian Paetz, Jonathan Gershenzon, Axel Schmidt, Martin Kaltenpoth

3B_402-Symbiosis
Monday, June 23, 2014 10:30 AM-10:45 AM

Mutualistic microbial partners of insects are commonly reported to be engaged in nutritional and defensive interactions with their hosts. However, they have also been described to be involved in the detoxification of noxious compounds contained in their host´s food source. This, although well described in symbioses between insects and fungus or yeasts, needs more support for mutualistic bacteria. So far, only one example of bacterial detoxification of a noxious compound has been demonstrated in insects, showing experimentally that pesticide-resistant strains of Burkholderia can establish stable symbiotic relationships with broad-headed bugs conferring them resistance.

The pine weevil (Hylobius abietis, Coleoptera) feeds on bark and phloem of Norway spruce (Picea abies), which contains resin ducts filled with a complex mixture of resin acids. Ingested mono, sesqui and diterpenes -conifer main secondary metabolites- can cause neural damage and disruption of gut membranes in insects. However, they seem to have no negative effect on H. abietis.

We are interested in how the large pine weevil copes with the terpenes in the host bark and cambium. Preliminary studies have shown that weevils do not avoid terpenoid-containing tissues and that antibiotic-treated individuals cannot digest these compounds as efficiently as non-treated ones suggesting a possible role of symbiotic bacteria in terpene detoxification. To identify putative detoxifying candidates we have characterized the gut microbial community from weevils from different geographical areas, both using culture-dependent and independent methods. Our results show a geographically stable community dominated by Enterobacteria and Firmicutes similar to that of bark beetles occupying similar ecological niches. Additionally, we have isolated and purified the natural mixture of diterpenes present in bark and are using a transcriptomic approach on artificial diet with and without this mixture to identify the enzymes involved in terpene degradation. In addition, we can supplement an artificial diet with a pure C13-labeled diterpene mixture to identify the metabolic products of the detoxification and whether they are used as nutrients and are incorporated into the insect tissues.

Elucidating the fate of these compounds will shed some light on how insects cope with plant induced defenses and how some symbionts allow their hosts to exploit otherwise inaccessible food sources.

Gene expression during parasitoid adaptation to symbiont-conferred resistance

Alice Dennis, Christoph Vorburger

3B_402-Symbiosis
Monday, June 23, 2014 10:45 AM-11:00 AM

Parasitoids are organisms which require, but ultimately kill, a host for reproduction. Thus there is strong reciprocal selection for the hosts to avoid parasitism and the parasitoids to successfully reproduce. In these systems, rapid experimental evolution has been observed such that parasitoids may overcome a static host defense system in just a few generations. The parasitoid wasp Lysiphlebus fabarum lays eggs within the black bean aphid (Aphis fabae); to develop, this egg must overcome not only the aphid immune system, but also defenses of a protective endosymbiont (Hamiltonella defensa). It is this bacterial defense that largely prohibits parasitoids from developing. To investigate the basis of rapid parasitoid evolution, we have experimentally evolved lines of L. fabarum, on three aphid hosts: two lines of aphids housing different endosymbiont isolates and a third line which lacks a protective bacterium. After just 10 generations, we observed an increased ability for wasps to infect the symbiont-protected aphid lines on which they have evolved. To explore the genomic basis of this adaptation, we are employing RNAseq to investigate shifts in gene expression associated with increased infectivity.

Assessing eco-evolutionary feedbacks among pea aphids, defensive symbionts, and natural enemies

Jacob Russell, Andrew Smith, Piotr Lukasik, Kerry Oliver

3B_402-Symbiosis
Monday, June 23, 2014 11:00 AM-11:15 AM

The microbiome can significantly impact eukaryotic phenotypes and serve as an additional source of heritable genetic variation. While patterns across eukaryotes are consistent with a role for symbiotic microbes in host macroevolution, few studies have examined symbiont-driven host evolution or the ecological implications across short timescales. In this study we report seasonal shifts in the frequencies of heritable defensive bacteria from the pea aphid, Acyrthosiphon pisum, across two host races and geographic regions. These shifts were consistent with symbiont responses to host-level selection and, indeed, findings from one population suggested symbiont-driven adaptation to seasonally changing parasitoid pressures. Conversely, symbiont levels seemed to influence enemy success when measured across host races, revealing ecological impacts of microbiome divergence. But overall the lack of clear patterns for several symbionts suggests disruption of symbiont-driven host-enemy dynamics, a finding of broad significance given the widespread nature of defensive microbes across plants and animals.

The Effects of Endosymbionts Across Food Webs: How Aphid Endosymbionts Affect the Survival of the Predatory Invasive Lady Beetle Harmonia axyridis

Jennifer Kovacs, Candice Gaul, Seth Wolf, Dene Voisin, Nicole Gerardo

3B_402-Symbiosis
Monday, June 23, 2014 11:15 AM-11:30 AM

Non-essential, facultative, symbiotic microbes can provide their hosts with protection from parasites, pathogens, and predators. Recent work has found that two facultative secondary symbionts Serratia symbiotica and Hamiltonella defensa, provide their host, the phloem-feeding insect the pea aphid (Acyrthesiphon pisum), with protection against predation from the lady beetle Hippodamia convergens. Lady beetle larvae fed a diet of aphids with secondary symbionts had significantly reduced survival both to pupation. We have recently extended this work to look at the fitness effects of aphid secondary symbionts (Serratia symbiotica, Hamiltonella defensa, and Regiella insecticola) in another aphid predator, the invasive lady beetle Harmonia axyridis. Similar to previous results, we found the survival of juvenile lady beetles to be significantly reduced for those that were fed aphids with secondary symbionts Serratia, as well as Regiella, however no fitness costs were found for those fed aphids with Hamiltonella or no symbionts. Also, unlike our previous findings in Hi. convergens where larval survival was reduced, pupal survival was reduced in this lady beetle species, Ha. axyridis, while larval survival was unaffected by the presence or type of aphid symbiont in the larval diet. Additionally, Ha. axyridis larvae fed aphids without symbionts or with the Hamiltonella symbionts were significantly heavier as adults than those fed aphids with the Serratia and Regiella symbionts. The presence of aphid symbionts in the larval diet of Ha. axyridis was also found to significantly affect development time to adulthood. Therefore this is yet another example of aphid endosymbionts, by reducing the fitness of the aphid predator, indirectly defending their host against predation, since aphids reproduce clonally and are often found in large genetically identical groups. Interestingly, the survival effects appear to be different between the species of predator, with one species being most affected during larval development and the other during pupal development. Additionally, for both predator species, different symbionts had different affects suggesting that each symbiont reduces the survival of the predator through a different mechanism. This work provides yet another example of the often far-reaching and unexpected effects that endosymbionts can have in ecological systems and highlights the importance of expanding our study of endosymbionts to include the many ecological interactions of their host species.

A twisted view of ecology and speciation

John Wiens

3B_BalC-ASN Solicited Symposium: Beyond reproductive isolation: microevolutionary controls on macroevolutionary speciation dynamics
Monday, June 23, 2014 10:15 AM-10:45 AM

Ever since Darwin, ecological divergence between populations has often been thought to play a pivotal role in speciation. At the same time, allopatric speciation is often considered the predominant geographic mode of speciation. Here, I review the idea that a key part of allopatric speciation may actually be the failure of niches to diverge over time (i.e. niche conservatism). Specifically, niche conservatism may ultimately be responsible for the initial geographic isolation of allopatric populations (and thus their separation into different lineages). In much of the speciation literature, this initial phase of allopatric speciation is ignored, although a “geographic barrier” is sometimes invoked. However, these “geographic barriers” can be conceptualized as areas of divergent ecological conditions to which the species is not adapted, making the failure to adapt to these conditions over time a key part of allopatry and allopatric speciation. This model does not rule out the importance of ecological divergence (and many other processes) at other points during the process of allopatric speciation, but does suggest that an exclusive focus on ecological divergence may miss an important aspect of allopatric speciation. Furthermore, consideration of this model also raises the question of whether many of the processes that are traditionally studied in regards to allopatric speciation actually pertain to the origin of new lineages or instead to their maintenance over time. In this talk, I will review empirical and theoretical evidence for the model of speciation through niche conservatism and future areas for research in its study.

The genetic architecture of hybrid inviability in Drosophila

Daniel Matute

3B_BalC-ASN Solicited Symposium: Beyond reproductive isolation: microevolutionary controls on macroevolutionary speciation dynamics
Monday, June 23, 2014 10:45 AM-11:15 AM

I investigate the genetic basis of reproductive isolation by applying a combination of classical genetics, field collections, and population genomics primarily to understand the genetic basis of phenotypes involved in reproductive isolation. In particular, I have concentrated on the genetic interactions that lead to hybrid lethality. Dissecting the genetic basis of hybrid inviability not only reveals the role of molecular evolution in keeping species distinct, but also sheds light on coevolution required for genes to interact normally in pure species. My main research focus is the hybrids between two diverged species: Drosophila melanogaster and D. santomea. I have identified eight genes that regulate early embryonic development in pure species but cause inviability in hybrids. Though they are thought to have conserved functions over broad evolutionary scales, the fact that these genes cause inviability in Drosophila hybrids hints at cryptic divergence in their molecular functions. This research entails the use of classical, population, and developmental genetics to understand the evolution of developmental pathways that can cause hybrid inviability in mel/san hybrids. Identifying the genes involved in hybrid incompatibilities in Drosophila will reveal the molecular and developmental mechanisms of postzygotic isolation—that is, how do genes that behave normally within species cause developmental problems when interacting in hybrids?

What can theoretical studies of microevolutionary speciation processes tell us about macroevolutionary patterns?

Maria Servedio

3B_BalC-ASN Solicited Symposium: Beyond reproductive isolation: microevolutionary controls on macroevolutionary speciation dynamics
Monday, June 23, 2014 11:15 AM-11:45 AM

Many advances have been made in theoretical studies of speciation mechanisms on a microevolutionary scale, but the extent to which these studies inform macroevolutionary patterns remains unclear. Theoretical studies can suggest evolutionary scenarios or forces that may be found, in comparative studies, to lead to higher or lower species richness. I focus on two potential sources of disconnect between studies of microevolutionary process by theoreticians and of macroevolutonary pattern by empiricists. First, theoreticians are primarily (but not exclusively) interested in speciation with gene flow because of the complex theoretical challenges posed by this process; if most speciation is in fact allopatric then a discrepancies between studies of process and pattern would be expected. Second, speciation with gene flow may lead to the evolution of isolating barriers that are incomplete or impermanent, and which may thus not be observed at macroevolutionary scales.

Joint effects of pollen limitation and pollen competition on offspring quality in a wind-pollinated herb

Anne-Marie Labouche, John Pannell

3C_201-Pollination
Monday, June 23, 2014 1:30 PM-1:45 PM
Pollination intensity regulates both seed set and offspring quality, with pollen-limited plants producing fewer seeds and progeny produced under high pollen loads and thus intense pollen competition expressing potentially better genotypes. Moreover, low seed production may result in larger seeds due to size-number tradeoffs. Surprisingly, however, these links between pollen competition and pollen limitation have seldom been made. We measured several components of fitness for progeny produced by females of the wind-pollinated dioecious plant Mercurialis annua under different levels of pollen limitation and thus pollen competition. Specifically, we tested the effect of pollination intensity on offspring performance in a design that allowed us to distinguish genetic and seed-size effects on offspring quality. We found that pollination intensity and maternal effects significantly affected offspring performance. Most of the first seedlings to emerge has been sired under high pollen loads. Pollen-limited mothers produced larger seeds, and larger seeds enjoyed growth advantages over smaller ones after emergence. We also found significant genetic and maternal effects on reproductive effort that depended on the competitive environment. Our results illustrate for the first time the contrasting genetic and maternal effects of pollen limitation on offspring quality.

Pollen competition in style: Is bigger always better?

Shu-Mei Chang

3C_201-Pollination
Monday, June 23, 2014 1:45 PM-2:00 PM
Most flowering plants are hermaphroditic and can gain fitness through both male (pollen) and female (ovule) functions. While mechanisms underlying the variation in female fitness (often measured as seed production) have been studied extensively, ones that influence variation in male fitness (pollen siring success) remain poorly understood, resulting in a biased towards using female fitness for evolutionary interpretation in many cases. This study aims to understand the causes and patterns of variation in male fitness by focusing on the influence of one of the male traits – pollen size. Specifically, by taking this “bottom up” approach this study will examine the relationship between pollen size and variation in male fitness. Pollen size varies greatly among different angiosperms species (diameter ranges from 5 ~ 250 μm) but is often considered to have little variation within a species; presumably due to a strong selection for the optimal pollen size for specific pollination conditions in each species. However, similar to several recent studies, we found that significant phenotypic and genetic variation still exist within and among natural populations of the common morning glory, Ipomoea purpurea, making it a suitable system for this study. In the current study, we test the hypothesis that variation in pollen size, presumably an index of pollen quality, will lead to variation in male fitness. We generated plants with divergent pollen sizes using an artificial selection approach. In a pollen competition experiment, we found that genotypes with larger pollen sizes sired significantly more ovules than those with smaller pollen sizes. We also investigated whether differential pollen tube growth rates were responsible for this pattern. Results will be discussed in the context of sexual selection in flowering plants.

Selection on floral traits through male and female fitness in two species of milkweed that differ in pollen limitation of seed set

Raffica La Rosa, Jeffrey Conner

3C_201-Pollination
Monday, June 23, 2014 2:00 PM-2:15 PM
Milkweeds have unusual floral traits that are likely adaptive for insect pollination, but are not well understood. The flowers are hermaphroditic, so individual floral traits may be adaptive for male fitness, female fitness, or both. In populations or species where female fitness is resource limited rather than pollen limited, we predict selection on floral traits will be through male fitness only, following Bateman. In populations where female fitness is instead limited by pollen receipt, we predict selection through both male and female fitness. We measured selection on floral traits in two species, Asclepias incarnata and A. exaltata; female fitness is pollen limited in the latter but not in the former. Female fitness was estimated as seeds set and male fitness as seeds sired using molecular genetic paternity analysis.

The consequences of pollinator declines on the quantity and quality of offspring in two New Zealand tree species

Megan Van Etten, Jennifer Tate, Alastair Robertson

3C_201-Pollination
Monday, June 23, 2014 2:15 PM-2:30 PM
Birds provide a variety of ecosystem services, such as pollination and seed dispersal, leading to concerns about how declining numbers of birds worldwide could affect other trophic levels. One such “trophic cascade” of concern is the potential for decreased pollination services leading to increased production of unfit selfed seeds and, ultimately, population declines of bird pollinated species. This effect could be especially drastic in New Zealand where the flora is heavily reliant on birds for pollination and almost half of the bird species have become extinct in the past ~700 years of human habitation. To determine the effect of bird declines on the population dynamics of the plants they pollinate, we examined pollinator abundances, selfing rates and inbreeding depression of two endemic tree species, Fuchsia excorticata and Sophora microphylla. We found high pollen limitation, high selfing rates and high inbreeding depression in most populations of both species.

Due to these high selfing rates (50-70%) and that nearly all selfed seeds die prior to adulthood, most of the seeds produced will not contribute to population growth and could lead to cryptic recruitment failure.

Dad saves the day: biparental plastid inheritance rescues cytonuclear incompatibility

Karen Barnard-Kubow, Laura Galloway

3C_206-Plant Organelles
Monday, June 23, 2014 1:30 PM-1:45 PM
There is a growing appreciation for the role cytonuclear incompatibilities play in the development of reproductive isolation and subsequent speciation. Theory proposes they may be among the first genetic incompatibilities to arise during the speciation process. However, this theory is predicated, in part, on uniparental organelle inheritance. While organelle inheritance is predominantly maternal, around 20% of angiosperms show biparental plastid inheritance. How might biparental plastid inheritance impact the dynamics of cytonuclear incompatibility? We address this question in Campanulastrum americanum, a plant species that has a strong intraspecific cytonuclear incompatibility (up to 75% decrease in survival). Preliminary data had also suggested the possibility of biparental plastid inheritance occurring in this species. By measuring plastid inheritance patterns and survival in multiple intraspecific crosses we show that although a strong cytonuclear incompatibility has arisen in C. americanum, biparental plastid inheritance rescues intraspecific hybrids from this incompatibility. Interestingly, our results also show that biparental inheritance occurs at a moderate level in this species regardless of genetic distance or the existence of cytonuclear incompatibility.

Contrasting patterns of plastid and mitochondrial genetic diversity in gynodioecious Lobelia siphilitica (Campanulaceae)

Andrea Case, Binaya Adhikari, Hannah Madson, Eric Knox, Christina Caruso

3C_206-Plant Organelles
Monday, June 23, 2014 1:45 PM-2:00 PM
In flowering plants, mitochondrial and plastid genomes should be maternally co-inherited, thus cytoplasmic haplotypes are expected to be in linkage disequilibrium (LD). The absence of LD may be caused by differences between genomes in mode of inheritance, recombination, or the effects of evolutionary forces. In gynodioecious plants, such evolutionary forces are likely to include selection on mitochondrial male sterility (CMS) genes. CMS genes prevent pollen production, converting some hermaphrodites into females. Theoretical models of gynodioecy predict that populations containing a higher frequency of females should contain multiple CMS genes as a result of frequency-dependent selection. Therefore, mitochondrial haplotype diversity is predicted to be higher in high-female populations, but no such relationship is predicted for the plastid (pt) genome except through LD with mitochondria (mt). Here, we documented haplotype diversity in both mt and pt genomes using populations of Lobelia siphilitica varying in sex ratio from 0% to >80% female. We observed high haplotype and nucleotide diversity as well as strong population structure in both genomes. Population sex ratio was positively correlated with mt haplotype and nucleotide diversity, but not pt diversity. Although diversity in both genomes was structured geographically, there was no LD between pt and mt. A reticulate mt haplotype network suggests that recombination has contributed to mt diversity, while significant positive correlations with population sex ratio indicate frequency-dependent selection. The absence of either of these characteristics in the pt dataset is consistent with decoupling of the evolutionary dynamics of cytoplasmic genomes in L. siphilitica.

The plastomes of mycoheterotrophic Ericaceae exhibit extensive gene loss and rearrangements

Thomas Braukmann, Sasa Stefanovic

3C_206-Plant Organelles
Monday, June 23, 2014 2:00 PM-2:15 PM
Heterotrophic plants show a wide range of evolutionary degradation of photosynthetic ability and rely entirely or partially on their hosts to supply water and nutrients. These plants are divided into two distinct, but evolutionary artificial groups: parasitic and mycoheterotrophic plants. Haustorial parasitism has evolved at least 11 times independently and there are at least 10 independent origins of mycoheterotrophy in angiosperms. Ericaceae, the heather family, is a large and diverse group of plants with elaborate symbiotic relationships with mycorrhizal fungi, including several mycoheterotrophic lineages. Based on previous hybridization results, the plastomes of 10 representative Ericaceae species with different life histories and trophic levels, including multiple representatives from the hemi-mycoheterotrophic pyroloids and holo-mycoheterotrophic monotropoids were sequenced using a nextgen sequencing approach (Illumina). Our results indicate that rearrangements of the large single copy region as well as expansion and contraction of the inverted repeat regions of the plastome are typical for most member of Ericaceae. Both non-synonymous (Ka) and synonymous substitution (Ks) rates were evaluated to determine if a relaxation of the plastid genes occurred prior to the transition to mycoheterotophy, a pattern that has been observed in parasitic plant lineages. The plastomes of monotropoids exhibit extensive loss of genes relating to photosynthetic function and retain genes with possible function outside photosynthesis. Furthermore, hemi-mycoheterotrophic plants retain most genes relating to photosynthesis but are polymorphic for the presence of the plastid 'ndh' genes. Our results extend previous inferences that plastid gene losses occur prior to becoming holo-heterotrophic and that mycoheterotrophic Ericaceae exhibit gene loss similar in pattern to parasitic plants.

Organellar phylogenomics of green plants

Matthew Gitzendanner, Brad Ruhfel, Guanqiao Feng, Greg Stull, Claudia Segovia, Gane Ka-Shu Wang

3C_206-Plant Organelles
Monday, June 23, 2014 2:15 PM-2:30 PM
Recent advances in sequencing technologies and computational approaches have dramatically changed the equation for balancing depth of taxon sampling and amount of data used for phylogenetic inference, enabling the construction of large genomic-level datasets. Using transcriptome data from the One Thousand Plants

Initiative (1KP, onekp.com) and previously published organellar genomes, we generated nearly complete datasets of chloroplast and mitochondrial genes for 1,300 green plants. The chloroplast genome has long been the workhorse of plant phylogenetics and, due to within-individual homogenization and its low levels of recombination, is simpler to analyze than the nuclear genome. Similarly, mitochondrial gene space is relatively easy to isolate and analyze. In addition to presenting the overview of relationships inferred from these two data sources, we will focus on the challenges encountered in assembling and analyzing datasets on this scale.

Horizontal gene transfer in the mitochondrial genome of Monsonia emarginata

Logan Cole, Jeffrey Mower, Jeffrey Palmer

3C_206-Plant Organelles
Monday, June 23, 2014 2:30 PM-2:45 PM

Recent studies have shown that plant genomes have been involved in horizontal gene transfer (HGT). The mitochondrial genomes of plants have been especially subject to HGT when compared to the organellar and nuclear genomes of other eukaryotes. Phylogenetic analyses suggest HGT as the source for copies of many genes recovered from the assembly of the mitochondrial genome of Monsonia emarginata, a member of the angiosperm family Geraniaceae. These analyses suggest that potential donors are restricted to the angiosperms. Though the mitochondrial genomes of the Geraniaceae contain many examples of unusual molecular evolutionary phenomena, there is no evidence for such HGT in other members of this family. This may suggest the recent derivation of the propensity for HGT in this lineage. Some of the transferred copies are intact, which indicates functionality and/or the recent occurrence of HGT. This work contributes to the growing body of evidence that HGT has had a significant impact on the evolution of genomes in eukaryotes. The current scope of the comparative genomics work in the mitochondrial genomes of the Geraniaceae will allow us to further investigate the evolutionary processes that underlie the occurrence of HGT in these mitochondrial genomes.

A comprehensive evaluation of species tree methods in the presence of incomplete lineage sorting

Diego Mallo, Siavash Mirarab, Shamsuzzoha Bayzid, Tandy Warnow, David Posada

3C_301A-Phylogenetic Methods
Monday, June 23, 2014 1:30 PM-1:45 PM

Recent advances in sequencing technologies have furnished the expansion of phylogenomic studies, unveiling extensive phylogenetic conflict among different genomic regions (genes). This incongruence is partially explained by the presence of evolutionary processes decoupling species and gene histories, like duplication and loss (GDL), horizontal gene transfer (HGT) and incomplete lineage sorting (ILS). Currently, ILS may be contemplated as most challenging, since HGT and GDL are usually putatively purged before final inference. Accordingly, the species tree / gene tree incongruence has received a lot of attention in recent years, and a plethora of species tree reconstruction methods have been proposed, in particular around ILS. Nevertheless, in our opinion, their benchmarking has been often partial, including a few methods and/or simple scenarios. Here we present a comprehensive and realistic simulation study, with thousands of replicates in which multiple genes were evolved inside species trees, including different sources of branch length heterogeneity and where parameter values were sampled from statistical distributions representing a very broad set of conditions. These simulations have allowed us to assess the relative performance of a broad sample of species tree methods (Concatenation, MP-EST, MRP, MRL, Greedy consensus, NJst, STAR, STEAC, and *BEAST among others) under a continuous evolutionary landscape, and to establish the correlation between species tree accuracy and different evolutionary parameters. We hope this study will provide a guide for phylogeneticists to choose the most appropriate method for the data at hand, given different compromises between accuracy and computational resources, conditioned on key dataset features, and connecting species tree methodologies with real data analysis.

---

guenomu: a Bayesian supertree program for species tree reconstruction

Leonardo de Oliveira Martins, Diego Mallo, David Posada

3C_301A-Phylogenetic Methods
Monday, June 23, 2014 1:45 PM-2:00 PM

Most species tree reconstruction methods assume a single source of disagreement between the gene and species trees, hindering the inclusion of all available sequences in the analysis. Furthermore the elusive pursuit of high-quality data sets – which usually translates into actively discarding sequences and genes – stifles the contemplation of alternative phylogenomic scenarios.

Here we extend the concept of Maximum Likelihood supertrees (Steel and Rodrigo 2008) where a hierarchical Bayesian structure describes how a species tree generates a collection of gene families. This model makes use of a multivariate distribution that penalizes gene trees far apart from the species tree according to several distances. The distances employed in the current implementation are based on most parsimonious reconciliations as well as on the mul-tree generalization of the RF distance, although other distances can be easily implemented. Importantly our model does not assume that the paralogy and coalescence relations are known a priori, allowing for all available data from a gene family to be taken into account.

We implemented this model into the program guenomu, which receives as input a collection of gene tree files as well as a list of species names, and returns the posterior distribution of species trees compatible with the set of genes. Each input gene file is assumed to have a posterior sample of trees from a gene family, such that their posterior frequencies are used as importance weights. We examine the performance of the program on synthetic data sets simulated under complex models. We show that guenomu can estimate reasonable species trees, while at the same time greatly reducing the gene tree uncertainty.

Computing the Quartet Distance for Sets of Heterogeneous Phylogenetic Trees

Ralph Crosby, Tiffani WIlliams

3C_301A-Phylogenetic Methods
Monday, June 23, 2014 2:00 PM-2:15 PM

Modern gene tree and supertree methods produce sets of phylogenetic trees containing dissimilar, heterogeneous, sets of taxa.

In order to understand the relationships between the trees distance methods are a powerful tool. The popular Robinson-Foulds (RF) distance is not usable in the heterogeneous case due to it's reliance on bipartitions. The quartet distance is not subject to these constraints. This talk describes a new algorithm, QuickQuartetHet for determining the all-pairs quartet distance for sets of heterogeneous phylogenetic trees. Experimental results on biological data verify that the algorithm performs within a constant factor of the existing QuickQuartet algorithm. In order to better understand the impact of heterogeneity synthetic trees were generated with varying levels of heterogeneity and experiments performed to show that even small levels of heterogeneity have large impacts on the quartet distance.

Mean and Variance of Phylogenetic Trees

Megan Owen, Daniel Brown

3C_301A-Phylogenetic Methods
Monday, June 23, 2014 2:15 PM-2:30 PM

Mean and variance can be defined for a set or distribution of phylogenetic trees in a way that is analogous a definition in Euclidean space, but with the underlying space being the space of phylogenetic trees constructed by Billera, Holmes, and Vogtmann (2001). A property of this space (non-positive curvature) ensures that there is a unique shortest path between any two trees, that the mean of a set of trees is unique, and that both can be practically computed. We compare the the mean and variance to existing consensus tree and summary methods, and show that the variance is particularly well-behaved compared to other measures of variation.

Polymorphism-aware Phylogenetic Model (PoMo): An allele frequency-based approach for species tree estimation

Carolin Kosiol, Nicola De Maio, Dominik Schrempf

3C_301A-Phylogenetic Methods
Monday, June 23, 2014 2:30 PM-2:45 PM

Incomplete lineage sorting (ILS) causes incongruences in the phylogenetic tree relative to different genes. If these incongruences are not accounted for, it is possible to incur several biases in species tree estimation. Here, we present a maximum likelihood approach that accounts for ancestral variation and ILS.

We use a POlymorphisms-aware phylogenetic MOdel (PoMo) that we have recently shown to efficiently estimate mutation rates and fixation biases from within and between-species variation data (De Maio et al., 2013). PoMo is a phylogenetic Markov model with states that represent fixed alleles and states representing polymorphic alleles at different frequencies. A substitution is thus modeled from mutation, through the transient polymorphic stage, and to fixation (or loss). Polymorphic states can be observed in the tips of the phylogeny as well as at ancestral nodes. We extend this model for species trees estimation. We test the performance of PoMo in several different scenarios of ILS using simulations and compare it with existing methods both in accuracy and computational speed.

In contrast to other approaches, our model has very few parameters, and in particular does not suffer from over-parametrization. We show that PoMo is well suited for genome-wide species tree estimation and that it is faster and more accurate than previous approaches. In our first analyses, a simple Nearest Neighbor Interchange algorithm (NNI) has been combined with PoMo. Currently, we implement our model into an efficient and easy-to-use software package IQ-TREE (Minh et al., 2013). It offers a very fast bootstrap technique that promises an additional, significant reduction of run-time.

We applied PoMo with species tree inference to data of a recent study on the genetic diversity and population history of the great apes (Prado-Martinez et al., 2013). This dataset includes all six great ape species with seven subspecies divided into a total number of 12 populations (with up to 23 individuals per population). The great apes constitute one of the most prominent examples for ILS. Using PoMo, we inferred the topology and branch lengths showing that our approach is accurate and that it can cope with data from many populations with many individuals each. Previous approaches based on coalescent theory can neither be applied genome-wide nor on 12 populations, whereas our analysis runs for about 25 hours on a personal computer. We expect that with the new implementation in IQ-TREE we can infer species trees for 20 to 100 populations opening new applications.

Molecular systematics of the North American tiger salamander radiation using parallel tagged amplicon sequence data

David Weisrock, Eric O'Neill, Brad Shaffer, Gabriela Parra Olea

3C_301B-Phylogenetics and Systematics
Monday, June 23, 2014 1:30 PM-1:45 PM

Resolving the evolutionary history of the North American tiger salamander complex has historically been a challenging endeavor due to limited access to variable sequence-based markers and the idiosyncratic patterns of evolution at traditionally informative markers (e.g., mtDNA). In recent years, our lab has made use of next generation amplicon sequencing to generate sequence data from a large number of genome-wide markers across a large number of individuals distributed across the taxonomic and geographic range of tiger salamanders. These data have been highly informative in delimiting species across the complex, often yielding fine-scale resolution of cryptic species lineages not previously recognized in earlier studies. In addition, these data have been informative in producing a robustly resolved species tree for the complex. None of these results were arrived at easily, as we faced numerous challenges in effectively implementing analyses with large genome-scale data sets. In this talk we will discuss our systematic disentanglement of the tiger salamander complex, including some of the analytical strategies used to identify robust estimates of phylogenetic history and regions that remain uncertain in their resolution.

Phylogenomic analysis of yellowjackets and hornets (Hymenoptera, Vespidae)

Federico Lopez-Osorio, Kurt M. Pickett, James M. Carpenter, Bryan Ballif, Ingi Agnarsson

3C_301B-Phylogenetics and Systematics
Monday, June 23, 2014 1:45 PM-2:00 PM

The Vespidae is a family of wasps exhibiting solitary and social phenotypes and thus a useful system for discovering genes that might have evolved novel roles linked to sociality. Within the Vespidae, hornets and yellowjackets are all social and show considerable diversity in their behavior. According to the traditional phylogenetic hypothesis, the yellowjackets are monophyletic and sister to the hornets. Recent genetic evidence, however, contradicts or fails to support the traditional phylogenetic hypothesis. Here, we test for the first time the genus-level relationships of hornets and yellowjackets using a phylogenomic approach. We sampled six species and sequenced their transcriptomes to conduct a phylogenetic analysis. Our study includes 105 orthologs (121,909 aligned sites) that were chosen on the basis of two criteria: presence in all species and sequence length longer than 800 characters. Our results show, contrary to the traditional view, that hornets nest within yellowjackets, rendering the latter paraphyletic. The results of this phylogenomic study will be the foundation for future studies of molecular evolution across solitary and social lifestyles in the Vespidae.

Disentangling phylogenetic relationships in an explosive bird radiation

Carl Oliveros, Michael Andersen, Robert Moyle

3C_301B-Phylogenetics and Systematics
Monday, June 23, 2014 2:00 PM-2:15 PM

Rapid evolutionary radiations allow tremendous insights into speciation and biogeographic history. However, a major challenge in studies of these brief bursts of diversification has been poor resolution of species' phylogenetic relationships owing to short internodes among ancestral lineages, incomplete lineage sorting, long-branch attraction, and homoplasy. As a consequence, too few robust phylogenetic hypotheses are available to document such radiations. This study aims to resolve relationships within a very rapid and diverse radiation using both simulated and empirical data to illuminate underlying processes of lineage splitting and dispersal.

The passerine family of white-eyes (Zosteropidae) presents an ideal system for investigating one of the most striking evolutionary radiations known among vertebrates. The distribution of this group of 120 species spans a vast area in the Old World, from the eastern Atlantic to the Western Pacific. A vast majority of this lineage is estimated to have begun diversifying only in the early Pleistocene, resulting in the highest speciation rate yet documented among land vertebrates. The relatively recent diversification of this clade minimizes problems of long-branch attraction and homoplasy confounding phylogenetic inference. Hence, this young and species-rich group provides an excellent system in which to examine macro-evolutionary and biogeographic patterns in rapid radiations, lines of research that depend on a robust estimate of phylogenetic relationships. Data from three mitochondrial genes and two nuclear introns yield a poorly-resolved phylogeny, but simulations suggest that increasing the number of loci to ~100 may improve resolution considerably. As predicted, DNA sequence data from hundreds of ultraconserved elements provide a much better resolved estimate of phylogenetic relationships in this rapid radiation.

Resolution of phylogenetic relationships within Zosteropidae is vital to opening novel research avenues in historical biogeography and population genetics across several archipelagos and understanding the process of speciation in a species-rich but morphologically conserved group. More broadly, this study provides methodological insights into paths toward resolving relationships in other rapid evolutionary radiations across the tree of life.

Phylogeny, morphology and ontogeny of the Spikethumb Frogs (Hylidae: Plectrohyla)

David Sanchez

3C_301B-Phylogenetics and Systematics
Monday, June 23, 2014 2:15 PM-2:30 PM
D.A. Sánchez, E.N. Smith and J.A. Campbell

Amphibian and Reptile Diversity Research Center, University of Texas at Arlington

Middle American Tree Frogs (Hylidae: Hylinae: Hylini) diversified into more than 180 species in Tropical Central America and dispersed to South America, North America, Asia and Europe. They have an incredible diversity of shapes and sizes as adults, but more astonishing is that of their larvae, hardly comparable to any other anuran lineage. Hypotheses of evolutionary relationships of this group of frogs are available since 2005, with studies involving questions about ecology, speciation rate and evolution of morphological novelty. The largest genus in the tribe, Plectrohyla, with more than 40 species, currently includes species assigned to the genus before 2005, and frogs previously assigned to the Hyla bistincta group of Mexico, West of the Isthmus of Tehuantepec. A group of only a few species originally in Plectrohyla have been previously included in phylogenetic analyses. In this study, we reconstruct a phylogeny of the species in this genus using mitochondrial and nuclear markers, and with a thorough species sampling. We analyze some external adult and larval morphology, and together with geometric morphometry of available skulls we derive an evolutionary hypothesis of development, in ontogenetic and genealogical times.

Increasing phylogenetic resolution in a hyperdiverse radiation of blood feeding flies

Keith Bayless, Brian Cassel, Brian Wiegmann

3C_301B-Phylogenetics and Systematics
Monday, June 23, 2014 2:30 PM-2:45 PM

Tabanus is a lineage of hematophagous horse flies containing 1340 described species, and many more undescribed. Adult size and patterning are variable, and the predatory larvae can withstand a range of semi-aquatic and arid environments. Comprehensive comparative studies on this group, which includes disease vectors, are stymied by a lack of modern taxonomic syntheses. A study focusing on the phylogeny of worldwide Tabanus is needed in order to understand the drivers and patterns of the evolution of this lineage and to make future taxonomic work feasible. We extracted five genes totaling 6 kb of nucleotide data from one hundred species in the Tabanus group, including nearly all genera of Tabanini and at least one species from every biogeographic region. Molecular phylogenetic investigation of this data shows that Tabanus includes at least fourteen other genera containing over 900 species, including morphologically distinct genera such as Haematopota. Neotropical species are the successive sister groups to the rest of Tabanus. The rest of the species of Tabanini s.l. fall into about 8 major groups, some of which correspond to previously established genera. Relationships among these major groups have no resolution or support. New methods of data analysis and data sources are discussed in order to provide a useful and illuminating framework phylogeny.

What drives genetic and phenotypic divergence for Iris hexagona

Jenna Hamlin, Michael Arnold

3C_302A-Speciation
Monday, June 23, 2014 1:30 PM-1:45 PM

Given that landscapes are heterogeneous in nature, the consequences of these fragmented landscapes include small isolated populations. Within these small populations divergence at both genetic and morphological level can occur. However, genetic and morphological divergence across populations could be the product of limited dispersal, also known as isolation-by-distance, or adaptation. Within plants, selection on various floral morphologies has been well documented and shown to be influenced by both abiotic and biotic factors. We are examining the relative roles of isolation-by-distance and isolation-by-adaptation in promoting morphological divergence within a species, Iris hexagona, a member of the species complex known as the “Louisiana irises.” Using a genotyping-by-sequencing approach, we sampled a large number of single nucleotide polymorphisms across I. hexagona genome. We generated a panel of 750 SNPs and used population genetic analyses to test whether patterns of neutral genetic divergence across I. hexagona populations are better explained by isolation-by-distance or isolation-by-adaptation. We then compared the amount of divergence among populations at neutral and non-neutral SNPs with the magnitude of phenotypic differences in vegetative and floral traits. We show that high levels of genetic differentiation exist for non-neutral SNPs compared to neutral SNPs. There is not an overall relationship between pairwise genetic distance, computed for neutral SNPs, and geographic distance, which is consistent with isolation-by-adaptation. Additionally, we show that non-neutral genetic differentiation is correlated with both geographic distance and morphological divergence, which is consistent with isolation-by-distance. For I. hexgaona, it appears that both isolation-by-distance and isolation-by-adaptation are at play in generating divergence.

Genome divergence at the onset of speciation with gene flow

David Marques, Laurent Excoffier, Ole Seehausen

3C_302A-Speciation
Monday, June 23, 2014 1:45 PM-2:00 PM

Gene flow has long been regarded as a force opposing speciation, but recent studies have shown that speciation can occur despite gene flow when it is associated with divergent natural or sexual selection. Although patterns of genomic differentiation between recently formed species have been investigated in several cases, few studies have investigated the earliest stages of this process. We explore here genomic patterns of divergence in three-spine stickleback ecotypes that began to form less than 150 years ago, presumably in response to divergent selection between different habitats. We studied anadromous lake and resident stream ecotypes from two replicate streams. One stream was sampled along a habitat gradient where stream and lake ecotypes breed in sympatry with much opportunity for gene flow. The other stream ecotype pair is parapatric with little expected gene flow. While previous studies found no or very limited replication in genomic divergence between lake and stream ecotypes, our two ecotype pairs show one large and several small regions that repeatedly diverged in these replicates, despite extensive gene flow in one of them. These results indicate an important role of standing genetic variation and genomic architecture in adaptation to similar habitats and thus to the earliest stage of ecological speciation.

Major Ecological Shifts both Promote and Retard Speciation in Timema Stick Insects

Daniel Funk, Patrik Nosil

3C_302A-Speciation
Monday, June 23, 2014 2:00 PM-2:15 PM

This study investigates the consequences of level of ecological divergence (taxonomic disparity of host plants) for habitat isolation and sexual isolation across dozens of independent allopatric and parapatric population pairs of Timema while controlling for genetic distance in order to evaluate the generality of ecological speciation across this genus. Ecological divergence is not associated with sexual isolation and no evidence of reinforcement of sexual isolation was found. However, Ecological divergence was strongly associated with habitat divergence. Moreoever, habitat divergence was inversely related to sexual isolation among parapatric but not sympatric population pairs. This suggests that habitat isolation is interfering with reinforcing selection by reducing the frequency of interpopulation matings on which reinforcing selection depends. Thus, major shifts in host use seem to be driving speciation via habitat isolation, which in turn is retarding speciation by negating reinforcement.

Insight into the speciation process: patterns of reproductive isolation in five stickleback species pairs that span the speciation continuum

Alycia Lackey, Jenny Boughman

3C_302A-Speciation
Monday, June 23, 2014 2:30 PM-2:45 PM

To understand how new species form and what causes their collapse, we study how reproductive isolation evolves across the speciation continuum from the early stages of divergence to strongly isolated species to cases where isolation is lost. From this, we can determine which barriers contribute to total isolation early and late in the speciation process, infer the order in which barriers evolved during divergence or collapse, and gain insight into the selective and genetic mechanisms that underlie reproductive isolation. We explore these ideas by taking advantage of decades of previous work as well as our own data in stickleback fish. We examine five species pair systems that span the speciation continuum and measure many reproductive barriers in each species pair, often with multiple measures of each barrier from which we can calculate confidence intervals. We evaluate the importance of the type and number of barriers, pre- and postmating isolation, and asymmetrical isolation at different stages of the speciation process. Our study shows that two premating barriers, habitat and sexual isolation, are likely essential for initiating speciation, while intrinsic postmating isolation may be necessary to restrict reversal. Sexual isolation also seems to play an important role in furthering forward movement along the continuum, and, importantly, its loss facilitates reversal. We found asymmetries in individual premating and extrinsic, but not intrinsic, postmating barriers. Yet these asymmetric individual barriers combined to yield essentially no asymmetry in total isolation between species. By measuring many barriers across many species pairs that span the speciation continuum, we test fundamental predictions of ecological speciation and generate insight into the order in which barriers evolved during divergence and collapse, which is often intractable in studies that focus on a few barriers or a single species pair.

Faster rates in snakes? Molecular evolution of the insulin signaling pathway in amniotes

Suzanne McGaugh, Tonia Schwartz, Chih-Horng Kuo, Anne Bronikowski

3C_302B-Molecular Evolution / Genetics of Adaptation
Monday, June 23, 2014 1:30 PM-1:45 PM

Metabolic differences associated with ectothermy and resistance to environmental extremes (e.g. freeze, anoxia, and starvation resistance), may also result in differential selection pressures for stress and nutrient pathways in non-avian reptiles than for mammals and birds. Recent studies have started to uncover clues that the genetic underpinnings of stress response are indeed very different in reptiles relative to mammals. For instance, IGF-1 contains more substitutions along the snake and lizard branch and more diversity in reptiles generally as compared to mammals, leading to the hypothesis that the insulin signaling pathway in reptiles may be considerably different from mammals. Here we provide the most comprehensive examination to date of the molecular evolution of the insulin signaling pathway to address whether components of this pathway have experienced faster evolution in snakes and lizards. To do so, we leveraged coding sequence data from 32 mammals, 10 birds, and 24 non-avian reptiles, the latter of which included 18 liver transcriptomes that we generated from six lizard species, seven snakes, four species of turtle, and alligator.

Coupling between protein level selection and codon usage optimization in the evolution of bacteria and archaea

Wenqi Ran

3C_302B-Molecular Evolution / Genetics of Adaptation
Monday, June 23, 2014 1:45 PM-2:00 PM
ABSTRACT

The relationship between the selection affecting codon usage and selection on protein sequences of orthologous genes in diverse groups of bacteria and archaea was examined by using the Alignable Tight Genome Clusters database of prokaryote genomes. The codon usage bias is generally low, with 57.5% of the gene-specific optimal codon frequencies (Fopt) being below 0.55. This apparent weak selection on codon usage contrasts with the strong purifying selection on amino acid sequences, with 65.8% of the gene-specific dN/dS ratios being below 0.1. For most of the genomes compared, a limited but statistically significant negative correlation between Fopt and dN/dS was observed, which is indicative of a link between selection on protein sequence and selection on codon usage. The strength of the coupling between the protein level selection and codon usage bias showed a strong positive correlation with the genomic GC content. Combined with previous observations on the selection for GC-rich codons in bacteria and archaea with GC-rich genomes, these findings suggest that selection for translational fine-tuning could be an important factor in microbial evolution that drives the evolution of genome GC content away from mutational equilibrium. This type of selection is particularly pronounced in slowly evolving, “high-status” genes. A significantly stronger link between the two aspects of selection is observed in free-living bacteria than in parasitic bacteria and in genes encoding metabolic enzymes and transporters than in informational genes. These differences might reflect the special importance of translational fine-tuning for the adaptability of gene expression to environmental changes. The results of this work establish the coupling between protein level selection and selection for translational optimization as a distinct and potentially important factor in microbial evolution.

IMPORTANCE

Selection affects the evolution of microbial genomes at many levels, including both the structure of proteins and the regulation of their production. Here we demonstrate the coupling between the selection on protein sequences and the optimization of codon usage in a broad range of bacteria and archaea. The strength of this coupling varies over a wide range and strongly and positively correlates with the genomic GC content. The cause(s) of the evolution of high GC content is a longstanding open question, given the universal mutational bias toward AT. We propose that optimization of codon usage could be one of the key factors that determine the evolution of GC-rich genomes. This work establishes the coupling between selection at the level of protein sequence and at the level of codon choice optimization as a distinct aspect of genome evolution.

Into the ant nest: molecular evolution of chemoreception and host specialization in predatory paussine beetles

Tanya Renner, Amanda Romaine, Wendy Moore

3C_302B-Molecular Evolution / Genetics of Adaptation
Monday, June 23, 2014 2:00 PM-2:15 PM

In insects, olfaction plays a major role in many behaviors, including host preference. Localization and identification of a host by an insect begins with processing of volatiles by small antennary proteins such as odorant-binding proteins, which transport odorant ligands in the air-fluid interface to odorant receptors located in the antennal sensilla. As specificity for certain ligands can be high, OBPs are thought to play a significant role in the selectivity of the insect olfactory system. Our current work focuses on the molecular evolution of chemoreception and host specialization in an ecologically and evolutionarily interesting group of flanged bombardier beetles with myrmecophilous relationships, Paussinae. We reconstruct the evolutionary history of odorant binding protein and odorant receptor chemoreception genes while also examining functional divergence to explore the influence of molecular evolution on life history in predatory paussine beetles. In addition, we investigate the functional importance of the OBP binding pocket that is essential for interaction between these proteins and their respective ligands by studying evolutionary selection acting on specific sites.

Characterizing independent adaptive mutations in yeast experimental evolution using DNA barcodes

Sandeep Venkataram, Dmitri Petrov, Gavin Sherlock, Barbara Dunn, Jessica Chang, Yuping Li, Jamie Blundell, Sasha Levy, Daniel Fisher

3C_302B-Molecular Evolution / Genetics of Adaptation
Monday, June 23, 2014 2:15 PM-2:30 PM

The study of adaptation suffers from the lack of a sufficiently large set of adaptive events for a statistically meaningful analysis. Consequently we still have a cursory understanding of the rate of adaptation, the distribution of effect sizes of individual adaptive mutations, and the possible molecular targets for adaptation in most systems. Here we utilize an innovative DNA barcoding approach to track the frequency trajectories of ~500,000 otherwise identical clones of the budding yeast Saccharomyces cerevisiae evolving in a single experiment under a glucose limited regime. From the trajectories, we identify and isolate 300 independent adaptive clones relatively early in the evolution, when most clones are likely to contain only a single adaptive mutation. We then sequence the genomes of all of these clones to isolate the putative adaptive mutations present on each lineage. We will discuss our findings in relation to the types of mutations that are adaptive e.g. point mutations, short indels, copy number variants or structural variants and whether these mutations are regulatory or in protein-coding regions as well as their predicted functional impact. We will also consider whether particular genes or pathways are common targets for adaptation under our conditions, and whether the strength of the fitness effects cluster by genetic target or the number of putative adaptive mutations identified in each clone.

Uncovering genome-wide targets of convergent evolution along a re-established flowering time cline in the introduced range of Arabidopsis thaliana

Billie Gould

3C_302B-Molecular Evolution / Genetics of Adaptation
Monday, June 23, 2014 2:30 PM-2:45 PM

Rapid evolution in response to new environments is repeatable, at least at the phenotypic level. In cases of convergent evolution however, the question remains whether the same heritable components are the repeated targets of selection. Do new or rare, locally restricted alleles facilitate adaptation, or does standing genetic variation and widespread gene pleiotropy largely constrain evolution to the same pathways and alleles at the molecular level? We addressed this question by studying the ecological genetic basis of flowering time adaptation in introduced populations of Arabidopsis thaliana. Using outlier analyses and genome-wide scans, we have identified variants associated with flowering-time differences along a re-established longitudinal cline in eastern North America. We compare these with variants with the genetic basis of flowering time adaptation in the native European range and discuss implications for the role of standing genetic variation in underpinning convergent phenotypic adaptation, particularly with regard to species introductions.

Periodic Social Niche construction

Philip Poon, Jessca Flack, David Krakauer

3C_302C-Sociality
Monday, June 23, 2014 1:30 PM-1:45 PM

Social niche construction describes the creation of social networks and institutions that influence individual fitness. Niche construction involves multiple timescales, including the relatively short time required to build a niche, and the longer time required to learn how to build a niche.

We explore a number of different learning rules for niche construction and deconstruction in relation to competition between constructing species or agents. We are particularly interested in the dynamics of institutional switching.

Using a learning rule in which construction effort is proportional to the effort put in by competing agents generates cycles in population density. Technically, the system undergoes a Hopf-bifurcation with a transition from a stable solution to a periodic solution.

Hysteresis (path-dependence) in key competition parameters provides evidence of top-down causal memory from the institutions, leading to increased resistance to change between stable and periodic states. This is due to the different stability criteria for a periodic solution as dictated by Floquet's theory.

We also find evidence for greater stability in a two niche or institution setting than a single institution setting. We relate these results to prior discussion of stability induced in bi-polar versus unipolar social systems.

Explaining the novel axes of adaptive phenotypic diversification in complex societies using the turtle ants

Scott Powell, Shauna Price

3C_302C-Sociality
Monday, June 23, 2014 1:45 PM-2:00 PM

How the process of adaptive radiation unfolds in taxa that live in complex societies has received little attention, despite the tremendous diversity and ecological dominance of many of these lineages. In complex societies, like those of ants and other social insects, the colony is the adaptive unit, with its members functionally dependent on each other. The major evolutionary transition to complex social living introduces a number of novel axes of phenotypic diversification that do not exist in lineages of solitary or weakly social animals. Among the most striking is the differentiation of colony members into different specialized morphotypes, or "castes", that serve as different traits of the functionally integrated colony. Here, we analyze the evolution of a specialized soldier morphotype within the turtle ants (Cephalotes), a diverse lineage of arboreal ants that has radiated throughout the Neotropics. Turtle ant soldiers have heavily armored heads, which they use to block the entrances of the colony's arboreal nesting cavities. Consequently, we also examine the ecological correlates of soldier evolution, focusing on cavity properties known to interact with soldier cavity defense. Our analyses of soldier morphology emphasize the evolutionary transitions among distinct soldier morphotypes and the evolution of soldier head size. Our results show a degree of lability in soldier evolution that is unexpected based on classical predictions for caste evolution. Furthermore, we show that soldier morphology is significantly correlated with the properties of the cavities that each species chooses to inhabit. Overall, these analyses suggest that soldier evolution is a major axis of adaptive morphological diversification in the turtle ant radiation, shaped by the evolution of cavity selection. Historically, work on the ecology of caste evolution has been isolated from mainstream work on the ecology of adaptive radiation. Broadly, these analyses show the value of adopting modern phylogenetic comparative approaches to address caste evolution within a framework of adaptive radiation in complex societies.

Fairness and wisdom: the emergence of leadership

Jeremy Auerbach, Sergey Gavrilets, Mark Van Vugt

3C_302C-Sociality
Monday, June 23, 2014 2:00 PM-2:15 PM

Groups make decisions with various strategies: quorums, consensus, leadership, or some combination thereof. Leadership, where an individual or a subgroup who can increase the effectiveness of coordinated activities not through increased skill of performing the task but by other social mechanisms (e.g. monitoring or punishment), is not only ubiquitous in human culture but has significantly impacted the course of human history. To determine how and why leadership has evolved we must explore the costs and benefits of the various decision making strategies and we attempt to do so through an individual-based model for group decision making. Here, individuals are involved in speaker-listener interactions, representing the decision making structure of our ancestors, and they differ in their preferred course of action, personality traits and intelligence. We conducted a comparison of the various decision making strategies by analyzing the costs incurred by foregoing individual preferences and the time it takes for the group to reach a decision. Consensus strategies favor individual preferences over speed and can tap into the ``Wisdom of Crowds'' phenomena while more despotic strategies opt for speed while sacrificing the preferences of the conspecifics. If timeliness outweighs preferences, e.g. between group warfare and exploitation of resources, we observe more despotic styles of leadership emerging and along with them their correlated personality traits (e.g. stubbornness). However, extant small scale communities tend to actively discourage following leaders with these personality traits, instead preferring to follow those who are wise (knowing the optimal course of action) or fair (reducing the loss of individual preferences). To account for this discrepancy we propose and explore possible mechanisms for the development of a reputation for being wise or being fair, which dynamically alters the social network. Future work could possible extend these results to explain why other species favor more despotic styles of group decision making, such as baboons and hyenas.

Looking for signatures of social conflict in secondary metabolites of cooperative amoebae

jeff smith, Joan Strassmann, David Queller

3C_302C-Sociality
Monday, June 23, 2014 2:15 PM-2:30 PM

In the study of microbial cooperation, one of the earliest and strongest predictions of social evolution theory was that microbes would have adaptations to exploit unrelated social partners. So far, some evidence is consistent with this prediction but cannot rule out nonadaptive alternative explanations. Here we use phylogenomics to test whether Dictyostelium amoebae use polyketides—small secondary metabolites that often act as antimicrobials—for interference competition when forming multicellular fruiting bodies. In particular, we examine polyketide synthases for signatures of an evolutionary arms race: rapid evolution via positive selection to create new products expressed during development.

Stepwise evolution of social complexity in ground-dwelling squirrels

Katherine Brooks

3C_302C-Sociality
Monday, June 23, 2014 2:30 PM-2:45 PM

Understanding why sociality evolved in its many present day forms is a central question in evolutionary biology. The Marmotini, a clade of ground-dwelling squirrels, exhibits considerable variation in social structure. This variation provides an excellent system in which to explore both the way in which social complexity evolves and its ecological and life history correlates. Early studies on ground-dwelling squirrels proposed that social systems evolved in successive stages from less to more complex. In this study, I use a molecular phylogeny to test this prediction. I show that social complexity does evolve in a linear stepwise manner, with transitions occurring most often between adjacent social grades. However, unlike earlier predictions, social evolution is not constrained to increases in complexity. I also find that more socially complex species live in visually open habitats and exhibit delayed sexual maturation. These results suggest that predation risk, which is generally considered to be higher in more visually open environments, played a role in ground-dwelling squirrel social evolution. Life history and evolutionary history also constrain social evolution in this clade. Species that exhibit delayed sexual maturation, also delay dispersal and live in natal family groups longer, thereby increasing chances for cooperation. In most cases, delayed maturation has led to complex social systems where individuals of multiple generations cooperate with one another. Together, my results highlight the importance of considering both shared evolutionary history and local adaptation when studying the evolution of sociality and other behavioral traits.

Evolutionary origins and genomic consequences of hybridogenesis in Pogonomyrmex harvester ants

Sara Helms Cahan, Andrew Nguyen, Yihong Zhou

3C_303-Hybridization
Monday, June 23, 2014 1:30 PM-1:45 PM

Hybridization between species provides the opportunity for two independently evolving genomes to recombine, which may have both negative consequences when co-adapted gene complexes are broken up, as well as positive effects if globally adaptive alleles are able to cross the species boundary. At the same time, hybridization can produce evolutionarily novel reproductive systems, such as sperm-dependent parthenogenesis and hybridogenesis, that may reduce genetic homogenization while maximizing the heterotic benefits of producing hybrid progeny. We investigated the evolutionary origins and genomic consequences of hybridogenesis in harvester ants, which must interbreed in every generation to produce sterile hybrid workers yet virtually always produce non-hybrid reproductive offspring. Using a combination of RADtag genotyping and comparative transcriptome sequencing, we investigated the ancestry of interbreeding hybridogenetic lineages to test whether they are derived from interspecific hybrid zones and identify their most likely source populations. To assess the role of hybridogenesis in shaping the genomic and fitness consequences of hybridization, we investigated the extent, directionality, timing, and genomic distribution of introgression between lineages. Our results indicate that hybridogenesis is derived from historical hybrid zones between P. barbatus and P. rugosus, with at least two independent origins involving different sub-populations of the parental species which became interdependent and then radiated together across the contact zone region. All hybridogenetic lineages show a marked reduction in genetic diversity, suggesting that hybridogenesis may be more likely to evolve in small and isolated populations cut off from populations in allopatry by geography and/or range contraction. Despite continually interbreeding, overall genetic exchange between lineages was low, with less than 5% of transcripts indicative of introgression. The introgression that did occur was most consistent with a single pulse of gene exchange when hybridizing populations first came into contact, which ceased once hybridogenesis shifted hybrids from the reproductive to the sterile worker caste. These results suggest that hybridogenetic systems in ants may function as “the best of both worlds”, reducing or eliminating the reproductive costs of hybrid ancestry once adaptive alleles have introgressed, while maintaining the non-reproductive heterosis advantages of a hybrid workforce over evolutionary time.

Hybrid Zones, Genomic Ancestry Patterns, and Genomic Scans for Hybrid Sterility Genes

John Hvala, Bret Payseur

3C_303-Hybridization
Monday, June 23, 2014 1:45 PM-2:00 PM

Hybrid zones provide natural laboratories for understaning speciation. Hybrid zones form when two lineages resume contact after a significant period of isolation. If the two groups are on the path to speciation, hybrid offspring are likely to exhibit reduced fertility. Hybrid sterility often results from deleterious epistatic interactions (known as Dobzhansky-Muller incompatibilities, DMIs) that accumulate between populations evolving in allopatry. If DMIs reduce fertility in naturally occurring hybrids to a degree that species differences can be maintained despite gene flow, they should affect patterns of genomic diversity in hybrid zones. In principle, genomic scans of gene flow in hybrid zones can be used to identify hybrid incompatibilities. Existing analytical approaches focused on clines are not specifically designed to detect epistatic selection and do not easily scale to the entire genome. Here we focus on an alternative measure of gene flow that overcomes these challenges. When hybrids form, recombination produces haplotypes that are mosaics of ancestry. The points where ancestry switches - ancestry junctions - are direct products of recombination in hybrids and are influenced by demographic as well as selective processes. We conducted individual based simulations to understand how genomic ancestry blocks are affected by population structure and selection against DMIs. First, we show how migration and drift affect the density of junctions across the genome in admixed Wright-Fisher populations and in a stepping stone model of a hybrid zone. Then, we demonstrate that the presence of a two locus DMI reduces the junction density at one or both loci. Our findings reveal the potential of using ancestry junctions to better understand the demographic history of hybrid zones and to detect DMI loci in genomic scans conducted in hybrid zones.

A Model of Genome-Wide Patterns of Ancestry in a Secondary Contact Zone

Alisa Sedghifar, Yaniv Brandvain, Peter Ralph, Graham Coop

3C_303-Hybridization
Monday, June 23, 2014 2:00 PM-2:15 PM

Differentiated populations, or subspecies, frequently come into secondary contact. Understanding genomic patterns in such contact zones can provide insights into population history and the loci underlying species maintenance in sympatry. For example, the sizes of introgressed regions, or extent of linkage disequilbrium of ancestry (ancestry-LD) can inform us of the age and extent of hybridization. Here we develop a neutral model to describe the lengths of admixed haplotypes and ancestry-LD in a geographically explicit setting. We use this model to explore the relationships between time, geography and genome-wide patterns of shared ancestry. This provides a suitable null model for investigating patterns of selection, and a tool for inference of the age of secondary contact zones.

The role of hybrid incompatibilities in hybrid zone structure

Molly Schumer, Rongfeng Cui, Gil Rosenthal, Peter Andolfatto

3C_303-Hybridization
Monday, June 23, 2014 2:15 PM-2:30 PM

Bateson-Dobzhansky-Muller (BDM) incompatibilities are the major genetic model for speciation, but so far have been studied primarily in model organisms. We recently mapped hybrid incompatibilities distinguishing two naturally hybridizing species of swordtail fish, Xiphophorus birchmanni and X. malinche. These two species form multiple natural hybrid zones in the Sierra Madre Oriental of Mexico, and these replicated instances of hybridization provide an opportunity to study repeatable dynamics of selection on hybrid genomes. Using our hybrid incompatibility mapping results, we model hybrid genomes in a range of scenarios and draw conclusions about the effects of incompatibilities on hybrid genomes. We further extend our simulations to understand the role of BDMIs in driving reproductive isolation at hybrid zones under a range of genetic architectures.

Shaking the parrotfish tree: hybridization in a peripheral environment produces phenotypic novelty

David Carlon, John H Choat, Kendall Clements, D. R. Robertson

3C_303-Hybridization
Monday, June 23, 2014 2:30 PM-2:45 PM

An increasing range of examples show that hybridization can play a creative role in generating new phenotypes and even new species. Yet there are few examples of hybrid zones among tropical reef-fishes, and these involve closely related species. We sequenced four nuclear introns in samples of the parrotfishes Scarus compressus, S. ghobban, and S. perrico from the Pearl Islands. These nuclear markers provide clear evidence that each of five S. compressus was an F1 hybrid resulting from crosses between S. ghobban and S. perrico. Each S. compressus sample was heterozygous at each locus, carrying diagnostic alleles for each parental species. Since the range of S. compressus (described in 1916) extends from the Gulf of California to Ecuador, this morphospecies is either maintained by constant (and frequent at some sites) hybridization, or is the product of homoploid hybrid speciation in which recombinant genotypes (F2 hybrids, etc.) have yet to be documented. We will further evaluate these two hypotheses with larger sample sizes and new genetic data from Baja California. Regardless of mechanism, to our knowledge this is the first evidence of the formation of a region-wide hybrid zone that involves hybridization between distantly related parrotfishes.

Developmental integration of an obligate intracellular symbiont

Alex Wilson, Hsiao-Ling Lu, Honglin Feng

3C_304-Symbiosis
Monday, June 23, 2014 1:30 PM-1:45 PM

Vertically transmitted symbionts are both developmentally and metabolically integrated into their hosts to generate the holosymbiont. In most systems remarkably little is known about the mechanisms mediating holosymbiont integration. Recently, facilitated by functional characterization and localization of amino acid transporter ApGLNT1, Price, Wilson and colleagues proposed a model of endosymbiosis regulation whereby amino acid biosynthesis in the holosymbiont is regulated by a symbiont-synthesized end product. By tracking the expression and protein localization of ApGLNT1 during asexual female embryogenesis we gain insight into the developmental and metabolic integration of the pea aphid, Acyrthosiphon pisum and its endosymbiont Buchnera aphidicola. In doing so, we find that the intracellular symbionts of asexual female pea aphids commence amino acid provisioning after birth and not before.

Allele changes during spore formation on the mycorrhizal fungi, Rhizophagus irregularis

Ivan Mateus, Frédéric Masclaux, Ian Sanders

3C_304-Symbiosis
Monday, June 23, 2014 1:45 PM-2:00 PM

Arbuscular mycorrhizal fungi (AMF) are endo-symbionts of plant roots. They provide mineral nutrients to the plant in exchange of photosynthesized carbon. In addition, AMF affects plant growth, plant community assembly and plant tolerance to heavy metals.

These fungi have been considered as ancient asexual organism that reproduce clonally by producing multinucleate spores. Recently whole-genome sequencing of in-vitro cultures of the model species Rhizophagus irregularis has shown little genetic polymorphism among coexisting nuclei in these cultures. However, single-spore cultures segregated from parental cultures alter differently rice growth, suggesting significant polymorphism between the single-spore cultures.

In order to understand if there is a genetic basis of this process, we tested whether single-spore cultures present genetic polymorphism. For this we produced single-spore cultures of R. irregularis (bottlenecked lines) and we used next generation sequencing to assess the genetic polymorphism. Contrary to the little polymorphism hypothesis, we found that there is big genetic polymorphism among the single-spore cultures. Moreover, we show that the genetic polymorphism is present in coding, non-coding, repetitive and non-repetitive regions. The most part of the polymorphism is due to allele loss or duplication. These results add more arguments to the debate whether this ancient asexual is genetically polymorphic.

Obligate insect endosymbionts exhibit increased ortholog length variation and loss of large accessory proteins concurrent with genome shrinkage.

Laura Kenyon, Zakee Sabree

3C_304-Symbiosis
Monday, June 23, 2014 2:00 PM-2:15 PM
Extreme genome reduction has been observed in obligate intracellular insect mutualists and is an assumed consequence of fixed, long-term host isolation. Rapid accumulation of mutations and pseudogenization of genes no longer vital for an intracellular lifestyle, followed by deletion of many genes, are factors that lead to genome reduction. Size reductions in individual genes due to small-scale deletions have also been implicated in contributing to overall genome shrinkage. Conserved protein functional domains are expected to exhibit low-tolerance for mutations and therefore remain relatively unchanged throughout protein length reduction while non-domain regions, presumably under less selective pressures, would shorten. This hypothesis was tested using orthologous protein sets from the Flavobacteriaceae (phylum: Bacteroidetes) and Enterobacteriaceae (subphylum: Gammaproteobacteria) families, each of which includes some of the smallest known genomes. Upon examination of protein, functional domain, and non-domain region lengths, we found that proteins were not uniformly shrinking with genome reduction, but instead increased in length variability and variability was observed in both the functional domain and non-domain regions. Additionally, as complete gene loss also contributes to overall genome shrinkage, we found that the largest proteins in the proteomes of non-host-restricted bacteroidetial and gammaproteobacterial species often were inferred to be involved in secondary metabolic processes, extracellular sensing, or of unknown function. These proteins were absent in the proteomes of obligate insect endosymbionts. Therefore, loss of large proteins not required for host-restricted lifestyles in obligate endosymbiont proteomes likely contributes to extreme genome reduction to a greater degree than ortholog shrinkage.

Genome duplication increases phosphorus limitation but does not enhance growth responses to Arbuscular Mycorhizal Fungi in an autopolyploid plant, Cha

Susan Hensen, Hafiz Maherali

3C_304-Symbiosis
Monday, June 23, 2014 2:15 PM-2:30 PM
Variation in the outcomes of generally mutualistic interactions, such as the symbiosis between arbuscular mycorrhizal (AM) fungi and land plants, can be modeled as an exchange of resources between symbiotic partners who vary in resource acquisition capabilities. Under this type of biological market model, benefit to a symbiotic partner can be predicted to depend on the relative cost of acquiring limiting nutrients such as carbon and phosphorus. This study tested the outcome of symbiosis with Glomus intraradices on diploid and tetraploid populations of Chamerion augustifolium, hypothesizing that tetraploids would be more phosphorus limited than diploids, and would therefore have a stronger mycorrhizal response. Results showed that tetraploids did respond more strongly to phosphorus application, providing support for the hypothesis that polyploids are more nutrient limited than diploids. However, the interaction between ploidy, AM colonization, and soil phosphorus was more complex than hypothesized; rather than a universally positive mycorrhizal response, diploid and tetraploid cytotypes showed a negative correlation between mycorrhizal responses in low and high phosphorus treatments. Tetraploids had a positive mycorrhizal response in high phosphorus treatments and a negative mycorrhizal response in low phosphorus treatments, while diploids showed the opposite trend. These results suggest that the nutrient requirements of the fungus play a larger role in mycorrhizal responses than is often assumed, and that further research into this area is necessary before the biological market model can be successfully applied to the plant-AM symbiosis.

Fitness feedbacks and alignment of interests in mutualisms

Erol Akcay

3C_304-Symbiosis
Monday, June 23, 2014 2:30 PM-2:45 PM
Some of the most striking examples of cooperation involve individuals from different species provide benefits to each other for mutual gain. For a mutualism to be stable, natural selection has to align the fitness interests of the interacting species, so that helping the other species returns a fitness gain to a focal individual. We term this a “fitness feedback”. While this principle has long been known, and various mechanisms for generating fitness feedbacks have been explored both in theory and empirical work, the relative importance of each mechanism, and interactions between them remain poorly understood. This is especially the case in interactions (such as the legume-rhizobium symbiosis) where there are phenotypic and fitness feedbacks operating simultaneously at multiple scales. In this talk, I will present initial results for a framework for modeling fitness feedbacks at multiple scales, using the legume-rhizobium mutualism as an example. My results highlight the consequences of the interactions between different feedback mechanisms for patterns of fitness covariation between species, and provide a framework in which to quantify fitness alignment between species.

Expression evolution in island snake venoms

Mark Margres, Darin Rokyta, Kenneth Wray, James McGivern, Margaret Seavy

3C_305A-Venom Evolution
Monday, June 23, 2014 1:30 PM-1:45 PM
Natural selection requires that individuals exhibit heritable phenotypic variation, and this variation must result in differential fitness (e.g., survival and/or reproduction) that enables the sorting of phenotypes in the next generation. Snake venoms are ecologically critical traits as they function in feeding and defense, and positive selection on venom genes suggests a coevolutionary arms race may shape venom composition as a result of resistance development in prey. Islands are natural experiments that have been run for thousands of years and thus are exceptional systems for addressing predator-prey coevolution because of changes in prey availability, limited gene flow due to isolation and low immigrant fitness, and accelerated evolution driven by positive selection on toxins and, if present, inhibitors/resistant alleles. We

used a joint transcriptomic-proteomic approach to construct a genotype-phenotype map for the venom systems of three species of venomous snakes and used the map in conjunction with a new statistical framework to compare island and mainland populations for each species to identify and quantify expression variation.

Uncovering venom neurotoxin gene family evolution from black widow and house spider genomes and transcriptomes

Jessica Garb, Kerry Gendreau, Robert Haney, Cheryl Hayashi, Thomas Clarke, Nadia Ayoub

3C_305A-Venom Evolution
Monday, June 23, 2014 1:45 PM-2:00 PM

Venoms are key adaptations that have independently evolved in several diverse animal lineages largely to facilitate rapid prey capture. Most venoms contain a wide assortment of toxins aimed at disrupting the nervous and circulatory systems of injected victims. Across divergent animal lineages, venoms also show remarkable similarities in their constituent proteins, implying the convergent recruit of homologous proteins for venom expression. However, determining the molecular diversity of venoms and deciphering the relationships of venom and non-venom proteins has been challenging, given the limited number of multi-tissue transcriptomes and genomes available for neglected venomous taxa. This talk will present recently completed and preliminary evolutionary analyses of the black widow latrotoxin venom gene family, based on high-throughput multi-tissue transcriptomes from the Western black widow (Latrodectus hesperus), and the recently sequenced genome of its non-hazardous close relative, the house spider (Parasteatoda tepidariorum). Previous work identified a single protein, alpha-latrotoxin, as the agent responsible for the extreme neurotoxicity of black widow venom, whereas the three other known latrotoxin paralogs were shown to be invertebrate neurotoxins. Results from a deeply sequenced L. hesperus transcriptome indicates the expression of at least 20 divergent latrotoxin paralogs in this species' venom. Moreover, phylogenetic analyses of latrotoxins from the P. tepidariorum genome show an unexpectedly large set of paralogs with highly variable domain structure, but all are very distantly related to L. hesperus latrotoxins, confirming the rapid evolution of this toxin family, and explaining the distinctly potent venom of black widows.

The secrets of staying young: Investigating the evolution of venom neoteny in the Timber Rattlesnake, Crotalus horridus.

James McGivern

3C_305A-Venom Evolution
Monday, June 23, 2014 2:00 PM-2:15 PM

Ontogeny is a source of phenotypic variation on which selection can act. However, the process by which selection can act on developmental patterns to give rise to fixed genetic differences remains unclear. To elucidate this process, the molecular mechanisms of ontogeny must first be unraveled in a context where the adaptive benefits can be established. Several species of Viperidae have been observed to undergo ontogenetic transitions in venom composition, including the Timber Rattlesnake (Crotalus horridus) a pit viper found across the eastern half of the United States. Two major venom types have been identified in separate populations of this species: a hemorrhagic venom type that undergoes a dramatic shift upon reaching adulthood, and a neurotoxic venom type that has evolved a unique neurotoxin and no longer undergoes the dramatic shift, instead retaining its juvenile venom. The presence/absence of key toxin classes in this ecologically critical trait likely represents evolutionary trade-offs. To better assess the genetic and proteomic differences between these venoms, we sequenced and analyzed the venom gland transcriptomes of a juvenile hemorrhagic venom-type prior to ontogenetic transition and an adult of each subtype. Putative toxin transcripts were confirmed in the venom using mass spectrometry. By comparing these individuals we determined genetic and proteomic differences between the subtypes and examined possible mechanisms by which these two venom types evolved. In addition, we sequenced microRNAs from the venom glands of each individual and compared them to assess the possible role of translational repression in the differences observed between juvenile and adult venoms.

All venoms are not created equal: the distribution and adaptive significance of venom types in the Timber Rattlesnake (Crotalus horridus)

Kenneth Wray, Mark Margres, Dragana Sanader, Darin Rokyta

3C_305A-Venom Evolution
Monday, June 23, 2014 2:15 PM-2:30 PM

Snake venom represents a polygenic, complex phenotype that possesses clear adaptive significance in feeding ecology. As such, venoms may be expected to vary across species and even within species. Somewhat surprisingly, however, it has been demonstrated that a few species have populations that vary from highly lethal, neurotoxic venoms (Type A) to less lethal, but tissue destroying, venoms (Type B), though relatively little is known about the geographic extent of this variation or its adaptive significance. We explore this variation in the Timber Rattlesnake (Crotalus horridus), a wide-ranging species that is currently threatened or endangered in at least 11 U.S. states and in Canada. We apply standard PCR techniques to test for the presence/absence of the acidic and basic subunits of canebrake toxin (the type II phospholipase neurotoxin responsible for Type A venoms) throughout the range of C. horridus. We then use comparative transcriptomics and proteomics to characterize the venoms of a Type A population and a Type B population from less than 100 miles apart. Finally, we use mitochondrial sequencing and morphometrics to put the venom variation between these two populations into an adaptive context. We extend the known range of the medically important Type A venom and reveal previously undescribed variation correlated with the different venom types, which could impact current management strategies.

Evolution of the venom gland transcriptome in widow spiders

Robert Haney, Nadia Ayoub, Thomas Clarke, Cheryl Hayashi, Jessica Garb

3C_305A-Venom Evolution
Monday, June 23, 2014 2:30 PM-2:45 PM

Spiders are the largest taxon of venomous metazoans, and are important predators in nearly every terrestrial food web. Their venom plays a critical role in successfully obtaining prey, and can also function in deterrence of both competitors and spider predators. The expansive spider Family Theridiidae currently contains close to 2400 species, several of medical importance due to human envenomations. Among these are the notorious black widows of the genus Latrodectus and the closely related false widows of the genus Steatoda. The venom of these and other spiders is a complex mixture of small molecules, peptides and proteins, most of which have never been fully characterized, despite their potential for pharmacological development. Widow spiders are unusual in their possession of a family of atypically large neurotoxins (~1100-1400 amino acids) called latrotoxins, which form pores in the presynaptic membrane of their prey, causing massive and uncontrolled neurotransmitter release. We identified a set of venom gland specific transcripts (VSTs) from three widow spider species (L. hesperus, L. geometricus and S. grossa) using RNA-Seq data from replicates of three tissue types (venom gland, ovary and cephalothorax). Among these VSTs we find numerous latrotoxin transcripts, greatly increasing the diversity of this toxin family. We also identify transcripts corresponding to members of other toxin families, including inhibitory cystine knot (ICK) toxins, CRISP family toxins, enzymes with toxic potential and putatively novel small toxins. As venom gland transcriptome evolution may proceed by changes in the number of transcripts of a given type, by changes in the primary sequence of expressed proteins, or via the magnitude or spatial pattern of expression of its component transcripts through regulatory mechanisms, we explore each of these potential avenues. We test for changes in gene family membership in VSTs of the three species, whether VSTs are more rapidly evolving at the sequence level or undergo more positive selection than more broadly expressed genes, and whether positive selection is involved in driving the molecular evolution of specific toxins. We explore to what extent transcripts exhibit conserved patterns of venom gland biased expression across species, and whether expression levels of VSTs in general evolve more rapidly across species or exhibit signatures of lineage-specific positive selection more often than broadly expressed transcripts.

A new dynamic model for the phylogenetic assembly of the ecological community

Alex Pigot

3C_305B-Phylogeny and Community Assembly
Monday, June 23, 2014 1:30 PM-1:45 PM

The application of phylogenetic data to community ecology has promised to provide new insights into the mechanisms structuring community assembly. However, progress has been hindered by a reliance on static null models that ignore the dynamic context within which assembly takes place. Here we address this by developing a new time-based model of community assembly by colonisation and local extinction, with speciation taking place in the wider species pool. We show that accounting for these processes fundamentally alters the phylogenetic structure of communities expected due to chance. We demonstrate how this new dynamic model can be used to infer both the historical rates of community assembly and the role of niche-based mechanisms in regulating community structure. We argue that a new generation of dynamic phylogenetic null models can greatly advance our understanding of the processes governing ecological communities.

Phylogenetic Skew: A New Index of Community Diversity

Hungyen Chen, Kwang-Tsao Shao, Hirohisa Kishino

3C_305B-Phylogeny and Community Assembly
Monday, June 23, 2014 1:45 PM-2:00 PM

The distribution of divergence times among community members, which depends on species sampling patterns, is an important aspect of community phylogenetic structure. Nevertheless, the incorporation of information regarding divergence time distribution is lacking from current phylogenetic diversity measures. Community genetic diversity may be translated into an effective community size for a hypothetical community generated by random speciation, extinction, and species sampling. In this study, we formulated a new index of community diversity, the phylogenetic skew index. We analyzed its statistical behavior using data from a monthly-monitored fish community at nuclear reactor water intakes in northern Taiwan, and developed a correction method to compensate for small sample size bias. We also performed a Bayesian analysis of variance under a gamma distribution model to detect annual and seasonal variation patterns in phylogenetic skew in the fish community. We show that our new phylogenetic skew index provides additional information regarding community diversity.

High-throughput sequencing characterization of meiofaunal communities in northern Gulf of Mexico

Pamela Brannock, Damien Waits, Jyotsna Sharma, Kenneth Halanych

3C_305B-Phylogeny and Community Assembly
Monday, June 23, 2014 2:00 PM-2:15 PM

Metagenomic approaches are widely used to examine prokaryotic community composition, but less often applied to eukaryotic organisms. Studies employing these approaches to study eukaryotic communities have mainly used the 454 platform. We have been using a novel high-throughput Illumina sequencing approach to characterize meiofaunal community composition within the Gulf of Mexico (GOM). Meiofauna, which comprise animals less than 1mm living between sediment grains, are important in food webs and nutrient exchange between the benthos and water column. These animals were dramatically affected by the Deepwater Horizon Oil Spill in both intertidal and subtidal locations. Unfortunately, knowledge of seasonality and variability of meiofaunal communities in most of the GOM is lacking. Previous research exploring meiofauna variation in this geographic region has used traditional methods of sieving and microscopy to taxonomically identify individuals. This method requires experts to properly identify organisms and, therefore, researchers typically focus on a few taxonomic groups within meiofauna, limiting the ability of studies to be extrapolated across the community. To better understand the spatial and temporal variation in GOM meiofaunal communities a whole, high-throughput amplicon sequencing targeting the eukaryotic specific hypervariable V9 region of the small subunit ribosomal RNA (SSU rRNA) gene was employed to examine intertidal and subtidal communities. Results show that high-throughput sequence approaches proved useful in examining the meiofauna community composition in the GOM. This approach can detect clear changes and differences in community composition over both spatial and temporal scales. In addition, this research provides a fundamental baseline to examine community impacts of future natural and anthropogenic disturbances in the Gulf of Mexico region and suggests the community shifts seen in sites impacted by the spill cannot be attributed to seasonal or geographic variability.

The role of deleterious mutations in influenza's antigenic evolution

Katia Koelle, David Rasmussen

3C_306A-Pathogen Evolution
Monday, June 23, 2014 1:30 PM-1:45 PM

The evolutionary dynamics of RNA viruses, as all organisms, depend on the occurrence of beneficial, deleterious, and neutral mutations. Yet, despite evidence for strong genetic linkage, the majority of studies on viral adaptive evolution focus exclusively on the role that beneficial mutations play in this process. This is particularly the case in modeling studies examining patterns of antigenic evolution in acute, semi-immunizing viral pathogens such as influenza. Here, we develop a model to address the dynamic interplay between beneficial mutations that enable immune escape and deleterious mutations that reduce between-host viral transmission. In an application of this model to influenza viruses in humans, we show that deleterious mutations are expected to make antigenic evolution occur in a punctuated manner, a pattern that has been empirically observed in these viruses. We further show that deleterious mutations are expected to substantially limit influenza's genetic and antigenic diversity in the long-run. Finally, we show that the dynamical effect of deleterious mutations provides a parsimonious explanation for two empirical observations in influenza: the occasional occurrence of within-subtype reassortment preceding an antigenic cluster transition and the tendency of antigenic clusters to arise from Asian, or more generally, tropical regions. This work highlights the critical importance of deleterious mutations in shaping patterns of viral adaptive evolution, even if they are not themselves the source of adaptation.

Signatures of Selection on RNA Structures in Influenza Genomes

Yang Ding, Joshua Plotkin

3C_306A-Pathogen Evolution
Monday, June 23, 2014 1:45 PM-2:00 PM

Influenza viruses are negative-sense RNA viruses that cause significant human morbidity and mortality each year. Rapid evolution of antigenic surface proteins allows the virus to re-infect hosts who have recovered from prior strains. It is thus important to understand the selective pressures that constrain the evolutionary trajectories of the influenza viral genomes. Most previous research has been focused on identifying amino acid residues that experience positive or negative selection, whereas selection on RNA structures in the anti-sense viral genome has received little attention. To address this, we developed an algorithm that scans along the viral genome to identify regions with excessive signals of purifying or positive selection on RNA structure, by comparing the average pairwise structural distances between actual viral RNA sequences with a null distribution. Unlike other algorithms that identify structural constraints, our approach accounts for the phylogenetic relationships between viral sequences, as well constraints on the amino-acid sequence. Moreover, our algorithm can detect recent selective pressures, which are of considerable practical interest. Our results on regions of negative selection on RNA structure largely agree with prior studies; and we provide the first evidence of recent positive selection on influenza virus RNA structures.

The Contribution of Migration and Mutation to the Population Shift Following Widespread Rotavirus Vaccination in the United States

Robert Woods, Daniel Zinder, Mercedes Pascual

3C_306A-Pathogen Evolution
Monday, June 23, 2014 2:00 PM-2:15 PM

The underlying evolutionary and ecological mechanisms that generate and maintain observed patterns of diversity in viral populations are often poorly understood. Dominant concepts of these mechanisms have been derived from a handful of iconic examples, such as HIV and influenza A, where the dynamics are driven by newly arising mutations. We investigate the evolution of rotavirus, a globally ubiquitous and genetically diverse cause of gastroenteritis and leading cause of childhood mortality, which has a distinctive pattern of geographically asynchronous serotype replacement. We take advantage of the introduction of two rotavirus vaccines in the United States in 2006, which created an intense but well defined perturbation. Publicly available sequences of the dominant antigenic protein, VP7, were used to show that in the United States the average genetic distance to the vaccine has increased following routine vaccination. Bayesian phylogenetic analysis combined with stochastic state reconstruction was used to estimate both sequence evolution and migration among geographic regions. We measure the contribution of three alternative population dynamics processes in the shift away from the vaccine, namely mutation, migration, and differential selection of local variants. We identify migration as the dominant process and show that the genetic shift occurred in serotypes independent of their inclusion in the vaccines. These results suggest that the asynchronous local dynamics maintain a diverse global metapopulation that in turn provides migrants that can rapidly respond to local changes in patterns of host immunity. We also find that genetic variation at higher resolution than that typically considered at the coarser, serotype, level may be of relevance to vaccine escape.

Intrahost competition in mixed-strain malaria infections may slow the evolution of resistance in high-transmission settings

Mary Bushman, Venkatachalam Udhayakumar, Jacobus de Roode

3C_306A-Pathogen Evolution
Monday, June 23, 2014 2:15 PM-2:30 PM

Most infections with the malaria parasite Plasmodium falciparum consist of a mixture of genetically distinct strains; the mean number of strains per host increases with the frequency of infective mosquito bites received. Mathematical models have suggested that within-host intraspecific competition between drug-sensitive and drug-resistant malaria parasites (in untreated asymptomatic infections) could inhibit transmission of resistant strains, slowing the evolution of resistance. This effect would have the greatest impact in high-transmission settings such as sub-Saharan Africa, where higher frequency of infective mosquito bites raises the probability of co-infection with sensitive and resistant parasites. Consistent with this, resistance to antimalarial drugs has typically been slower to spread in sub-Saharan Africa than in low-transmission settings.

We set out to test the hypothesis that intraspecific competition between drug-sensitive and drug-resistant P. falciparum occurs in human malaria infections. We used quantitative real-time PCR to determine the densities of chloroquine-sensitive and chloroquine-resistant P. falciparum in 1,358 pre-treatment blood samples from children in three African countries (Angola, Ghana and Tanzania). The average density of CQ-resistant parasites was found to be significantly lower when CQ-sensitive parasites were present, and vice versa, suggesting that intrahost competition between sensitive and resistant parasites does occur. Additional analysis of neutral genetic variation showed that total parasite density does not increase with the number of strains present, indicating density-dependent regulation of the overall parasite population. Finally, two lines of evidence suggested a fitness cost of resistance to chloroquine. First, the densities of CQ-resistant parasites were consistently lower than those of CQ-sensitive; second, we observed a rapid decline in the CQ-resistant allele following cessation of chloroquine use in Ghana. These findings suggest that intrahost competition may have helped to slow the spread of drug-resistant malaria in Africa, and may enhance selection against resistant alleles in the absence of drug selection. This work advances our understanding of the conditions that favor the spread of drug resistance and may ultimately help with design of better strategies to prevent and contain drug-resistant malaria.

Temporal Dynamics of a Ranavirus Outbreak in Chelonians with Mosquitoes as Possible Vectors

steven kimble, Ajit Karna, April Johnson, Jason Hoverman, Rod Williams

3C_306A-Pathogen Evolution
Monday, June 23, 2014 2:30 PM-2:45 PM

Ranaviruses are significant pathogens of amphibians, reptiles and fishes, contributing to mass mortality events worldwide. Despite an increasing focus on ranavirus ecology, our understanding of ranavirus dynamics, especially among reptilian hosts, remains limited. Specific knowledge deficits in chelonians includes mode of transmission, temporal dynamics during an outbreak, how infection covaries with environmental factors such as temperature and precipitation, and the efficacy of current noninvasive sampling techniques. To address these knowledge gaps, we repeatedly sampled a captive population (n = 317) of eastern box turtles (Terrapene c. carolina) during an outbreak of the ranavirus strain frog virus 3 (FV3). We also trapped and sampled mosquitoes to test the prediction that ranaviruses can be transmitted among Chelonians by arthropod vectors. Three mosquito samples tested positive for FV3 by qPCR, suggesting that mosquitoes may be involved in virus transmission as a mechanical or biological vector. Mortality was high, with at least 149 known mortalities by the end of the active season. Prevalence of FV3 ranged from 6.3% to 85.3%. Prevalence followed precipitation temporal trends but not temperature. Sampling by standard oral swabbing and blood draw revealed suggested that FV3 can either become quiescent periodically or that clearing and reinfection is common, perhaps by mosquito vectors.

Evidence for natural selection of phenotypic plasticity in Plantago lanceolata

Matthew Marshall

3C_306B-Plasticity
Monday, June 23, 2014 1:30 PM-1:45 PM

In natural populations phenotypic plasticity often increases with latitude and altitude. For example, in Plantago lanceolata temperature-sensitive plasticity of inflorescence reflectance/color is positively correlated with latitude and altitude among European populations. This observation suggests plasticity is adaptive in cooler environments. However, this geographic pattern may have arisen via neutral evolutionary processes. I estimated differences in neutral genetic AFLP markers, plasticity, and environmental conditions among 14 European populations of P. lanceolata to test the following hypotheses: 1) Neutral evolutionary forces alone are sufficient to explain differences in plasticity among populations, and 2) Local adaptation of plasticity has occurred via natural selection. The first hypothesis was rejected because neutral genetic differences were too small to explain phenotypic differences. Data supported the hypothesis that natural selection has driven differences in thermal plasticity.

Soil microbial communities cause differential selection and plasticity of flowering time in the wild mustard Boechera stricta

Maggie Wagner, Derek Lundberg, Devin Coleman-Derr, Susannah Tringe, Jeff Dangl, Tom Mitchell-Olds

3C_306B-Plasticity
Monday, June 23, 2014 1:45 PM-2:00 PM

The timing of flowering in complex natural habitats is known to be both genetically controlled and sensitive to multiple biotic and abiotic environmental stimuli. However, the impact of soil-dwelling microbes on flowering time and on patterns of natural selection has rarely been considered. We transplanted seedlings from 48 naturally inbred populations of the wild crucifer Boechera stricta into potting soil inoculated with a soil microbial community extracted from each of 4 natural B. stricta habitats. We then measured plant height and leaf number, date of first flower, and number of fruits produced. Microbial community did not affect plant size, but shifted flowering time by up to 2.2 days. The two B. stricta subspecies showed a nearly significant difference in the extent of flowering time plasticity in response to soil microbes, but we found no evidence for within-subspecies genetic variation for plasticity. Soil microbes also altered the relationship between flowering time and fruit set, even reversing the direction of selection in one community. Deep 16S rDNA sequencing revealed three phyla (Proteobacteria, Crenarchaeota, and Acidobacteria) and several families that were differentially abundant in soils associated with slowest and fastest flowering. Our results show that soil microbes have the potential to alter flowering time as well as the intensity of selection on flowering time in nature.

Why wait? The optimal waiting time between an environmental cue and a plastic response

Hamish Spencer

3C_306B-Plasticity
Monday, June 23, 2014 2:00 PM-2:15 PM

An adaptive plastic response to an environmental cue results in an organism developing a phenotype that is in some way appropriate to the future conditions forecast by the cue. Clearly, the more accurate the forecast the more likely it is that the response will be appropriate (although plasticity is favoured by selection for surprisingly inaccurate cues) and the higher the expected fitness benefit to organisms employing such a cue. Selection, then, may be expected to favour the evolution of accurate cues. Everything else being equal, cues that induce an immediate developmental response might be expected to be more accurate than cues that occur some time before the response is initiated because there is less opportunity for unexpected environmental changes and the correlation between the cue and the future environment will be higher. Nevertheless, many plastic responses (so-called “predictive adaptive responses”) are induced by cues that occur long before any developmental changes occur. In this talk, I will explore the reasons why it it may be better to wait. These results can be used to predict what sorts of traits may be influenced by predictive adaptive responses.

Predator-induced phenotypic plasticity within- and across-generations

Matthew Walsh, Steve Munch

3C_306B-Plasticity
Monday, June 23, 2014 2:15 PM-2:30 PM

Much work has shown that the environment can induce phenotypic changes that span multiple generations. Theory predicts that similar conditions (i.e., predictable environmental variation) favor the evolution of within- and across-generation plasticity. We explored the relationship between within- versus across-generation plasticity by evaluating the influence of predator cues on the life history traits of Daphnia ambigua. We manipulated the duration of exposure to fish-conditioned water and tracked responses across multiple generations. We show that predator exposure during embryonic development causes faster development and increased reproductive output. Such effects are detectable two generations removed from predator exposure. Most importantly, we found a negative correlation between within- vs. across generation responses. Although many models address transgenerational plasticity, none of them predict all features of this work. Our results highlight the need to refine the theory of transgenerational plasticity.

Plasticity in offspring growth maximizes potential fitness in unpredictable environments

Robert Aldredge, Peter Lowther

3C_306B-Plasticity
Monday, June 23, 2014 2:30 PM-2:45 PM

In ideal conditions postnatal growth should be limited primarily by the ability of tissues to differentiate because suboptimal growth due to resource limitation can have immediate and long-term consequences for fitness. However, conditions rarely are ideal and growth rate often exhibits considerable variation from the optimum. Passerines are a large and diverse group of animals that maximize postnatal growth to the rate at which skeletal tissue can differentiate. By maximizing growth rates, parents increase the number of possible nesting attempts per season and hence the total number of offspring they can produce, but limit the variation in nestling growth strategies. I analyzed growth rates for more than 5,000 nestlings in three populations of a multi-brooded songbird, the house sparrow Passer domesticus, over 32 years (2,901 nestlings from 1975-1978 in Kansas, 2,047 nestlings from 1988-2013 in Illinois, and 257 nestlings from 2012-2013 in North Carolina). Growth rate shows substantial spatial and temporal variation. Despite this extensive variation, growth rate and nestling survival are highest in rural populations in Kansas and North Carolina, and are consistently low in a residential population in Illinois. Faster growth rates during cicada emergences in 1990, 2002, and 2007 suggest that poor growth in Illinois is caused by limited food availability. However, growth in these superabundant food years never exceeded the maximal rate seen in Kansas birds. These results show that house sparrows maintain considerable plasticity in offspring growth strategies, and support the assertion that growth rate may be limited in some populations and years by the ability of tissues to differentiate. Plasticity in postnatal growth likely enables parents to maximize fitness in unpredictable food environments and may have facilitated the rapid expansion of house sparrows across North and Central America, as well as the successful colonization of house sparrows in diverse environments around the world.

A tradeoff between natural and sexual selection underlies evolution of sexual signal diversity in Bahamas mosquitofish

Justa Heinen-Kay, Kirstin Morris, Nicole Ryan, Samantha Byerley, Rebecca Venezia, Nils Peterson

3C_306C-Visual Signaling
Monday, June 23, 2014 1:30 PM-1:45 PM

It has long been assumed that conspicuous, brightly colored traits are subject to tradeoffs between natural and sexual selection, but surprisingly few empirical investigations of this hypothesis exist.

We directly tested this notion in a model system for adaptive diversification: livebearing Bahamas mosquitofish (Gambusia hubbsi) inhabiting blue holes across Andros Island. Male G. hubbsi possess bright orange dorsal fins that they display during female courtship and male-male competition. The degree of fin coloration has evolved differences between populations isolated in the presence or absence of a piscivorous fish (Gobiomorus dormitor) for thousands of years. We constructed 3D-printed model replicas of male G. hubbsi and painted them to exhibit the average fin color of males found in low-predation (more colorful fins) or high-predation (less colorful fins) populations. We paired high- and low-predation models to test for a tradeoff between natural and sexual selection using in situ predator trials in blue holes and lab-based female mate choice trials. Predatory fish approached and spent more time inspecting more colorful models than less colorful models, suggesting that bright orange dorsal fins are more conspicuous to predators. Virgin female G. hubbsi born in the lab spent more time associating with the more colorful model fish, with significant heritability for female preference. Thus, our study provides much needed empirical evidence supporting a tradeoff between natural and sexual selection for a conspicuous sexual signal.

Ecological variation affects signal reliability in Gambusia hubbsi

Sean Giery, Craig Layman

3C_306C-Visual Signaling
Monday, June 23, 2014 1:45 PM-2:00 PM

In many models of sexual selection, conspicuous ornaments are preferred by mates because they indicate heritable signaler viability. To function as indicators, ornaments must maintain a proportional relationship between expression and viability. These indicators are called condition dependent signals. To maintain condition dependence, signaling costs must prevent males with low viability from expressing disproportionate conspicuous signals. Given ecological variation in signaling costs, it is likely that the strength of condition dependence varies concomitantly. In this study, we assess the effect of variable signal cost, predation risk, on the strength of condition dependence among 15 wild populations of Bahamas mosquitofish (Gambusia hubbsi) that use colorful dorsal fins in courtship displays. We found that the signal of interest, fin coloration, predicted body condition. However, this relationship was only seen in populations subject to predation from piscivorous fish. In contrast, populations without predators showed no signs of condition dependence suggesting that variation in ecological costs has important effects on communication system evolution. In summary, while our study addresses only one type of sexual signal (coloration), uses only one estimate of viability (condition), and focuses on a single type of signaling cost (predation), we confirm a crucial role for ecological signaling cost in communication.

Warning signals are seductive: Relative contributions of color and pattern cues to predator avoidance and mate attraction in Heliconius butterflies

Susan Finkbeiner, Adriana Briscoe, Robert Reed

3C_306C-Visual Signaling
Monday, June 23, 2014 2:00 PM-2:15 PM

Visual signaling in animals can serve many uses, including predator deterrence and mate attraction. In many cases signals used to advertise unprofitability to predators are also used for intraspecific communication. Although aposematism (warning signaling) and mate choice are significant forces driving the evolution of many animal phenotypes, the interplay between relevant visual cues remains little explored. Here we address this question in the aposematic passion-vine butterfly Heliconius erato by using color- and pattern-manipulated models to test the contributions of different visual cues to both mate choice and warning coloration. We found that the relative effectiveness of a model at escaping predation was equivalent to its effectiveness at inducing mating behavior in males, and in both cases wing color cues were more predictive of fitness benefits than pattern cues. Overall, however, a combination of the appropriate color and pattern cues were most successful for both predator deterrence and mate attraction. By exploring the relative contributions of color versus pattern composition in predation and mate preference studies, we have shown how both natural and sexual selection can work in parallel to favor the evolution of specific animal color patterns.

Directional Selection on Aposematic Coloration in the Dyeing Poison Frog (Dendrobates tinctorius)

J.P. Lawrence, Antoine Fouquet, Bibiana Rojas, Elodie Courtois, Johanna Mappes, Brice Noonan

3C_306C-Visual Signaling
Monday, June 23, 2014 2:15 PM-2:30 PM

Aposematic (warning) coloration is a defensive strategy found throughout the animal kingdom. The phenomenon relies on frequency dependence of an aposematic signal for local predators to learn and associate the signal with unpalatability. Theory predicts that more common signals (morphs) should be favored against novel forms. Previous research supports the role of purifying selection on phenotype, consistent with current evolutionary theory. Many aposematic species, however, display polytypism (interpopulation variation), which is counterintuitive. Here we studied how signal polytypism may evolve in the Dyeing Poison Frog (Dendrobates tinctorius). This species is found throughout the Guiana Shield of South America and exhibits a wide variety of color and pattern combinations. We examined predator response to novel colors and patterns by placing plasticine clay models in two different sites in French Guiana where color but not pattern differ. Models placed in each area had either the local color and pattern, local color and novel pattern, or local pattern and novel color. At one site, avian predators attacked the local morph more often than expected by chance, but had equal avoidance of all models in our second site. These results suggest directional selection towards a more efficient aposematic signal. This provides a mechanism for novel signals to evolve and be pushed to a new signal optimum, which could explain how polytypism may evolve in aposematic species.

Parasite-mediated sexual signaling: what do females gain?

Amanda Hund, Joanna Hubbard, Rebecca Safran

3C_306C-Visual Signaling
Monday, June 23, 2014 2:30 PM-2:45 PM

The Hamilton-Zuk hypothesis proposes that host-parasite co-evolution maintains the honesty of sexual traits and predicts that attractive males with the greatest degree of sexual trait expression have lower parasite loads. Accordingly, this hypothesis also predicts that females use these signals as indicators of parasite resistance. Parasites are common in many species and represent a cost to their host as they can limit investment in reproduction and affect breeding success. Using parasite-linked sexual traits in mate selection could confer benefits to females in at least three ways: attractive males could 1) have greater genetic resistance to parasites that can be passed to offspring, 2) offer a better nest environment with lower parasite risk, and/or 3) help to offset the costs of parasitism through behaviors such as provisioning . In a breeding population of North American barn swallows Hirundo rustica in Colorado, I applied a reciprocal cross-fostering design where I experimentally manipulated parasites in nests to establish the degree to which females use male ventral coloration – a sexual signal in this population of barn swallows - for information about parasite-resistant genotypes or parasite-free environments. I also observed provisioning behavior of these birds to see if behavior changed with parasites and sexual trait expression. Because parasites differ across spatial scales, parasite-mediated signaling may be based on different suites of parasites in different populations. This study will help me to tease apart the role of parasites in driving sexual selection and mate choice in North America before conducting larger comparative studies on barn swallow subspecies with divergent sexual selection on different plumage-based traits.

Detecting the genes responsible for local adaptation

Michael Whitlock, Katie Lotterhos

3C_402-ASN Vice Presidential Symposium:Modern approaches to local adaptation
Monday, June 23, 2014 1:15 PM-1:45 PM

We present a new method for identifying the genes underlying local adaptation from genomic data. A great difficulty for identifying genes that are more differentiated than expected for neutral genes is that hte null odel depends on demographic details. As a result, model-based inference is challenging and prine to high false discovery rates. The new method, OutFLANK, is derived from the Lewontin Krakauer test, but the null distrbution is inferred from a trimmed distirbution of Fst by loci. We show that over a broad range of simulated cases the method has appropriate false discovery rates and outperforms alternative approaches.

Theoretical perspectives on local adaptation in heterogeneous environments

Florence Débarre

3C_402-ASN Vice Presidential Symposium:Modern approaches to local adaptation
Monday, June 23, 2014 1:45 PM-2:15 PM

The spatial and temporal variation in environmental, and hence, selective, conditions is an important factor for the emergence and maintenance of diversity. Yet, heterogeneous environmental conditions do not always lead to a greater genetic or phenotypic variation: gene flow, drift, or genetic constrains can impose limits on local adaptation. The potential for local adaptation also depends on how selection varies over space. Here, I consider various theoretical models of local adaptation, and I show in particular how modelling spatial structure explicitely may affect the predictions derived from models that neglect explicit spatial structure (e.g., island models).

Reconciling population and quantitative genetic models of local adaptation: Critical assumptions about genetic architecture

Sam Yeaman

3C_402-ASN Vice Presidential Symposium:Modern approaches to local adaptation
Monday, June 23, 2014 2:15 PM-2:45 PM

Population genetic models of local adaptation predict that polymorphism can be lost when migration rates exceed certain critical values, defined mainly by the strength of selection. By contrast, quantitative genetic models typically assume that standing variation is always maintained and that mean trait values evolve under the balance between migration and selection. As such, these two approaches can yield conflicting predictions in certain regions of parameter space, when migration is strong relative to selection on individual alleles. Here, I will review some of the predictions of these models and discuss the importance of assumptions we make about the genetic basis of trait variation (number of loci, effect size distributions, and linkage relationships). I will also discuss an alternative model based on recurrent conditionally deleterious mutation that can generate genotype x environment interactions for fitness resembling local adaptation.

Emerging methods in phylogenomics, transcriptomics, and the evolution of gene expression

J. Chris Pires

3C_BalC-SSB Symposium: Phylogenomics, transcriptomics, and the evolution of gene expression
Monday, June 23, 2014 1:15 PM-1:30 PM

Functional genomic data are no longer the realm of a few model organisms – they are now collected across the tree of life. Gene expression analyses in particular, mediated by technical advances in mRNA-seq, are providing entirely new approaches to understanding the relationships between genes and phenotypes in many different species. Most such studies, though, still focus on one species at a time. Phylogenetic comparative analyses of gene expression will be critical for synthesizing information across organisms, investigating the evolution of gene expression, and for using the diversity of phenotypes within clades to understand gene function. In this symposium, we propose to explore how transcriptomic data are being used to make phylogenies and other evolutionary inferences (detect polyploidy and hybridization, assess function, metagenomics, etc.); and how phylogenies are being used to make inferences about gene expression evolution. The intersection of phylogenomics, transcriptomics, and the evolution of gene expression also offers the systematic biology community a rich area to develop new approaches and statistical methods. To address these issues, we have assembled a diverse set of junior and senior investigators who use transcriptomic and phylogenomic approaches in various lineages of life.

What can the evolution of gene expression tell us about the evolution of genomes and other phenotypes?

Casey Dunn

3C_BalC-SSB Symposium: Phylogenomics, transcriptomics, and the evolution of gene expression
Monday, June 23, 2014 1:20 PM-1:45 PM
Most species on Earth will never be grown in the lab, precluding many of the genetic and experimental tools that have been used to understand the relationships between genotypes and phenotypes. This puts most phenotypes beyond the reach of current tools. Gene expression analyses have been proposed as a means of understanding gene function in these difficult-to-study species. The perspective they provide is quite narrow, though, and they have multiple technical limitations. I will describe how phylogenetic analyses of gene expression can overcome some of these challenges, while also directly addressing central questions about the evolution of genomes and phenotypes.

Transcriptomic fingerprints of development and circadian cycles in marine invertebrates

Ann Tarrant

3C_BalC-SSB Symposium: Phylogenomics, transcriptomics, and the evolution of gene expression
Monday, June 23, 2014 1:45 PM-2:15 PM
Animal physiology, behavior and morphology change both during development and in response to environmental conditions, many of which vary on daily and/or seasonal cycles. The copepod Calanus finmarchicus can facultatively enter dormancy during its last juvenile stage (C5). During the C5 stage, C. finmarchicus stores wax esters in an organ called the oil sac in order to provide energy reserves needed for molting, reproduction and sometimes dormancy. We have identified genes that change in expression during progression through the C5 molt stage, including evidence for a wide-ranging metabolic transition. Gene expression comparisons between developmental stages, between closely-related species and between populations that differ in their dormancy patterns have begun to provide insight into regulation of Calanus dormancy. The prevalence of transcriptional profiling studies provides an unprecedented opportunity for comparative analyses with existing datasets. We have used such a comparative approach to identify homologous genes with a strong circadian signal in both an anemone and a coral species. These shared genes are strong candidates for playing a central role in circadian clock function.

Comparative Transcriptomics of Queen and Worker Castes in Hymenoptera

Ali Berens, James Hunt, Amy Toth

3C_BalC-SSB Symposium: Phylogenomics, transcriptomics, and the evolution of gene expression
Monday, June 23, 2014 2:15 PM-2:45 PM
The presence of queens and workers defines eusocial insect societies and constitutes a spectacular example of biological complexity expressed as alternative phenotypes from a single genome. Given multiple origins of eusociality in Hymenoptera (bees, ants, and wasps), it has been proposed that caste phenotypes evolved convergently through common genetic “toolkits”. An alternative hypothesis posits that “novel” genes are responsible for evolution of the worker phenotype. Here, we combine data from previously published studies on ants and bees with new data for Polistes paper wasps and present the first comparative transcriptome-wide analysis of caste determination among three major Hymenopteran social lineages. Polistes wasps are an ideal system to study social evolution because they have flexible caste differences that are biased during early development via nutritional differences. Therefore, we also investigated the transcriptomic impacts of high and low nourishment levels as environmental determinants of caste in P. metricus larvae. Overall, we found few shared caste differentially expressed transcripts across the three social lineages. However, there is substantially more overlap at the levels of pathways and biological functions. Thus, genetic toolkits appear to be relatively “loose”, i.e. different lineages converge on similar metabolic pathways and molecular functions but not on the exact same genes. By comparing RNA-seq data from two paper wasp species, we found no support for the idea that “novel” transcripts are important for caste differences. At the same time, nutritional inequalities only partially biased wasp gene expression patterns toward one caste or another; thus there must also be non-nutritional, likely social environmental, determinants of caste in Polistes.

Condition-dependent alternative reproductive tactics in territorial damselflies: the role of wing shape in territory-holding potential

David Outomuro, Frank Johansson

3D_201-Reproductive Strategies
Monday, June 23, 2014 3:15 PM-3:30 PM
Territorial contests between males without weaponry are based on costly displays and can result in condition-dependent alternative reproductive tactics that maximize male fitness. Physiological and morphological traits such as fat content, body size or the expression of secondary sexual traits have been shown to contribute to male territory-holding potential. When territorial contests are based on flight displays, wing shape is expected to contribute to the territory-holding potential of a male through its effects on flight performance. We explored whether wing shape contributed to the territory-holding potential of males of three species of Calopteryx damselflies. Males of these species show two

distinct, condition-dependent behavioral tactics: territorial and nonterritorial. Previous studies have shown that territorial males have higher fitness than nonterritorial males. We used mark-recapture to determine male tactics within the populations and compared wing shape, size and wing colored spot size (a secondary sexual trait) between tactics. Territorial males of all three species had shorter and slightly broader hindwings than nonterritorial males. In two species, forewings of territorial males were longer and broader than forewings of nonterritorial males. Wing size and wing spot size did not differ between tactics. We suggest that the wing shape of territorial males might confer better flight maneuverability, which would be advantageous for territorial contests. Therefore, wing shape is likely to be an important trait contributing to territory-holding potential in condition-dependent alternative reproductive tactics based on flight displays.

Maintenance of a conserved trait: natural selection on stamen lengths in wild radish

Jeffrey Conner, Anne Royer, Zhigang Zhao, Vanessa Koelling, Keith Karoly

3D_201-Reproductive Strategies
Monday, June 23, 2014 3:30 PM-3:45 PM
Tetradynamy, the presence of four long and two short stamens within each flower, is a diagnostic trait of the mustard family Brassicaceae, but the reasons for the maintenance of this trait across most of the 3700+ species in the family are unknown. Previous functional studies of pollen removal and selection through male fitness (seed siring success) suggested that the short stamens function to reduce per-visit pollen removal, which increases male fitness under high pollinator visitation rates (Conner et al. 2003 Evolution). To further test this hypothesis, we expanded the phenotypic variance of the difference in stamen heights through artificial selection, and measured selection on this trait across multiple days that naturally varied in pollinator visitation rate.

Battle of the sexes? Investigating the evolution of multiple mating types in Dictyostelium

Tracy Douglas, David Queller, Joan Strassmann

3D_201-Reproductive Strategies
Monday, June 23, 2014 3:45 PM-4:00 PM
Theory indicates that the number of mating types expressed in a system should tend towards infinity or remain at two. This means it is a puzzle that dictyostelids often have only 3 or 4 mating types, a question that has yet to be addressed in these species. In the model organism Dictyostelium discoideum, there are three self-incompatible mating types, which cannot mate with themselves but can mate with any other type. Although sex is rarely observed in this species, we know from previous studies that sex is an important part of the life cycle based on evidence of little or no linkage disequilibrium. Because so little else is known about the characteristics of the D. discoideum mating types, we predict that many factors could contribute to the maintenance of this system. To start, we investigated common measurements for evidence of conflict between mating types and selection on mating systems: gamete size and mating type distribution. While gamete size measurements revealed no evidence of differing selective pressures within D. discoideum, showing that gametes across mating types are homologous in size, mating type distributions show potentially interesting dynamics. Though we found an overall even distribution, we also found population-specific mating type distributions, suggesting a possibility for location-driven differential selective pressures on these mating types. In addition to these traditional measures, we will also discuss current efforts to identify conflicts between mating types caused by differential contributions to macrocyst production and insight into how these conflicts could lead to constraints on the evolution of many mating types in D. discoideum.

Evolution of sexual dimorphism in floral scent.

Tomoko Okamoto

3D_201-Reproductive Strategies
Monday, June 23, 2014 4:00 PM-4:15 PM
Animal-pollinated flowers often emit various signals, e.g. color and scents, to attract pollinator insects. In plants with unisexual flowers, such signals are similar between the sexes because attraction of the same animal to both sexes is essential for reproductive success. We focused on the reproductively highly specialized clades of the tribe Phyllantheae (Phyllanthaceae) which are pollinated by species-specific, seed-parasitic Epicephala moths (Gracillariidae). Female adults of Epicephala moths pollinate actively – they purposefully collect pollen on male flowers and deliberately pollinate female flowers to secure food for their seed-feeding larvae. Thus, Epicephala moths may have the ability to distinguish male and female flowers, which is crucial for successful reproduction of both the moths and the plants. Here, we present the findings undermine commonly accepted theory that floral signals should be similar between sexes in flowering plants.

We found the major qualitative differences in scent between male and female flowers in Epicephala-pollinated Phyllantheae plants. In a choice test, mated female Epicephala moths preferred the scent of male flowers over that of female flowers, suggesting that male floral scent elicits pollen-collecting behavior. Epicephala pollination evolved multiple times in Phyllantheae, at least thrice accompanied by transition from sexual monomorphism to dimorphism in floral scent. This is the first example in which sexually dimorphic floral scent has evolved to signal an alternative reward provided by each sex, provoking the pollinator's legitimate altruistic behavior.

An experimental test of the causal mechanisms linking flowering time to male fitness in a hermaphroditic annual plant

Emily Austen, Arthur Weis

3D_201-Reproductive Strategies
Monday, June 23, 2014 4:15 PM-4:30 PM
Individuals of sexual species accrue fitness by producing (female role) or siring (male role) offspring. Understanding trait evolution requires that the targets and agents of selection be identified for both gender roles.

We aimed to understand how and why selection acts on flowering time in Brassica rapa. As for most plant traits, little is known about selection on flowering time through male fitness, but both direct and indirect selection are possible. The latter may include indirect effects through phenotype-environment correlation with the social environment (quantity and quality of conspecifics) or with the non-social environment (pollinators, florivores, abiotic stress, etc.) experienced during flowering.

To tease apart these effects, we manipulated the correlation between age at flowering (AAF) (i.e., flowering time) and flowering Julian Date (FJD) (i.e., non-social environment). Specifically, we staggered planting dates to create populations in which AAF and FJD were positively, negatively, or uncorrelated.

Genetic paternity analysis revealed that direct selection strongly favoured young AAF in two populations, and tended towards the same in the third. Decreasing male success with older AAF, regardless of FJD, suggests indirect selection through correlation with the non-social environment was weak.

To assess effects of correlation with the social environment, we repeated paternity analysis using seeds sampled uniformly across mothers. This sampling eliminated variance in dam quality, and thus, covariance between sire AAF and dam quality. Selection gradients estimated from the uniform sample matched those estimated by the previous, proportional, sample, suggesting selection through correlation with the social environment was also weak.

Finally, to explore the direct effect of flowering time on male fitness, we conducted path analysis of AAF and correlated traits on four multiplicative fitness components. In all populations, older AAF led to fewer mates reached per flower. Thus it seems that AAF (or an unmeasured, genetically correlated trait) directly affected attractiveness to pollinators and/or efficiency of pollen transfer to pollinator bodies.

We previously reported that selection through female fitness in this experiment tended to favour early FJD, regardless of AAF. Taking the positive correlation between AAF and FJD to be the closest approximation of a natural population, we infer that early flowering likely enhances both male and female function in B. rapa, but for different reasons. This mechanistic difference has evolutionary consequences: selection to maintain optimal AAF for male function could slow response to selection on FJD through female function in a changing environment.

Evolutionary responses of plants to urban environments

Mohamed Yakub, Peter Tiffin

3D_206-Evolution in Human-altered Environments
Monday, June 23, 2014 3:15 PM-3:30 PM

Urban environments are hotter, drier, and have altered air quality than their rural surroundings, and therefore provide a natural experiment to examine evolutionary responses to new habitats. Using seeds collected from Minneapolis and St. Paul and neighboring rural areas we conducted greenhouse and reciprocal transplant experiments. We detected phenotypic differences between urban and rural plants, with plants from rural sources reproducing later but plants from urban sources growing larger. In the field, urban plants were larger in the urban environment and rural plants were larger in the rural environment, consistent with local adaptation. Analyses examining selection and fitness differences are currently underway. Understanding if and how plant populations have adapted to urban environments may provide insight into niche expansions as well as plant responses to future climates, which are expected to be characterized by shifts in abiotic factors similar to those in urban environments.

Phenotypic shifts in urban areas in the tropical lizard Anolis cristatellus

Kristin Winchell, R. Graham Reynolds, Sofia Prado-Irwin, Alberto Puente-Rolón, Liam Revell

3D_206-Evolution in Human-altered Environments
Monday, June 23, 2014 3:30 PM-3:45 PM

Urbanization is an important dimension of global change and human-dominated landscapes are increasing in both spatial extent and intensity worldwide. How populations of urban-persistent species might be adapting to these habitats is a topic of interest to evolutionary biology and conservation. We studied populations of a common neotropical lizard, Anolis cristatellus, in paired urban and natural habitats in three of the most populous regions of Puerto Rico to test the hypothesis that populations are adapting to urban conditions. We found significant evidence of a morphological shift in urban areas in this species. We are presently using a common-garden rearing experiment combined with natural selection studies in the wild to help determine if this shift is genetically-based and in the direction predicted by differences in natural selection between environments.

An elemental perspective of intraspecific variation and its impact on key eco-evolutionary processes

Priyanka Roy Chowdhury, Punidan Jeyasingh

3D_206-Evolution in Human-altered Environments
Monday, June 23, 2014 3:45 PM-4:00 PM

Explaining the origin and maintenance of variations across multiple levels of organization, from sub-cellular to community level, is an important challenge in contemporary biology. Integrating the mechanistic framework of ecological stoichiometry (ES) with contemporary –omics mechanisms can serve as an important tool to quantify such variations and understand their interactions across key levels of organization. ES uses information on the content of elements in individuals to predict key ecological functions such as nutrient recycling. While much work in ES has focused on interspecific variation, little is known about the ecological consequences of intraspecific variation in elemental content and excretion. To that effect, we first quantified intraspecific variation in P-use in four resurrected genotypes of Daphnia pulicaria from South Center Lake (MN) sediments that has a history of cultural eutrophication. We further tested whether such genotypic variations in P-use results in differential excretion, consequently affecting the quality and quantity of algal cultures via differential consumer-driven-nutrient-recycling. Second we quantified the ionomic profiles of individual genotypes in response to P-supply, to identify correlated shifts in the processing and excretion of other biogenic elements co-varying with dietary P-supply. Our results showed significant genotypic variations in P-use physiology which in turn affected both the algal quality and quantity indicating the potential of such variations to alter ecosystem functions. Ionomic profiles indicated that altering P-supply alone can invoke extensive changes in the somatic concentrations of several elements, some of which can play significant ecological roles. Together, this study highlights the importance of intraspecific variation in trophic interactions, and the utility of ecological stoichiometry in understanding the ecological consequences of such variation.

Tainted resurrection: Metal pollution is linked with high juvenile mortality in Daphnia egg banks

Mary Rogalski

3D_206-Evolution in Human-altered Environments
Monday, June 23, 2014 4:00 PM-4:15 PM

The life history strategy of many taxa relies on long-lasting resting stages to transit harsh conditions. Plants, insects, zooplankton, algae, and fungi (to name a few) all produce resting stage propagules capable of temporal dispersal. Some of these propagules can persist for decades or even centuries before hatching or germinating. A wealth of research has focused on the functioning and evolutionary importance of these propagule banks; however relatively little is known about the effects of the abiotic environment experienced during dormancy on this complex life history strategy. This study examines the developmental success of Daphnia hatched from resting eggs from several lakes and time periods experiencing varying levels of heavy metal contamination. I hatched a total of 274 animals from resting egg banks going as far back in time as the early 1900s to the present day. I found strong evidence of increased juvenile mortality in Daphnia hatching from sediments contaminated by heavy metals. Post-hatching juvenile mortality ranged from 0% to 45%. This trend emerges from analysis of three polluted lakes and three different Daphnia species. Animals from a reference lake that experienced limited metal contamination had the lowest mortality rates. The mechanisms driving this trend will require further study. Heavy metals could have affected the eggs via maternal effects or bioaccumulation or directly through years of exposure to metal contaminated sediments. Regardless of the specific mechanism, exposure to heavy metals may impose strong selection on Daphnia hatched from resting egg banks.

Time-after-time: assessing ecological and genetic variation in Daphnia resting egg banks

Lawrence J. Weider, Dagmar Frisch, Philip Morton, Priyanka Roy Chowdhury, Bily Culver, Joaquin Munoz

3D_206-Evolution in Human-altered Environments
Monday, June 23, 2014 4:15 PM-4:30 PM

The use of population genetic and genomic methods in assessing genetic changes in dormant propagule banks is a valuable tool in the study of resurrection ecology. Coupling this approach with comparative, long-term studies of populations that have been subjected to differential environmental histories is essential to assess the impact of anthropogenic environmental change. In lakes and ponds, such historic changes can be detected using paleolimnological methods to reconstruct environmental histories from lake sediments that harbor long-term records of changes in water chemistry (e.g., heavy metals, organo-pollutants, nutrients). For our study, we focused on a number of lakes that have served as study sites in a long-term monitoring program (Minnesota Sentinel Lakes Program, MN, U.S.A) that has been assessing the role of phosphorus (P) loading as a key driver of eutrophication, resulting in impacted water quality. In particular, we studied changes in the temporal population genetic structure of the keystone aquatic herbivore, Daphnia pulicaria, using resting eggs extracted from centuries-old sediments in two lakes (South Center, Hill). These two lakes showed striking differences in environmental histories prior to and after European settlement, with South Center showing dramatic temporal shifts in genetic structure through time that closely paralleled changes in anthropogenic impacts (i.e. human population growth, land-use, P-loading), while Hill showed no such shifts, paralleling weaker human-impacts in its watershed. Using a variety of molecular markers (i.e., microsatellites, SNPs) distributed across the entire Daphnia genome, we identify possible relationships between environmental variables and genetic structure in these lake populations.

Investigating parameterization in RAD-tag phylogenetic inference

Clive Darwell, David Rivers, David Althoff

3D_301A-Phylogenetic Methods
Monday, June 23, 2014 3:15 PM-3:30 PM

The advent of modern genomic, next-generation sequencing (NGS) technologies offers the chance to unravel complex, hitherto obfuscated evolutionary and ecological patterns in non-model organisms. However, a number of unresolved issues from a phylogenetics perspective mean that widely accepted methodologies for the implementation of these datasets are currently being heavily debated and are still in development. Among the issues, is whether there is value in employing standard methods of nucleotide sequence evolution modeling on the short sequence reads (~90bp) generated across these huge datasets and whether the typical inclusion of large amounts of missing data across taxa when compiling sequence alignments for phylogenetic inference is problematic. Here we present an empirical investigation of the effects of these two issues placed against the backdrop of evaluating taxonomic relationships among a previously considered problematic species complex of yucca moths (Prodoxidae). Our main conclusion is that the huge volume of raw sequence information made available by RAD-tag technologies means that the manipulation and parameterization of data in order to optimize Bayesian and maximum likelihood phylogenetic inference has minimal impact on final results. Taxonomic relationships among yucca moths were resolved unambiguously under different modeling schemes across all inferred phylogenies, almost always with 100% node support. Moreover, statistical comparison of pairwise branch length distances found that all phylogenies are of similar topological structure. Additionally, we removed sequence data information and coded restriction site loci as present or absent, thus mimicking an AFLP-type dataset. Here we found that at deeper nodes, where much missing data is encountered in RAD-tag sequencing, relationships were resolved whereas more recent evolutionary events were unclear. These findings suggest that presence/absence information may contribute significantly to determining more ancient relationships in these NGS datasets. We suggest that the large amounts of data and the unequal distribution of restriction sites found in RAD-tag datasets means that many of the salient theoretical issues surrounding phylogenomic inference are of a different nature to those relevant to standard PCR-based, multi-gene phylogenetic reconstruction.

A New Age of Experimental Phylogenetics: Digital Evolution and the Population Processes that Reduce Phylogenetic Accuracy

Cory Kohn, Barry Williams

3D_301A-Phylogenetic Methods
Monday, June 23, 2014 3:30 PM-3:45 PM

Accurate inference of historical relationships, i.e. phylogenetics, is central to evolutionary biology. Methods for phylogenetic inference have improved through increasingly advanced theoretical and statistical approaches as well as increasingly sophisticated computational tools. However, methods used to evaluate phylogenetic accuracy have been less well developed. Tests of phylogenetic accuracy rely almost exclusively on computational simulations, which are superb tools for generating large amounts of data under defined parameter values. A drawback of simulations is that they cannot be used to evaluate emergent or unknown properties present in complex systems with enigmatic interactions among factors. Our perception of phylogenetic accuracy has been constrained to inferences that can be gleaned using simulations specified under simple evolutionary models. Alternative, but rarely used, approaches to evaluate phylogenetic accuracy are analyses of data from natural or experimental taxa with a known evolutionary history. Major drawbacks to these approaches are the labor- and time-intensiveness required to observe evolutionary change. The digital software platform Avida is a rapid and highly manageable, yet freely evolving, artificial life system. Since digital experimental evolution is amenable to phylogenetic inference and able to incorporate complex biologically relevant processes, it is an attractive alternative for the evaluation of phylogenetic accuracy.

Using Avida, we examined the effects of natural selection, recombination, and the extent of lineage evolution on phylogenetic accuracy. While varying the strength of each factor, known evolutionary histories were evolved through replicate rounds of experimental evolution. Through periodic cladogenesis, an ancestral population evolved a history of a rooted, symmetrical eight-taxon tree topology, comparable to those from a landmark study of experimental phylogenetics using T7 bacteriophage. Under experimental conditions where evolution proceeded by random genetic drift alone or in the presence of either natural selection, recombination, or differing branch lengths, both maximum likelihood- and Bayesian inference-based methods exhibited high accuracy. Experimental evolution with a combination of these factors reduced clade accuracy due to complex among-factor interactions. In such cases, analyses of the entire set of 135,135 tree topologies demonstrated that the ‘best’ tree identified was indeed the most likely or most probable evolutionary history, though was often rather distant from the true tree in “tree space.” We highlight several such instances in order to identify the mechanisms behind phylogenetic error in these experiments. This work demonstrates the potential value of experimental phylogenetics using digital evolution as being a powerful tool for the evaluation of phylogenetic accuracy.

Capturing single-copy nuclear genes and its applications in phylogenetics

Chenhong Li, Zhizhi Liu, Dong Liu

3D_301A-Phylogenetic Methods
Monday, June 23, 2014 3:45 PM-4:00 PM

Single-copy nuclear genes often have slower rate in their coding region than non-coding gene markers. They are easy to be aligned and often were studied with well-characterized molecular evolution models. Thus, single-copy nuclear genes are naturally good markers for phylogenetics. We have developed a cross-species hybridization method to enrich target genes and applied next-gen sequencing on the enriched library to collect sequences of thousands of genes and hundreds of species. Here we present results from our phylogenetic studies on fishes, snakes and other vertebrates using this method.

PASTA: A new method to co-estimate alignments and trees (even on ultra-large datasets) with high accuracy and speed

Siavash Mirarab, Nam-phuong Nguyen, Tandy Warnow

3D_301A-Phylogenetic Methods
Monday, June 23, 2014 4:00 PM-4:15 PM

Multiple sequence alignment (MSA) is a basic step in many bioinformatics analyses, including predicting the structure and function of RNAs and proteins and estimating phylogenies. SATe (Liu et al., Science 2009 and Systematic Biology 2012) provided a fast and highly accurate method to co-estimate alignments and trees, and has been used to analyze many biological datasets. Yet, even SATe is unable to analyze extremely large datasets with more than 50,000 sequences, whereas phylogenetic analyses of sequence datasets containing more than 100,000 nucleotide sequences are being attempted by at least two groups that we are aware of: the iPTOL project and the Thousand Transcriptome project (1KP).

We present PASTA, “Practical Alignments using SATe and TrAnsitivity”, a new method to co-estimate alignments and trees for nucleotide or amino-acid sequences. The key to the accuracy and scalability of PASTA is the novel technique it uses for estimating an alignment on a guide tree. As in SATe, PASTA uses the centroid edge dataset decomposition technique and computes MAFFT-linsi alignments on the subsets; however, PASTA and SATe merge these subset alignments into an alignment on the full dataset using very different techniques. While SATe uses Opal to hierarchically merge all the subset alignments into a single alignment, PASTA uses Opal only to merge pairs of adjacent subset alignments, producing overlapping alignments, then treats each resultant alignment as an equivalence relation and uses transitivity to merge these larger alignments. The result is a very fast re-alignment method that is highly parallelizable and easily scales to large datasets.

PASTA is dramatically faster than SATe on large datasets, and produces much more accurate alignments and trees than SATe. We demonstrate PASTA's speed and accuracy on a collection of datasets, including large protein datasets, RNA datasets, and a simulated 200K-sequence RNASim dataset. All these analyses – including the 200,000 sequence dataset, complete in less than 24 hours using PASTA on a 12-core machine.

PASTA is available in open source form, uses the same GUI as SATe, and can be obtained from

http://www.cs.utexas.edu/users/phylo/software/pasta/index.html

---

A phylogenetic model for measuring departures from the mutation-selection balance

Nicolas Rodrigue, *Nicolas Lartillot*

3D_301A-Phylogenetic Methods
Monday, June 23, 2014 4:15 PM-4:30 PM

Codon substitution models have traditionally been used to measure selective pressures in protein-coding genes by evaluating the ratio of rates of nonsynonymous to synonymous substitutions. Recently, we have proposed a mutation-selection framework in which site-specific purifying selection at the amino acid level is explicitly modeled. Loosely speaking, under this model, substitutions at a given position occur at the neutral or near-neutral rate when they are either synonymous, or when they correspond to replacements within a sub-set of suitable amino acids---substitutions to ill-suited amino acids have much lower rates. As an alternative to traditional methods, we explore the idea of using our recent model as the null against which to test for deviations from the neutral/nearly-neutral regime. We present applications of this approach on a few data set of protein-coding genes, and discuss how the null model can be extended so as to test for different reasons for measured deviations, such selection on codon usage.

Convergent evolution and photosynthetic diversity in the grass tribe Paniceae

Jacob Washburn, *James Schnable, Gavin Conant, J. Chris Pires*

3D_301B-Phylogenies and Phenotypic Diversification
Monday, June 23, 2014 3:15 PM-3:30 PM

Most plants convert sunlight into chemical energy using C3 photosynthesis. However, a modified pathway, C4 photosynthesis, allows some plants to be more drought tolerant and fertilizer-use efficient. Strikingly, C4 photosynthesis has evolved independently in dozens of different plant lineages, a testament to its diversity and advantages in many common terrestrial environments.

Currently, massive international efforts are focused on breeding and bioengineering C4 photosynthesis into C3 rice and other food and sustainable energy crops. What these efforts often overlook is that there is no "one" C4 photosynthesis. In fact, with its 60-plus distinct evolutionary origins, 20-plus anatomies, and 3 basic enzymatic sub-types, C4 is more of a diverse syndrome than it is one generalized photosynthesis type. Because the various C4 sub-types have evolved in diverse environments, different sub-types may be more efficient for different agricultural applications.

Our study uses the grass tribe Paniceae to investigate the evolution and diversity of C4 photosynthesis within a phylogenomic context. The Paniceae are ideal for this investigation because they are the only plant lineage with representatives that primarily utilize each of the C4 enzymatic subtypes. This allows us to answer questions such as: How are different types of C4 photosynthesis related to each other? Which C3 and C4 species are ideal model organisms for studying C4 evolution in the Paniceae? Which tribe Paniceae species are best suited for development as sustainable energy, food, health, and forage crops?

Sex determination and the birth and death of species.

Nicole Valenzuela, *Itay Mayrose, Niv Sabath, Shai Meiri*

3D_301B-Phylogenies and Phenotypic Diversification
Monday, June 23, 2014 3:30 PM-3:45 PM

What promotes speciation and extinction? This question remains an unsolved evolutionary mystery. Sex determination is expected to influence species diversification because it influences sex ratio, population growth, post-zygotic isolation, and consequently, the origination and demise of species. Yet, the impact of the evolution of sex determination on diversification in clades such as reptiles remains obscure. Using phylogenetic likelihood methods of trait evolution we find evidence that sex determination (whether genotypic – GSD, or temperature-dependent – TSD) affects diversification patterns by modifying speciation rates, but it does so in opposite directions in turtles and squamates. Geo-climatic niche evolution appears to mediate the observed differences. We propose that the contrasting longevity between turtles and squamates might explain the reverse patterns between groups. Our approach includes a novel test of the effect that including taxa with unknown states has on the uncertainty of the analyses.

Evolution of sexual dimorphism within puppet beetles

Traci Grzymala

3D_301B-Phylogenies and Phenotypic Diversification
Monday, June 23, 2014 3:45 PM-4:00 PM

The puppet beetles (Coleoptera: Aderidae) represent one of the taxonomically and systematically poorest known beetle families. There has never been a phylogenetic tree published for the group. These beetles exhibit secondary sexual dimorphism in the form of elaborate male antennae or the presence of large setal patches on the hind legs. The first molecular phylogeny for the Aderidae is presented based on nuclear and mitochondrial sequence data. Sexually dimorphic morphological characters are mapped onto this phylogeny and ancestral state character reconstructions are performed to examine their evolutionary history.

Testing Darwin's hypothesis on the evolution of ornamental eyespots in peafowl and their relatives

Rebecca Kimball, Keping Sun, Kelly Meiklejohn, Edward Braun, Brant Faircloth, Travis Glenn

3D_301B-Phylogenies and Phenotypic Diversification
Monday, June 23, 2014 4:00 PM-4:15 PM

The most striking feature of peafowl (Pavo) is the males' elaborate train, which exhibits ocelli (ornamental eyespots) that are under sexual selection. Two additional genera within the Phasianidae (Polyplectron and Argusianus) exhibit ocelli, but the appearance and location of these ornamental eyespots exhibits substantial variation among these genera, raising the question of whether ocelli are homologous. Within Polyplectron, ocelli are ancestral, suggesting ocelli may have evolved even earlier, prior to the divergence among genera. However, it remains unclear whether Pavo, Polyplectron, and Argusianus form a monophyletic clade in which ocelli evolved once. We estimated the phylogeny of the ocellated species using sequences from 1966 ultraconserved elements (UCEs) and three mitochondrial regions. The three ocellated genera did form a strongly supported clade, but each ocellated genus was sister to at least one genus without ocelli. Indeed, Polyplectron and Galloperdix, a genus not previously suggested to be related to any ocellated taxon, were sister genera. The close relationship between taxa with and without ocelli suggests multiple gains or losses. Independent gains, possibly reflecting a pre-existing bias for eye-like structures among females and/or the existence of a simple mutational pathway for the origin of ocelli, appears to be the most likely explanation.

Nutrition as a constraint on neural evolution: a comparative study across butterflies

Emilie Snell-Rood, Anne Espeset, Eli Swanson, Sarah Jaumann, Rhea Smykalski

3D_301B-Phylogenies and Phenotypic Diversification
Monday, June 23, 2014 4:15 PM-4:30 PM

The availability of energy and nutrients has been hypothesized to be an important factor in limiting the evolution of large brains. However, organisms readily adapt to low nutrient environments, calling into question whether diet can be a strong evolutionary constraint. Butterflies offer an attractive system to tackle this question because larval nutrition is relatively consistent within species, highly variable across species, and phylogenetic approaches can be used to estimate how long a species has been consuming their current diet. Here we present data from several butterfly families testing how nitrogen and sodium availability shape neural investment (relative eye size, total brain size and the size of neuron-dense brain regions). Nitrogen availability appears to be particularly important in the evolution of neural investment, even across species that have been feeding on their current diet for over 50 million years. Sodium availability and the timing of a diet shift are important correlates of neural investment within some lineages. We also use this data set to test for brain-life history tradeoffs across species. Overall, these results provide support for the idea that nutrition can constrain the evolution of large, costly brains.

Evidence for multiple barriers to reproduction between edaphic specialist populations of an Amazonian Tree: Protium subserratum (Burseraceae)

Tracy Misiewicz, Paul Fine

3D_302A-Speciation
Monday, June 23, 2014 3:15 PM-3:30 PM

Disentangling the strength and importance of barriers to reproduction that arise between diverging lineages is central to our understanding of diversification. To date, only a handful of studies have comprehensively quantified the strength of individual reproductive isolating mechanisms among closely related plant species. Even fewer studies have focused on tropical plants and those have focused on herbaceous lineages. In this study we examine multiple barriers to reproduction between diverging lineages of soil specialist ecotypes of Protium subserratum (Burseraceae), an Amazonian tropical tree. Specifically we aimed to (1) Quantify the contributions of pre-zygotic and post-zygotic barriers to isolation including ecogeographic isolation, flowering phenology, pollinator assemblage, pollen adhesion, pollen germination, pollen tube growth, fertilization/initial seed development and hybrid fitness and (2) Calculate the total amount of reproductive isolation as well as the relative contribution of each barrier to total reproductive isolation. We were able to identify four active barriers to reproduction including ecogeographic isolation, differential pollen adhesion, differences in pollinator assemblages, and low levels of hybrid seed development. We demonstrate that a combination of pre-zygotic and post-zygotic barriers to reproduction act to maintain near complete reproductive isolation between edaphically divergent populations of P. subserratum.

Do color-assortative female preferences generate reproductive isolation in a polymorphic frog?

Cori Richards-Zawacki, Matthew Dugas, Julia Berkey, Stephanie Strickler

3D_302A-Speciation
Monday, June 23, 2014 3:30 PM-3:45 PM

The extent to which sexual selection contributes to the generation of reproductive isolation among incipient species remains a question of theoretical and empirical interest in evolutionary biology. Studies of recently or nearly isolated lineages, where the action of current barriers can be directly observed, arguably provide the best test of sexual selection's role in reproductive isolation. The striking diversity in coloration exhibited by the poison frog Oophaga pumilio in and around the Bocas del Toro Archipelago of Panama is thought to have arisen recently and rapidly, suggesting the action of strong selection. Previous work has detected color-assortative female preferences in a number of populations suggesting the potential for behavioral isolation among morphs. However, a number of factors may influence the extent to which divergent preferences, which are often measured under controlled laboratory conditions, are expressed in the form of a pattern of assortative mating in nature. We asked, for O. pumilio populations where coloration is polymorphic, whether assortative female preferences lead to a pattern of assortative mating and behavioral reproductive isolation. Our results provide new insights into the role of sexual selection in generating reproductive isolation in this system and highlight the need for a clearer understanding of the conditions under which divergent mate preferences can be expected to translate to behavioral isolation in nature.

A role for male behavior in trait divergence and behavioral isolation in darters

Michael Martin, Tamra Mendelson

3D_302A-Speciation
Monday, June 23, 2014 3:45 PM-4:00 PM

Some of the most striking examples of biodiversity occur in groups with elaborate sexual signals and displays. Divergence in male sexual signals between allopatric populations is often considered a result of changing female preferences, driven by genetic drift or environmental differences. By comparison, male competitive interactions and preferences receive little attention as potential drivers of speciation among allopatric populations. By simulating secondary contact in the lab, we show that male competitive responses and color displays have coevolved in allopatric species of freshwater fish; as male color differences between species increase, interspecific aggression decreases. Male signal divergence also precedes divergence in competitive responses, a pattern consistent with mutation-order speciation. Measures of behavioral isolation do not correlate with color divergence but do correlate with male courting biases. These results highlight an important role for male competition and choice in trait divergence and the evolution of behavioral isolation in a diverse genus of fishes.

The identification and characterization of a behavioral isolation gene.

Amanda Moehring

3D_302A-Speciation
Monday, June 23, 2014 4:00 PM-4:15 PM

Behavioral divergence is thought to be among the earliest reproductive isolation barriers to develop during speciation. While genetic mapping has elucidated the genetic architecture underlying behavioral isolation, no individual genes have been identified, limiting our understanding of the underlying mechanisms that enable species to develop and remain discontinuous from one another. Here, I present the identification and characterization of a gene influencing species-specific female preference behavior between two species of Drosophila.

Speciation genomics and a role for the sex chromosome in the mallard and Mexican duck

Philip Lavretsky, Jeffrey DaCosta, Blanca Hernández-Baños, Andrew Engilis, Michael Sorenson, Jeffrey Peters

3D_302A-Speciation
Monday, June 23, 2014 4:15 PM-4:30 PM

Speciation is a continuous and dynamic process. Early in speciation, the genomes of incipient taxa are manipulated by evolutionary forces, and identifying their heterogeneous composition can reveal potentially important processes influencing species composition. We conducted genomic scans across the mitochondrial DNA (mtDNA) control region, 3563 autosomal loci, and 172 Z-chromosome loci in the mallard (Anas platyrhynchos; N = 17 individuals) and Mexican duck (A. [p.] diazi; N = 105 individuals from six Mexican and two US states) to disentangle their incipient evolutionary relationship. Between mallards and Mexican ducks, we found discordance in divergence estimates among autosomal (mean ΦST = 0.018), sex-linked (mean ΦST = 0.086), and mtDNA (ΦST = 0.14) markers, and five Z loci and one autosomal locus were more divergent than expected given background levels of divergence. In contrast, divergence in autosomal (mean ΦST = 0.012) and Z-linked markers (mean ΦST = 0.018) were tightly correlated within Mexican ducks, and divergence at only two autosomal loci strongly deviated from background levels. We conclude that speciation between mallards and Mexican ducks is likely proceeding via selection on a few sex-linked markers with large effects, whereas divergence at the remaining genome is the result of genetic drift. These results suggest post-zygotic isolating mechanisms. In contrast, divergence among Mexican duck populations is consistent with isolation-by-distance and large role for genetic drift. These results demonstrate that a large number of loci are necessary to better understand the speciation process between recently diverged taxa and provides a compelling example of the differential roles of selection and genetic drift across genomic regions.

Did the serpentine sunflower originate on serpentine soil? A population genomics analysis of Helianthus bolanderi

Gregory Owens, Loren H. Rieseberg

3D_302B-Microevolution
Monday, June 23, 2014 3:15 PM-3:15 PM

Serpentine soil is a challenging environment for plants due to its high levels of heavy metals and skewed Ca/Mg ratio. While many plants found on serpentine soil are restricted to serpentine, others are found on both serpentine and non-serpentine soil. Reciprocal transplant experiments have shown that these species are often locally adapted to their home soil environment. This would suggest that gene flow between soil types and the founding of cross-soil populations should be difficult. Thus, the relationships between populations inhabiting different soil provides insight into how local adaptation proceeds.

One species found on serpentine and non-serpentine soil is the serpentine sunflower, Helianthus bolanderi. We sampled populations across it's entire native range in northern California and genotyped them using Genotyping-By-Sequencing (GBS). Population structure analysis identified two groups corresponding to the east and west populations. Non-serpentine populations occur in both groupings, suggesting multiple transitions between soil types. We used the directionality index, psi, to triangulate the origin of the species on a serpentine patch in the coast mountain range. Lastly, we estimated gene flow between soil types and found little evidence for reduced migration between soils. Taken together, this suggests H. bolanderi originated on serpentine and transitioned onto normal soil with relative ease.

Clinal variation in floral color and flavonoids along alpine elevation gradients in Silene vulgaris

Andrea Berardi, Douglas Taylor

3D_302B-Microevolution
Monday, June 23, 2014 3:15 PM-3:15 PM

Spatial environmental heterogeneity can lead to divergent selection in populations, often leading to phenotypic divergence and local adaptation. The plant flavonoid biosynthetic pathway has been well characterized and is conserved among angiosperms, and the pathway structure allows us to make predictions about phenotypic divergence, which may co-vary across environmental gradients. We monitored populations of the widespread bladder campion, Silene vulgaris (Caryophyllaceae), spanning 700-2100 m in the French Alps for two years, measuring traits associated with the flavonoid pathway: floral color, floral and foliar flavonoids, and herbivory. We predicted that with increasing elevation, more non-anthocyanin flavonoids would be produced as a response to increased UV radiation, and that anthocyanins would accumulate to ameliorate stress associated with high elevation environments. We found evidence for adaptive divergence of floral color across elevational transects, where pairwise PST > FST. Anthocyanin-based floral color increased with elevation, as did flavonoids in leaves. However, there were no associations between the increase in flavonoid production with herbivory. Our results indicate that floral color and leaf flavonoid production are linked by means of shared upstream enzymes, and that selection likely acted on the flavonoid pathway, reinforcing the relationship.

Evolution as a work in progress: potential incipient adaptive change in a cave-dwelling salamander

Hilary Edgington, Colleen Ingram, Douglas Taylor

3D_302B-Microevolution
Monday, June 23, 2014 3:15 PM-3:15 PM

Studies of adaptive evolution generally strive for an understanding of the mechanisms behind an observed response to selection. However, by changing the focus to a system in which expected morphological change is not apparent we can potentially get a real-time perspective on the parameters that promote and constrain adaptation. Using phylogeographic and population genetic methods, we infer the history of Eurycea lucifuga, a cave-dwelling salamander that exhibits none of the suite of cave-associated traits that have evolved convergently in most cave-restricted taxa. We find that expansion into caves was most likely very recent, suggesting that the expected response to the strong selective pressures imposed by the cave environment may be incipient. This characterizes E. lucifuga as an important system in which to study adaptive evolution as it occurs in a natural population.

Rapid Divergence and Convergence of Functional Characters in Experimentally Evolved Populations of Drosophila

James Kezos, Thomas Barter, Larry Cabral, Grant Rutledge, Mark Phillips, Kevin Phung

3D_302B-Microevolution
Monday, June 23, 2014 3:15 PM-3:15 PM

We have examined a wide range of functional characters in 30 outbred Drosophila melanogaster populations all of which descend from one common ancestral population. These populations have well-known phylogenetic relationships and selection histories over the course of more than 30 years of sustained and replicated parallel selection. We have phenotypically compared these populations for the following functional characters: age-specific adult mortality rates, age-specific female fecundities, developmental timing, larval viability, starvation resistance, desiccation resistance, flight endurance, and cardiac performance. The 30 populations in this study include long-established populations (ACO1-5 , B1-5 , and CO1-5) and newly-established populations with corresponding recent selection regimes (AO1-5 , BO1-5 , and NCO1-5). The 15 ACO, B, and CO populations have been undergoing A, B, and C-type selection for 737, 837, and 290 generations, respectively. The 15 AO, BO, and NCO populations have been undergoing A, B, and C-type selection for only 146, 120, and 36 generations, respectively. These populations were used to determine (1) if phenotypic convergence has occurred between the long-established and newly-established populations recently sharing the same selection regime, and (2) whether the level of phenotypic divergence between the newly-established populations is equivalent to the level of divergence between the long-established populations despite the fewer number of generations of divergent selection. For most of the functional traits assayed, there was extensive convergence between parallel-selected populations, whether the selection regime was long-sustained or relatively recent. There was also rapid divergence among the populations newly subjected to the three different selection regimes. All told, these findings suggest that experimental evolution in outbreeding Mendelian populations can proceed with great rapidity.

Understanding Adaptation to Deserts in a Novel Model Organism, Peromyscus eremicus

Matthew MacManes

3D_302B-Microevolution
Monday, June 23, 2014 3:15 PM-3:15 PM

The maintenance of water balance in animals is one of the most important physiologic processes, and is critical to desert survival. Indeed, mammals are exquisitely sensitive to changes in osmolality, with slight derangement eliciting physiologic compromise. When the loss of water exceeds dietary intake, dehydration - and in extreme cases, death - can occur. Unlike most mammals, animals living in desert habitats are subjected to long periods of extreme heat and intense drought. As a result, desert animals have evolved mechanisms through which physiologic homeostasis is maintained despite severe and prolonged dehydration. This presentation will describe research that integrates physiology, evolutionary genomics, and computational biology to better understand how the cactus mouse (Peromyscus eremicus) survives in what appear to be unsurvivable conditions. Specifically, I will describe the newly assembled draft genome and results of an ongoing RNASeq experiment. These results will be presented in the context of studies of electrolyte balance collected using captive animals held in a specially designed desert chamber.

Exploring diversification rates in the monocot family Araceae at different taxonomical scales

Alejandro Zuluaga-Trochez, Kenneth Cameron

3D_302C-Diversification
Monday, June 23, 2014 3:15 PM-3:30 PM

Araceae is one of the most diverse monocot families with about 3500 described species. It is particularly abundant in the tropics, and exhibits remarkable morphological, anatomical, ecological, and geographical variation. Despite several recent phylogenetic studies, we still know rather little about the dynamics of lineage and species diversification across the family, or about the underlying drivers of diversification. We used a fossil calibrated Bayesian relaxed molecular clock phylogeny from a previous analysis (134 taxa), a new ‘supermatrix’ approach (with about 700 taxa), and a more complete dataset (ca. 100 taxa) for the species-rich subfamily Monsteroideae to explore these issues. First, we combined results from BiSSE birth–death models of diversification, MEDUSA, and a new Bayesian approach (BAMM), to evaluate the evolutionary patterns of species diversification in the family as a whole and for Monsteroideae. Preliminary analyses revealed dissimilar clade-specific processes that allow for species diversification in the family. We reviewed the abundant literature about morphological and ecological traits in Araceae, and offer possible explanations for shifts in diversification traits in terms of extrinsic factors or intrinsic trait evolution. We studied in more detail, rates associated with transitions to and from water-associated life forms, to more extreme aquatics, to strictly rheophytes, or toward dry-land geophytes and epiphytes of various kinds. Second, using literature, herbarium specimens, and field observations, we compiled a morpho-anatomical dataset for the subfamily Monsteroideae comprising 10 vegetative and ca. 25 floral characters. We studied the evolution of these traits using ancestral state reconstruction, and hypothesize their influence on at least two significant shifts in rates of diversification. We demonstrate that better sampled phylogenies that cover broad taxonomy and geographic ranges, and that are inferred from many genes, are promising for more accurate and precise modeling of rate shifts across aroids. In addition, assembly of equally densely sampled morphological, geographical and ecological datasets will be needed to properly test associations between these factors and clades showing different rates of species diversification.

The “dry diagonal” of South America as a driver of ecological diversification in turtle ants

Shauna Price, Scott Powell

3D_302C-Diversification
Monday, June 23, 2014 3:30 PM-3:45 PM

The South American “dry diagonal” is a distinct biogeographic region that has been implicated as an important driver of ecological diversification. Also known as the Chacoan region, the dry diagonal is comprised of the Cerrado, Caatinga and Chaco biomes that together create a continuous expanse of open and seasonally dry vegetation extending from northeastern Brazil to northern Argentina. The Chacoan region is known to have high levels of biodiversity and endemism, yet it has rarely been the focus of work addressing diversification dynamics in the Neotropics, especially compared to work that focuses on the adjacent Amazon region. Nevertheless, recent work on the turtle ants (Cephalotes), a species-rich genus of arboreal ants, has suggested that ecological opportunity in the Chacoan region has been important in driving the diversification dynamics of the lineage. More specifically, rates of diversification in the turtle ants have been shown to slow overall, while one subclade associated with the Chacoan region exhibits a recent, rapid burst of diversification. Moreover, species found in the region have been shown to be phylogenetically clustered and to have a higher rate of speciation than outside the region. Here, we use recently developed methods to further explore how ecological opportunity, represented by the relatively young vegetation of the Chacoan region, has shaped diversification dynamics in the turtle ant lineage. Our analyses include the use of a total evidence divergence time estimation analysis and methods for detecting patterns of diversity dependence that take missing species into account. We particularly focus on comparing the overall diversification dynamics of the lineage with those of the Chacoan subclade previously identified, and a second candidate subclade of Chacoan diversification. Our analyses reveal a signature of overall diversification consistent with diversity dependence (an early burst and then a decline in rates of diversification towards the present), but with an important role of the Chacoan biogeographic region in influencing recent radiations in a turtle ant subclades. Overall, our analyses highlight the important role of the understudied Chacoan region in Neotropical diversification, and how the region may represent a significant, recent ecological opportunity for some Neotropical lineages.

Physiological divergence as a driver of the Anolis adaptive radiation

Alex Gunderson

3D_302C-Diversification
Monday, June 23, 2014 3:45 PM-4:00 PM

Two important questions in the study of adaptive radiation are 1) how does selection shape phenotypes along important axes of ecological divergence? 2) how does this divergence facilitate species coexistence? West Indian Anolis lizards have served as an important model system to address these questions, driven by analyses of morphological specialization. However, morphological specialization cannot fully explain the Greater Antillean Anolis radiation because most cladogenic events have occurred within ecomorphological types. Here, I focus on physiological divergence among anoles, asking how thermal physiology evolves across two Greater Antillean islands: Puerto Rico and Jamaica. I find that both optimal temperatures for physiological performance and upper thermal tolerance limits evolve in response to divergent thermal regimes. Furthermore, I demonstrate that these divergence events have significant adaptive performance consequences under ecologically relevant thermal conditions. Finally, I demonstrate that these divergence events likely facilitate high community-level species diversity: across both Puerto Rico and Jamaica, if two morphologically similar species co-occur, they invariably differ in thermal physiology. These results demonstrate how physiological divergence can play an important, and often underappreciated, role in evolutionary radiations.

Does Energy Availability Predict Gastropod Reproductive Strategies?

Craig McClain

3D_302C-Diversification
Monday, June 23, 2014 4:00 PM-4:15 PM

The diversity of reproductive strategies in nature is shaped by a plethora of factors including energy availability. For example, because low temperatures and limited food availability could increase larval exposure to predation by slowing development, these habitats may select against pelagic larvae. In addition, the frequency of hermaphroditism could increase under low food availability as population density (and hence mate availability) drops. We test these hypotheses by exploring the relationships between reproductive/life-history traits and energy availability for 189 marine gastropod families. Only larval type was related to energy availability with the odds of having planktotrophic larvae versus direct development decreasing by 1% with every one-unit increase in the square root of carbon flux. Simultaneous hermaphroditism also potentially increases with carbon flux, but this effect disappears when accounting for evolutionary relationships among taxa. Our findings do not support current hypotheses on the nature of reproductive strategies and energy availability. Instead, they suggest that some reproductive strategies are too energetically expensive at low food availabilities and others serve to capitalize on opportunities for aggregation or increased energy availability.

Ecological opportunity is not sufficient to explain the origins of adaptive radiation in Caribbean pupfishes

Christopher Martin

3D_302C-Diversification
Monday, June 23, 2014 4:15 PM-4:30 PM

Adaptive radiation is thought to result from ecological opportunity: an abundance of under-utilized resources following colonization of a new habitat, mass extinction, or key innovation. However, it is unclear whether this ecological factor alone is sufficient to explain adaptive radiation: for nearly every example, similar taxa have failed to diversify in the exact same environment. Here I examine whether ecological and demographic factors are sufficient to explain two remarkably localized examples of adaptive radiation in Caribbean pupfishes. In situ diversification has occurred in only two isolated lake systems across the entire Caribbean. These young radiations share major features with classic examples: 1) morphological diversification rates up to 130 times faster than background, 2) trophic innovations such as scale-eating in micro-endemic specialist species, and 3) field experiments measuring the growth and survival of F2 hybrids confirm that multiple fitness peaks on the adaptive landscape drive diversification. However, a survey of similar lake environments on neighboring islands without specialists suggests that ecological opportunity is not the full story. These lakes are similar in area, geochemistry, flora, and fauna with identical depauperate fish communities. Furthermore, generalist pupfish populations in these lakes exhibit similar genetic diversity, morphological diversity, dietary isotopic diversity, and stomach content diversity relative to generalist populations in lakes supporting specialists. Despite extreme outlying diversification rates in these two localized adaptive radiations that do not form a continuum with rates in other clades, there are no smoking-gun ecological differences among these environments. This suggests the presence of empty fitness peaks on neighboring islands and additional intrinsic constraints on the origins of adaptive radiation.

Speciation and hybridization in Jamaican Streamertail Hummingbirds

Caroline Judy, Robb Brumfield, Gary Graves

3D_303-Hybridization
Monday, June 23, 2014 3:15 PM-3:30 PM

Trochilus polytmus and Trochilus scitulus are known to hybridize, but the hybrid zone has stayed shockingly narrow through time. The origin and maintenance of such a narrow hybrid zone linking species with high dispersal capabilities on a small oceanic island defies traditional explanations. The standard toolbox of techniques and genetic markers used to study hybrid zones has failed to reveal fixed differences that are generally needed to reconstruct speciation scenarios. We use genotyping-by-sequencing to gather a genomic single nucleotide polymorphism (SNP) dataset for both parental types and putative hybrids. We use these data to examine patterns of genomic differentiation and introgression and look for signatures of selection. We discuss the implications of these results for Trochilus, and also discuss ways these genomic data can be used in conjunction with other datasets for hybrid zone studies.

Genomic consequences of introgressive hybridization in Darwin's Finches adaptive radiation

Jaime Chaves, Andrew Hendry, Elizabeth Cooper, Jeffrey Podos, Al Uy

3D_303-Hybridization
Monday, June 23, 2014 3:30 PM-3:45 PM

Hybridizing species complexes provide one of the richest natural experiments in evolutionary biology. Interspecific hybridization can break up co-adapted genes, disrupt local adaptation and produce genomic extinction. But it could also be viewed as a creative force behind species formation, particularly at differing levels of gene flow in a so-called "mosaic of speciation". Here we explore the genomic consequences of introgressive hybridization in a hybridizing complex of closely related Darwin ground Finches. We identified more than 41,000 SNPs across the three sympatric species of ground finches (Geospiza fuliginosa, G. fortis, G. magnirostris), including the two distinct fortis morphs. We found that despite high levels of gene flow across all species, we could detect ~600 species-specific SNPs associated to "conventional" morphological categories, but no association was found when these SNPs where chosen randomly. These findings suggest genetic permeability across "porous" species boundaries where neutral loci can move freely but putative naturally selected loci get trapped. We suggest the importance of species bridges in creating and maintaining species identities and stress the important role of introgressive hybridization behind the radiation of Darwin's Finches.

Population genomics of two ecologically disparate Fundulus hybrid zones.

Jacob Schaefer, David Duvernell

3D_303-Hybridization
Monday, June 23, 2014 3:45 PM-4:00 PM

An earlier survey of ten replicate topminnow (Fundulus olivaceus and F. notatus) hybrid zones revealed that the species were typically distributed in an upstream-downstream manner with contact zones localized at confluences featuring abrupt shifts from tributary to river habitat. The rate of hybridization among drainages ranged from no hybrids in two drainages to near random mating in others. The best predictor of hybridization rate was the homogeneity of habitat through tributary-river confluences (ratio of river to tributary size). Phenotype differences between the species reflect predicted selection differences along stream gradients. Downstream populations (lower food availability and greater predator pressure) generally showed larger investment in reproduction (higher gonadal somatic index), smaller body size and lower somatic condition compared to upstream populations. In two drainages, the species typical up and downstream positions were reversed. Phenotypic differences between the species in the two reversed drainages were consistent with convergence of life history traits in the respective habitats. We sampled the middle of two ecologically disparate hybrid zones (one typical and one reversed) and used genotyping-by-sequencing to generate genome wide SNP libraries. We ask whether there is a greater rate of hybridization or directional introgression in converging populations from the "reversed" hybrid zone.

Consistent genomic signatures of reproductive isolation in a hybrid zone responding to climate change

Scott Taylor, Robert Curry, Thomas White, Valentina Ferretti, Irby Lovette

3D_303-Hybridization
Monday, June 23, 2014 4:00 PM-4:15 PM

Studies of hybrid zone dynamics often investigate a single sampling period and draw conclusions from that temporal snapshot, but stochasticity can result in loci with patterns that differ from neutral expectations. Comparing admixed populations from different geographic regions is one way to detect consistently divergent regions potentially involved in reproductive isolation. Temporal comparisons address the same problem, but have not been investigated. In North America, black-capped (Poecile atricapillus) and Carolina (P. carolinensis) chickadees hybridize in a contact zone extending from New Jersey to Kansas. The hybrid zone is likely maintained by strong intrinsic selection against hybrids, and it is moving north in response to climate change. We used a reduced representation genomic approach and temporally spaced sampling—two samples of ~80 individuals separated by a decade—to determine the pattern and consistency of selection and introgression in the chickadee hybrid zone. We report consistently low introgression for highly divergent loci between P. atricapillus and P. carolinensis in this moving hybrid zone. This is strong evidence that these loci are linked to genomic regions involved in reproductive isolation between chickadees. This spatiotemporal genomic analysis highlights the benefits of examining hybrid zones at multiple time points, and in different geographic contexts, when investigating reproductive isolation between closely related species.

Inferring differential introgression among Southern African White eyes

Guinevere Wogan, Ke Bi, Graeme Oatley, Gary Voelker, Rauri Bowie

3D_303-Hybridization
Monday, June 23, 2014 4:15 PM-4:30 PM

The Southern African White eyes. White eyes (Zosterops) have earned the moniker the "great speciators" by exhibiting the highest rate of diversification estimated among vertebrates. The rapid speciation among the birds of this group, and the extremely wide geographic distribution (Old World tropics) makes them an interesting group within which to examine speciation and hybrid zone dynamics. Previous work shows that the Southern African White eyes (Z. capensis, Z. pallidus, Z. senegalensis, and Z. virens) have diversified within the 1million years, with the most recent species split occurring within the past 300 thousand years. Each species is distinguishable based on plumage and song and each is endemic to its own biome/habitat type. Where the biomes meet hybrid zones form indicating a complex pattern of diversification seemingly related to environmental heterogeneity. However, differentiating between hybridization and introgression versus ancestral polymorphism and incomplete lineage sorting in this system is a challenge given its recent diversification, and to do so requires large numbers of independent markers. Using several thousand orthologous genome-wide SNPs we first compare a new informatics pipeline with existing pipelines to evaluate how upstream informatics decisions affect downstream biological inference. We then use these data to estimate a species tree, evaluate population structure and differentiation, assess introgression across lineages using statistical approaches, and look at associations between genetic and spatial structure. We recover strong signals of population differentiation accompanied by signals of introgression among lineages, however we find that informatics decisions made during the early stages of filtering, merging, alignment, and SNP calling of RAD data can have strong effects on downstream inference, such that different and often conflicting biological signals emerge.

Variation and duplication of the DQB MHC class II gene in Gulf of California blue whale (Balaenoptera musculus) Population.

DIANA DANIELA MORENO SANTILLAN, Eileen Lacey, Diane Gendron, Jorge Ortega

3D_304-MHC Evolution
Monday, June 23, 2014 3:15 PM-3:30 PM

The Major Histocompatibility Complex (MHC) is a multigenic family that is central to the immune response in vertebrates. MHC genes are generally thought to be under strong balancing selection from pathogens, as a result they are often among the most polymorphic loci in vertebrates genomes. Among mammals, MHC variation is reportedly lower among cetaceans, leading to speculation that the marine environment imposes reduced pathogen pressure compared to terrestrial habitats. As a first step toward exploring this hypothesis, we characterized MHC variability in a population of blue whales (Balaenoptera musculus). Specifically we genotyped exon 2 of the MHC Class II DQB locus for 80 Pacific blue whales resident in the Gulf of California during winter and spring. Twenty-two putatively functional DQB variants were identified; all of these variants were homologous with cetacean DQB sequences and none contained insertions or deletions. Up to 5 DQB alleles per individual were identified, suggesting duplication of the DQB locus. When all variants were considered, 20 polymorphic sites were evident. Overall haplotype diversity in the study population was the highest reported among baleen whales (suborder Mysticety: h=0.867). Estimates of rates of non-synonymous to synonymous substitutions ($\omega=93$) and neutrality tests provided potential evidence of strong positive selection acting on the peptide binding region of this exon. Phylogenetic analyses of DQB allele sequences revealed the occurrence of trans-specific evolution within cetaceans although no alleles were shared between species. This suggests that selection on this locus has acted over an extended period of time. Collectively, these findings reveal that immunogenetic variation in marine mammals is not always limited, thereby providing potential evidence against the hypothesis that marine taxa face reduced pathogen challenges.

Key words: Balaenoptera musculus, DQB, gen duplication, Major Histocompatibility Complex, PBR, positive selection.

Major Histocompatibility Complex diversity helps lemurs live longer and survive natural disasters

Kathleen Grogan, Michelle Sauther, Frank Cuozzo, Christine Drea

3D_304-MHC Evolution
Monday, June 23, 2014 3:30 PM-3:45 PM

At the interface between genetic make-up and survival, genes of the Major Histocompatibility Complex (MHC) are partially responsible for initiating the body's immune response to pathogens. Therefore, an individual that is genetically diverse at its MHC genes is hypothesized to be capable of mounting an immune defense against a greater variety of infections than is an individual that has little MHC diversity. Because of the direct link between MHC and health, MHC diversity is thought to play a role in differential survival between individuals. We investigated the influence of MHC diversity on ring-tailed lemur (Lemur catta) survival in both a captive (Duke Lemur Center, NC: n=105) and wild (Beza Mahafaly Special Reserve, Madagascar: n=151) population. All of the lemurs were genotyped at the second exon of the MHC-DRB gene, using parallel-tagged sequencing on 454 Titanium and Ion Torrent PGM platforms. Survival data came either from Duke's long-term life history records or Beza's census data, which has been collected monthly since 2003. Under the relatively stable environmental conditions in captivity, ring-tailed lemurs suffer from inbreeding depression, as individuals with fewer MHC alleles are more likely to die at younger ages (X2=4, p

---

MHC polymorphism and divergence in wild and domesticated zebra finches

Daniel Newhouse, Christopher Balakrishnan

3D_304-MHC Evolution
Monday, June 23, 2014 3:45 PM-4:00 PM

The zebra finch (Taeniopygia guttata) is a passerine bird comprising two subspecies native to Australia and the Lesser Sunda Islands, respectively. Domesticated populations in the United States have also been derived from the two subspecies. The Lesser Sundas zebra finch appears to have gone through a severe genetic bottleneck during the colonization of the islands from Australia. Previous studies of domesticated zebra finches also show divergence between wild and captive populations at neutral genetic loci. Comparisons utilizing functional loci, however, are lacking. Here, we characterize the polymorphism and divergence in the third exon of the highly variable major histocompatability complex (MHC) class I α chain, which encodes the α2 domain of the peptide binding region (PBR). Immune genes are thought to strongly rely on genetic variation to convey a greater resistance to pathogens. Genes of the MHC, a component of the vertebrate adaptive immune response involved in antigen presentation, have received considerable attention in immunogenetic studies due to their importance in the immune response. Despite historical bottlenecks in nature and during domestication, high MHC polymorphism persists in all zebra finch populations. We report higher levels of nucleotide diversity when compared with neutral loci and strong evidence of positive selection acting on important residues forming the PBR. Due to its importance in pathogen recognition, selection seems to have maintained variability of the MHC class I, even following population bottlenecks. Although there is high genetic diversity in all populations, we do find evidence of genetic differentiation between zebra finch subspecies and between wild and domesticated zebra finches, both potentially representing adaptation to novel environments.

Antagonistic effects on survival and reproduction maintain MHC variation in a natural population

David J Wright, Lewis G Spurgin, Hannah Dugdale, Jan Komdeur, Terry Burke, David Richardson

3D_304-MHC Evolution
Monday, June 23, 2014 4:00 PM-4:15 PM

Understanding the processes that generate and shape genetic variation among individuals is central to our understanding of evolution. Variation at Major Histocompatibility Complex (MHC) genes, which play a key role in the immune system of vertebrates, has been shown to influence susceptibility to pathogens and fitness. Consequently various mechanisms of balancing selection have been proposed to drive the extraordinary levels of polymorphism observed at these genes. However MHC variation has also been associated with many negative genetic disorders, especially in humans, thus leading to theories outlining the potential role of sheltered deleterious mutations in the evolution of the MHC. In the present study we used data and samples collected across 20 years to assess how MHC variation changes over time in a contained natural population of Seychelles warblers (Acrocephalus sechellensis) on Cousin Island, Seychelles. We have previously shown that in this species both fertilisation patterns and survival are positively influenced by higher levels of MHC variation. In addition, within a cohort of offspring a single MHC allele (Ase-ua4) was found to confer a substantial survival advantage throughout life. After massively extending the dataset we now find that the positive effect of Ase-ua4 on survival has been consistent in multiple cohorts across the 20 years. However, contrary to expectations, the frequency of this allele in the population overall did not increase over this period, but remained remarkably consistent at ca. 15%. Consequently we conclude that antagonistic effects must be restricting the reproductive success of individuals carrying the Ase-ua4 variant. I will outline how we have tested for such effects using the detailed life-history and reproductive success data we have for individuals and pairs within this population, and discuss how antagonistic effects on survival and reproduction can maintain MHC variation within a natural population.

Multi-tagged pyrosequencing reveals highly polymorphic MHC genes in the endangered San Joaquin kit fox

Tammy Wilbert, Masoumeh Sikaroodi, Brian Cypher, Christine Van Horn Job, Katherine Ralls, Jesus E. Maldonado

3D_304-MHC Evolution
Monday, June 23, 2014 4:15 PM-4:30 PM

The conservation of wild species and habitats is challenged by human population growth, urbanization, habitat fragmentation, and ever-increasing demands on natural resources. A metapopulation of approximately 3,000 endangered San Joaquin kit foxes (Vulpes macrotis mutica; SJKF) remains in a highly fragmented area in central California, with the third largest population residing in the city of Bakersfield. Disease is a particular conservation concern for the SJKF because scientists have documented cases of rabies, distemper (CDV) and parvovirus (CPV) in other natural populations of canids, and small population sizes make the SJKF vulnerable to extinction. In addition, carnivores that inhabit urban ecosystems have increased disease risks from interactions with domestic pets, raccoons, and skunks. One way that animals naturally resist disease is through the genes that support their immune system, and animals with the most diverse immune system genes are usually the healthiest. Major Histocompatiblity Complex (MHC) genes are crucial to an individual's ability to defend against disease, provide an important measure of functional genetic diversity, and have been implicated in mate choice and recognition of relatives. Therefore these genes may help foxes avoid inbreeding and resist disease, especially in urban environments. We used multi-tagged pyrosequencing to characterize genetic diversity of three MHC class II genes (DQA, DQB, and DRB) from a total of 96 individuals, half urban and half wild. Using rigorous bioinformatics methods to limit sequencing artifacts, we identified 11 DQA alleles, 13 DQB alleles, and 29 DRB alleles, which translated into 1, 6, and 25 unique antigen binding sites, respectively. The high polymorphism did not correlate with sequencing depth or sample location, but was present across individuals and indicated polygenic loci for DQB (2 gene copies) and DRB (3 copies). Using Tajima's D, we found support for negative selection in DQA (D=-1.71) and positive selection in DRB (D= 2.82). We did not find a significant difference in the number of alleles carried in wild or urban kit foxes. However, a few common DRB alleles found in the wild population were absent in the urban population, which may indicate an absence of functionally unique diversity in urban foxes. MHC diversity in the SJKF is similar or greater than MHC diversity of widespread canid species. These results will be used to further investigate strategies of inbreeding avoidance in urban kit foxes as well as the genetic diversity of 8 foxes that recently died during an outbreak of sarcoptic mange.

Fighting with ultrafast weapons: mantis shrimp win by striking more frequently

Patrick Green, Sheila Patek

3D_305A-Behavior
Monday, June 23, 2014 3:15 PM-3:30 PM

Animal weapons are often used in stereotyped fights that begin with the exchange of visual displays and then escalate to application of force; however, the use of ultrafast power-amplified weapons may alter fight dynamics. Mantis shrimp (Stomatopoda) fight using weapons that exert repeated high-force, transient strikes onto a competitor's impact-resistant tail plate (telson). Here we test whether strike frequency or strike force predicts fight performance. We measured whether the winners and losers of Neogonodactylus bredini fights differed in the number of strikes they delivered during a fight and in the maximum force with which they struck a force sensor. We collected individuals from seagrass habitats in Panama and measured each individual's body size, body mass, weapon morphology, and maximum strike force (highest out of 10 strikes). We then paired body size- and sex-matched individuals in fights over burrows, observing how frequently each individual struck its competitor during the fight and which competitor resided in the burrow at the end of the fight. Winners of fights did not produce greater maximum strike force than losers; however, winners struck more frequently during fights than losers. N. bredini fights almost immediately escalated to striking; this finding is in contrast to previous research showing that animals with weapons (including mantis shrimp) exchange weapon displays prior to escalated fighting. Thus, in size-matched fights, individuals win not necessarily by having weapons that produce higher force, but instead win by using their weapons more frequently. The ultrafast power-amplified weapons of mantis shrimp appear to shift fight dynamics from displays of size and applications of force to the repeated exertion of impact forces onto competitors.

From fast to ultrafast: the evolutionary dynamics of mantis shrimp power amplification

Sheila Patek, Thomas Claverie, Michael Rosario

3D_305A-Behavior
Monday, June 23, 2014 3:30 PM-3:45 PM

Mantis shrimp use a potent biomechanical combination of springs, linkages and latches to power their fast raptorial appendages. Most mantis shrimp species are fish-catching spearers (2-6 m/s, 103 m/s2, 3-25 ms), yet one group shifted to ultrafast shell smashing (16-30 m/s, 105 m/s2,

---

Behavioral drive and behavioral inertia in the tropical lizard, Anolis cybotes

Martha Muñoz, Jonathan Losos

3D_305A-Behavior
Monday, June 23, 2014 3:45 PM-4:00 PM
Behavior determines how organisms interact with their environment, and has long been posited as a pacemaker for evolutionary diversification. The classical view is that novel behaviors expose organisms to new selective pressures, in turn "driving" morphological and physiological evolution. Behavior can also restrain evolutionary change. The "behavioral inhibition" hypothesis suggests that some behaviors, such as thermoregulation, help organisms maintain a constant selective environment, obviating the need to adapt even in the face of changing environments. However, behavioral drive and inhibition are not necessarily mutually exclusive processes – in response to a changing environment, behavioral changes that keep a population in its ancestral niche with regard to one niche axis often will be accomplished by subjecting the population to novel selective pressures on a different niche axis. In this study we test the hypothesis that behavior simultaneously inhibits physiological evolution while impelling morphological evolution in the lizard, Anolis cybotes, a species that ranges from sea level to nearly 3000 meters on the Caribbean island of Hispaniola, and discuss the implications of our findings in the light of contemporary debates in evolutionary biology.

The anti-predatory behavioral repertoire of Drosophila melanogaster

Abhijna Parigi, Cody Porter, Megan Cremak, William Pitchers, Ian Dworkin

3D_305A-Behavior
Monday, June 23, 2014 4:00 PM-4:15 PM
Predation is among the major causes of mortality in most natural populations. Its importance as an agent of selection in shaping both morphology and behavior of prey populations can be inferred from the complexity and diversity of anti-predator traits that organisms express. Although predation, as an agent of selection has been widely investigated, most studies lack tools to explore the genomic and developmental consequences of evolutionary response to predation. Drosophila melanogaster, a well-characterized and tractable model organism with a large behavioral repertoire is well suited for this purpose. However, little is known about predation in D. melanogaster adults. As a starting point, we compiled a catalogue (or ethogram) of D. melanogaster's anti-predatory behavioral repertoire in response to two visual, invertebrate predators, Salticus scenicus (zebra jumping spiders) and juvenile Tenodera aridifolia sinensis (praying mantids) that primarily differ in hunting mode. Based on behavioral observations of a wild caught population in the laboratory, we show that D. melanogaster can alter its behavior in a predator specific manner. Recognizing anti-predatory behaviors that are persistent in natural populations is a prelude to understanding how these behaviors can evolve. To our knowledge, this is the first attempt at building an ethogram of D. melanogaster's anti-predatory behaviors.

Effective payoff matrix in spatial games

Ching-I Huang, Hsiu-Hau Lin, Chun-Chung Chen

3D_305A-Behavior
Monday, June 23, 2014 4:15 PM-4:30 PM
Biodiversity and extinction are central issues in the field of evolution. For well-mixed populations, the evolutionary dynamics is captured by the replicator equations characterized by the payoff matrix. However, previous studies show that local competitions in structured populations lead to different dynamical behaviors. For comparison with replicative dynamics, it is helpful to construct an effective payoff matrix for the global dynamics from the local competitions. In this work, we simulate the rock-paper-scissors spatial game numerically and extract the effective payoff matrix by the extinction time in different parameter regimes. The effective payoff matrix serves as a direct evidence of the robustness of biodiversity in the two dimensional network. The notion and the techniques developed here can be generalized to different systems with different spatial structures.

Evaluating the influences of polyploidy and reproductive mode on life-history variation in a snail model for the maintenance of sex

Katelyn Larkin, Claire Tucci, Maurine Neiman

3D_305B-Life History
Monday, June 23, 2014 3:15 PM-3:30 PM
Sexual reproduction is both extremely common and costly, suggesting that there are profound benefits associated with sex that can counter its costs. Here, we focus on potential life-history costs and/or benefits of sexual reproduction as well as of polyploidy, a trait commonly associated with asexual reproduction that itself may influence important life-history traits. We used a common-garden approach to address these questions, quantifying growth rate, time to reproductive maturity, and adult size in diploid sexual and triploid and tetraploid asexual Potamopyrgus antipodarum. This New Zealand freshwater snail is well suited for studying sex and ploidy-level evolution because sexual diploids and asexual triploids and tetraploids are ecologically similar and coexist in nature, allowing us to use comparisons of sexuals to asexuals and of triploid to tetraploid asexuals to in part decouple the effects of sex from effects of ploidy elevation. We detected significant variation in growth rate, time to maturity, and size at reproduction within each of the three ploidy levels, revealing genetic variation for these important life-history traits. We also found reproductive maturity is not achieved until ~4mm in length, indicating a size threshold that must be met before reproduction. Furthermore, individuals that grew more rapidly also reproduced at a younger age. These tight associations between size, growth rate, and age at maturity highlight the likelihood that growth rate is an important fitness-related trait in P. antipodarum. While sexual P. antipodarum grew more slowly and reproduced at a later age than the polyploid asexuals, there were no apparent life-history differences between triploid and tetraploid asexuals. The latter result suggests that ploidy level differences per se do not explain the relatively slow growth and maturation of sexuals, but instead indicates that reproductive mode itself may directly or indirectly influence life-history traits. Taken together, these data suggest that

the sexual diploid P. antipodarum persist in natural populations in spite of substantial life-history disadvantages.

Residency time as an indicator of reproductive restraint in male burying beetles

Ashlee Smith, Mark Belk, Curtis Creighton

3D_305B-Life History
Monday, June 23, 2014 3:30 PM-3:45 PM

The cost of reproduction theory posits that there are trade-offs between current and future reproduction because resources that are allocated to current offspring cannot be used for future reproductive opportunities. Two adaptive reproductive strategies have been hypothesized to reduce the costs of reproduction and maximize lifetime fitness. The terminal investment hypothesis predicts that as individuals age they will allocate more resources to current reproduction as a response to decreasing residual reproductive value. The reproductive restraint hypotheses predicts that as individuals age they will allocate fewer resources to current reproduction to increase the chance of securing an additional reproductive opportunity. In this study, we test for adaptive responses to aging in male burying beetles, Nicrophorus orbicollis. Burying beetles use facultative biparental care, but the male typically abandons the brood before the female. Previous work in male burying beetles has suggested several factors to explain variation in male residency time, but no study has observed male behavior throughout their entire reproductive lifetimes to determine whether males change residency time in an adaptive way with age. We compared residency time of males that reproduced biparentally, uniparentally, and on different-sized carcasses. Males did not increase residency time in response to advanced partner age when reproducing biparentally, but decreased residency time with age when reproducing uniparentally. A decrease in parental care with age is consistent with a reproductive restraint strategy. To our knowledge, this is the first test of adaptive reproductive strategies in male burying beetles and is one of the first studies to demonstrate reproductive restraint in males.

Sex, mating system, and the evolution of lifespan in Pristionchus nematodes

Cameron Weadick, Ralf Sommer

3D_305B-Life History
Monday, June 23, 2014 3:45 PM-4:00 PM

Most animals are gonochoristic, comprised of both males and females, but some species have replaced females with self-fertile hermaphrodites. Self-fertile hermaphrodites are powerful systems for studying the evolutionary roles of sex and mating, as the transition to hermaphroditism will alter the strength and form of selection on many traits related to reproduction. In particular, the capacity for self-fertilization will provide reproductive assurance and lower the average age of reproduction, which should result in altered selection on lifespan and ageing. Here, I employed a comparative approach to explore the relationship between mating system and lifespan in Pristionchus nematodes, a genus where hermaphroditism has evolved multiple times independently. Lifespan of unmated individuals under lab conditions was assayed for five hermaphroditic species and six gonochoristic species. Median survival time varied considerably among species, depending on both clade and sex; hermaphrodite lifespan ranged from 20-60 days whereas gonochorist lifespan ranged from 40-60 days for males and 50-90 days for females. Hermaphrodite lifespan was unrelated to brood size, suggesting that reduced hermaphdotie lifespan is not simply a consequence of reproductive costs. The degree of sexual dimorphism in lifespan varied among gonochorists, with females living significantly longer than males in three distantly related species. Further experiments were then conducted using hermaphroditic P. pacificus, a model species for evo-devo research, and its gonochoristic sister species, P. exspectatus. These closely-related species can form viable F1 progeny in the lab, yet P. exspectatus females can live approximately four times as long as P. pacificus hermaphrodites. Differences in lifespan were found among strains of P. pacificus, but this variation was small compared to the level seen between species. The capacity of unmated P. exspectatus females to reproduce declines with age faster than it does for conspecific males, suggesting the possibility of sexually dimorphic post-reproductive lifespan. Culturing females and hermaphrodites with conspecific males significantly reduced lifespan, with many females/hermaphrodites dying from matricide, the hatching of unlaid eggs within the mother, which suggests that mating bears costs and that the sexes may be in conflict over egg-laying rate. Nematodes have proven useful systems for studying the mechanistic basis of ageing; efforts are underway to explore molecular correlates of ageing within/among Pristionchus species using transcriptomic approaches. Taken together, this work demonstrates a large effect of mating-system on lifespan in Pristionchus nematodes and provides a foundation for future studies directed at uncovering the molecular changes underlying natural variation in ageing among species.

Hungry mothers' ability to abort and cannibalize their offspring enables the evolution of placentotrophy in a lizard

James Van Dyke, Oliver Griffith, Michael Thompson

3D_305B-Life History
Monday, June 23, 2014 4:00 PM-4:15 PM

Placentotrophy, the nourishment of offspring via a placenta, has evolved repeatedly in vertebrates, including six times in squamates. Prior studies have predicted that the evolution of placentotrophy requires that food resources be abundant and stable throughout gestation. If food availability is not consistently abundant enough to permit successful reproduction, theory predicts that placentotrophic females should be pre-adapted to recoup nutrition invested in reproduction. We tested these hypotheses in the placentotrophic skink, Pseudemoia entrecasteauxii. We fed pregnant females one of four diets (high constant, high stochastic, low constant, and low stochastic) and tested the effects of both food amount and stochasticity of food availability on maternal body composition, neonate composition, developmental success, and cannibalism rate. Low food availability significantly reduced developmental success, maternal growth, neonate size, and maternal and neonate energy, fat, and protein contents. Females on low food diets were significantly more likely to cannibalize both undeveloped eggs and developed offspring. Stochasticity of food availability did not significantly affect any maternal or offspring characteristic. Taken together, our results support the hypotheses that placentotrophy is most likely to be a successful strategy of offspring provisioning when food resources are abundant, and that abortion and cannibalism allows females to recoup nutrition provisioned to offspring if food resources are too low to permit successful reproduction.

Do placentation and superfetation facilitate living life in the fast lane? A preliminary field study

Bart Pollux, Andrew Furness

3D_305B-Life History
Monday, June 23, 2014 4:15 PM-4:30 PM

Placentation (extensive post-fertilization maternal provisioning via integrated materno-fetal tissues specialized for nutrient transfer) and superfetation (the ability to carry multiple, overlapping broods that are in different stages of embryonic development) are two complex female life history traits that evolved multiple times throughout the animal kingdom. The repeated evolution of these traits suggests that they convey an adaptive benefit to females, yet these potential benefits remain poorly understood. The 'locomotor performance hypothesis' proposes that placentation and superfetation evolved to reduce a female's reproductive burden during gestation (Pollux et al. 2009). This might be particularly beneficial to aquatic organisms living in environments characterized by high flow conditions. Here we test the prediction that placental and superfetatious livebearing fish occupy a wider ranger of flow conditions compared to sympatric species that lack placentas and superfetation. We used underwater visual census to study microhabitat use of four sympatric Poeciliid species in Costa Rican rivers. Two of these species, Poeciliopsis retropinna and P. paucimaculata, have well developed placentas and superfetation. The other two species, Poecilia gilli and Brachyrhaphis roseni, lack placentas and superfetation. We observed a strong difference in microhabitat use between these four species: P. gilli and B. roseni inhabit the shallow river margins and isolated side pools where current velocity is low, while P. retropinna and P. paucimaculata are found in a much wider range of current velocities. We propose that placentation and superfetation are life history traits that may have evolved to facilitate the exploitation of a wider ecological (flow) niche.

Genotype-by-Diet Interactions underlying Metabolomic Variation in Drosophila

Laura Reed

3D_306A-Hosts, Pathogens, and Diseases
Monday, June 23, 2014 3:15 PM-3:30 PM

Diseases linked to Metabolic Syndrome (MetS) such at type-2 diabetes and cardiovascular disease are rapidly increasing in humans due to the influences of a modern Westernized-life style, but the genetic, environmental, and physiological mechanisms linking the symptoms of MetS remain to be elucidated. Previously, we have shown that that there is a very substantial contribution of genotype-by-environment interactions to the phenotypic variation observed for MetS-like symptoms in a naturally genetically variable population of D. melanogaster. A major question in evolutionary biology is how can a maladaptive genetic trait like MetS affect such a large proportion of a population without being lost due to selection? Has a shift in environment facilitated the exposure of cryptic genetic variation for a maladaptive trait? We address this question by explicitly testing the genotype-by-diet interaction effect on metabolomic variation in the Drosophila Synthetic Population Resource genetic mapping population. We have mapped QTLs for the genotype-by-diet interaction effects in MetS-like phenotypes (e.g. body weight, triglyceride storage, blood sugar), as well as for metabolomic profiles. Generally we find that the QTLs for main the genetic effects are different from those mediating the genotype-by-diet interactions, and that each trait has a unique set of QTLs. We are finding both new and expected candidate genes as being associated with these metabolic traits.

Pathogen-Host Interactions within Freshwater Systems

Catherine Putonti, Kema Malki, Siobhan Watkins

3D_306A-Hosts, Pathogens, and Diseases
Monday, June 23, 2014 3:30 PM-3:45 PM

Bacteriophages play crucial roles in the maintenance of microbial communities, their impact far extending to the environments in which they are found. Their predation, however, drives bacterial species evolution, and thus the coevolutionary battle begins. In an effort to catch a glimpse into this dynamic system, bacterial and viral species were isolated from the Chicago nearshore waters of Lake Michigan. Using next-generation sequencing, taxa and coding regions present were predicted. The two sites frequently showed comparable bacterial compositions on a collection date, although the presence and relative abundance of each taxon varied over time. While the most prolific and ubiquitous species on earth, a very small fraction of bacteriophages have been characterized and sequenced. BLAST-based analyses of our environmental phage metagenomes repeatedly uncovered novel putative protein sequences, providing a glimpse – albeit narrow – into the phage species present. Correlations between phage and their bacterial host species were observed. Furthermore, composition-based analysis of the viral contigs assembled offers insight into possible host species for uncharacterized phage species.

Evolution of devil facial tumor disease: what it means for the survival of the Tasmanian devil

Janine Deakin, Yiru Zhang, Gayitha Sakthivel, Jennifer Schoning

3D_306A-Hosts, Pathogens, and Diseases
Monday, June 23, 2014 3:45 PM-4:00 PM

Tasmanian devils are the world's largest living carnivorous marsupials. They have experienced a turbulent history, becoming extinct on mainland Australia and surviving a couple of previous population crashes in Tasmania. However, it is right now that devils are perhaps fighting their toughest battle as they contend with an unusual contagious cancer. This fatal cancer, known as devil facial tumor (DFT) disease, is threatening the devil population with extinction. DFT disease appears to have arisen in a female devil in the mid 1990s. It is the tumor itself that is the infectious agent, having since spread through much of the population when devils bite each other and causing a dramatic drop in devil numbers across much of Tasmania. The only other example of a transmissible tumor in the wild is canine transmissible venereal tumor (CTVT), which has been spreading through dogs for over 1000 years. The most important difference between DFT and CTVT is that in most cases CTVT does not kill its host, with the tumor and host being able to co-exist in the population. Is there a chance that DFT could evolve to reach this more desirable scenario?

The initial DFT appears to have resulted from a shattering and rejoining of two chromosomes, followed by the accumulation of other structural mutations which resulted in the formation of several distinctive DFT marker chromosomes. Interestingly, these regions are not only extensively rearranged in DFTs but are also highly rearranged between different marsupial species, suggesting a potential link between tumor and evolutionary breakpoints. By studying DFT chromosomes isolated from individuals from different geographical locations, it has been possible to trace the evolution of this tumor as it ispreads through the population. Until recently, structural mutations in DFTs were seemingly restricted to particular genomic regions, predominantly regions consisting of chromosome 4, 5 and X material but a more recent karyotypic strain of the DFT with a duplication of chromosome 1 material has been detected in a population where DFT disease prevalence is reduced and there has been a limited effect on population structure compared to other areas affected by DFT disease. The implications of this relatively major chromosomal change on the impact of DFT disease will be discussed.

Embracing the complex causality of cancer with microbial experimental evolution

Katherine Liu

3D_306A-Hosts, Pathogens, and Diseases
Monday, June 23, 2014 4:00 PM-4:15 PM

Despite the progress reported in cancer research, cancer remains a huge burden on society. There are many biological, social, and conceptual reasons for this. Cancer is a complex process that involves high genetic and morphological variability. However, the dominant model by which we study cancer (the identification of molecular biomarkers) treats cancer as a static, homogenous entity. The primary systems used to study cancer, namely human tissues and cell cultures, also present these characteristics. Alternative models that embrace the process dynamics and cancer's heterogeneity do not have empirical systems – they depend on theoretical work or computer simulations. Here I discuss the development of a new model by which we can understand cancer with its evolutionary, ecological, and developmental complexity. As well, I argue that microbial experimental evolution systems are untapped resources ideal for studying aspects of cancer.

This novel model is a synthesis of the existing approaches and is based in evolutionary developmental biology (evo devo), particularly the phenomenon of modularity. Evo devo addresses problems of complex causality in the context of developing organisms, while attending to the intergenerational dynamics of evolving populations. A model that employs modularity shifts the attention away from entities to the relationships between the integration and individuation of parts and wholes, illuminating the changing dynamics between the cancer and non-cancer cells as the cancer progresses to malignancy.

A cancer model that embraces the evolutionary, ecological, and developmental dimensions requires a study system that can embrace those dimensions as well. Microbes are ideal for this because they are easy to manipulate, have short generation times, and large population sizes. Here I focus on the multicellular yeast system (Saccharomyces cerevisiae), which can also be used as a representative model of development. Using experimental evolution methods, we can understand evolutionary causality by tracking the selective history and relevant environmental information. More concretely, we can, among other things, investigate the conditions in which the level of selection changes, and how that shift can lead to cheating and defection.

While not modeling cancer proper, microbial experimental evolution systems give a tractable way to study the evolutionary, ecological, and developmental mechanisms involved in cancer progression. A better understanding of these mechanisms can help us understand and predict when there might be unwanted side effects or resistance to commonly used treatments such as chemotherapies.

Evolution of wild yeasts as opportunistic pathogens during experimental co-infection

Sujal Phadke, Serena Zhao, Calum Maclean, Timothy James

3D_306A-Hosts, Pathogens, and Diseases
Monday, June 23, 2014 4:15 PM-4:30 PM
Evolution of wild yeasts as opportunistic pathogens during experimental co-infection

Sujal Phadke, Serena Zhao, Calum Maclean, Timothy James

Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI 48109

Opportunistic pathogens likely emerge from the native and environmentally acquired microbial flora when host immune response is weakened. We studied the propensity of wild isolates of the yeast Saccharomyces cerevisiae to become pathogenic upon continued association with a model host, wax moth larvae of Galleria mellonella. We serially passaged through the host a consortium of 60 wild strains isolated from various habitats, including clinical isolates, and used illumina barseq analysis to identify strains recovered after 30 days inside the host. This serial passaging strategy allowed us to compare the fitness of strains inside a novel host with that estimated from growth in standard in vitro conditions. We found two strains, a generalist and a specialist, to repeatedly outcompete others in vivo, increasing in relative frequency by ~40%. The generalist strain also outcompeted others by ~30% increase in its relative frequency under in vitro conditions. Next, we tested pathogenic potential of the winner strains independently and in association with each other. Our results show that virulence is a dynamic trait and that the immediate biotic environment may be important early in the evolution of wild yeasts as opportunistic pathogens. Our results emphasize the need to study co-infection dynamics in addition to virulence factors to aid understanding of evolution of infectious diseases.

Strong selection drives reinforcement in Phlox

Robin Hopkins, Mark Kirkpatrick, Rafael Guerrero

3D_306B-Speciation and Cryptic Species
Monday, June 23, 2014 3:15 PM-3:30 PM
Reinforcement, the process of increased reproductive isolation due to selection against hybridization, is an important mechanism through which natural selection acts during speciation. The strength of selection driving reinforcement, however, has never been measured in a natural system. We quantify the strength of reinforcing selection in the native Texas wildflower Phlox drummondii using a strategy that weds a model with data. Reinforcement in this system is caused by variation in two loci that effect flower color. We quantify a sharp cline in flower color where this species comes into contact with its congener, P. cuspidata. We develop a spatially explicit population genetic model for these clines based on the genetics of flower color variation P. drummondii. By fitting this model to field observations, we find that selection on flower color genes generated by reinforcement is exceptionally strong. Our findings show that natural selection can play a decisive role in the evolution of reproductive isolation through the process of reinforcement.

Sexually-selected sperm competition genes also contribute to postmating species barriers (conspecific sperm precedence) between D. melanogaster and D.

Dean Castillo, Leonie Moyle

3D_306B-Speciation and Cryptic Species
Monday, June 23, 2014 3:30 PM-3:45 PM
Sexual selection and sexual conflict are often considered important drivers of speciation. Indeed, sister species are frequently primarily isolated by traits thought to have evolved by sexual selection and/or conflict, and models of speciation suggest that traits involved in intrapopulation sexual dynamics can ultimately lead to reproductive isolation. However, whether reproductive isolation between species evolves directly as a consequence of intrapopulation sexual dynamics remains empirically unresolved, in part because knowledge of the genetic mechanisms, if any, connecting these processes is limited. Here we provide evidence of a direct mechanistic link between intraspecies sexual selection and reproductive isolation. We examined genes with known roles in intraspecific sperm competition in D. melanogaster and assayed their impact on conspecific sperm precedence. We found that two such genes contribute to both offensive sperm competition and conspecific sperm precedence; knockdown lines had both lower competitive ability against D. melanogaster conspecifics, and were no longer able to displace heterospecific D. simulans in competitive matings. In comparison, another locus essential for intraspecific sperm competition--does not contribute to conspecific sperm precedence. These data indicate that several important molecular players in sperm competitive interactions have an additional role in similar interactions that enforce post-mating reproductive isolation between species, and show that sexual selection and reproductive isolation can act on the same molecular targets in a gene-specific manner. All three loci show elevated rates of molecular evolution compared to other known D. melanogaster sperm competition genes, indicating that rapid evolution per se is not responsible for this dual role in sexual competition and sexual isolation. Rather, comparatively less pleiotropic constraint, and/or differential involvement in the specific modality underlying sexual isolation, might explain the differential involvement of these loci in CSP.

Does Ecological Speciation Explain the Origin of Tropical Savanna Woody Flora?

William Hoffmann

3D_306B-Speciation and Cryptic Species
Monday, June 23, 2014 3:45 PM-4:00 PM
Tropical savanna is a relatively recent biome, arising in the past 6 to 10 million years, concurrent with the increased dominance of C4 grasses across many areas of the globe. Following this expansion of highly flammable grasses, there has arisen species-rich flora of woody plants that gave rise to the savanna biome. Using the Brazilian Cerrado as a case study, I examined three lines of evidence to explore the hypothesis that the highly diverse woody plant flora arose largely as a result of ecological speciation driven by vegetation-fire feedbacks. Using a published flora of the region and available phylogenetic information, I estimate that savanna woody plants have evolved from tropical forest lineages in at least 115 separate lineages, revealing that a large fraction of speciation events are associated with a switch in biome. Using trait data from a subset of species pairs, I fitted the Ornstein-Uhlenbeck model of evolution, revealing strongest selective pressure on traits that confer fire tolerance. Finally, using a demographic-based model of natural selection and trait evolution, I found that gradients in fire frequency across savanna-forest boundaries are sufficiently sharp to permit genetic differentiation over small spatial scales. The conditions necessary for this differentiation arise because of positive feedbacks between fire and vegetation that result in sharp transitions in flammability, vegetation structure and species composition. Together these results support the hypothesis of fire-driven ecological speciation and suggest that diversification was driven by evolutionary feedbacks that arose naturally from ecological feedbacks.

Analysis of nuclear and mitochondrial DNA reveals cryptic speciation in North American flying squirrels (Glaucomys)

Brian Arbogast, Katelyn Schumacher, Allison Bidlack, Joseph Cook, Jim Kenagy

3D_306B-Speciation and Cryptic Species
Monday, June 23, 2014 4:00 PM-4:15 PM
Phylogeographic studies of North American boreal forest mammals have frequently demonstrated a marked mitochondrial DNA (mtDNA) discontinuity in the Pacific Northwest. This pattern apparently results from historic vicariant event(s) that divided ancestral populations into coastal and interior lineages, followed by more recent secondary contact. We examined mtDNA variation in 205 northern flying squirrels, Glaucomys sabrinus, from across their range, with an emphasis on the Pacific Northwest. This analysis documented a strong phylogeographic break between a highly differentiated coastal clade and an interior clade, and also

allowed us to identify several geographic locations where the two clades come into contact in the Pacific Northwest. To assess levels of nuclear gene flow between these two divergent lineages, we examined microsatellite variation at 8 loci in 64 individuals straddling the mtDNA phylogeographic break. This analysis revealed no evidence of recent or ongoing gene flow between the coastal and interior lineages of G. sabrinus, despite close proximity of samples from the two groups. A similar suite of microsatellite loci have previously demonstrated recent gene flow and apparent hybridization in northeastern North America between the same interior lineage of G. sabrinus and a sibling species, the southern flying squirrel, G. volans. Our new evidence strongly supports the existence of a cryptic species of flying squirrel in the Pacific Northwest, which would add a third species to the genus Glaucomys.

Cryptic phyloendemism across the vast monsoonal tropics of northern Australia

Craig Moritz, Sally Potter, Jason Bragg, Renae Pratt, Gaye Bourke

3D_306B-Speciation and Cryptic Species
Monday, June 23, 2014 4:15 PM-4:30 PM

Phylogeographic analyses commonly reveal deeply divergent but morphologically cryptic lineages within species, a layer of diversity invisible to traditional morphology-based taxonomy. North Australia is dominated by an extensive and relatively intact tropical savanna biome, across which the true diversity is poorly explored. Phylogeographic analyses of low dispersal lizards, from mtDNA to genome-scale, indicate that the diversity and endemism of the region has been vastly underestimated. Revealing the true hotspots of endemism across the region will help prioritise and support large-scale ecological management and development of indigenous-controlled protected areas.

Molecular consequences of sperm competition in Agelaius blackbirds

Irene Liu

3D_306C-Reproductive Traits
Monday, June 23, 2014 3:15 PM-3:30 PM

In species with polyandry (multiple mating by females), sperm from different males compete for access to a female's eggs. Increasing polyandry can intensify selection on traits, such as proteins in the seminal fluid, that confer reproductive advantages to males. Though seminal fluid proteins (Sfps) and their evolutionary patterns have been documented in many species, they remain poorly characterized in birds, a taxon known for its polyandry but only recently studied at the molecular level. Using the Agelaius clade of New World blackbirds, I tested whether Sfps evolve faster in species with high levels of sperm competition than in species with low levels of sperm competition. I first measured the rate of extra-pair paternity (EPP) in three Agelaius species as a proxy for the intensity of sperm competition. All three exhibited similar levels of EPP, including a socially monogamous island endemic. I then used a combination of transcriptomic and proteomic analysis on field-collected samples to compile the first list of seminal fluid proteins in a passerine, the red-winged blackbird (A. phoeniceus). Using this list, I selected and analyzed six candidate Sfps and two control genes across the three species. Preliminary results from dN/dS tests revealed that not only is there no evidence for positive selection in any of these genes, there is strong evidence for purifying selection and furthermore very low levels of diversity within and divergence across species (although levels of diversity correspond with the census sizes of each species). These results contrast trends observed in non-passerines and in insects and mammals. Reasons for the differences could be both microevolutionary (the Sfps examined in this study could face mixed selective pressures, including selective constraints) or macroevolutionary (birds have a much slower tempo of molecular evolution than other taxa). Additional characterization of the transcriptome, as well as further evolutionary analyses, are ongoing to place these initial findings in context. By examining the effect of mating system on protein divergence, this work links sexual selection with DNA sequence evolution while generating behavioral, genetic, transcriptomic and proteomic resources for future comparative studies.

Contemporary co-evolution of sea urchin sperm and egg recognition proteins in response to changing population densities

Don Levitan

3D_306C-Reproductive Traits
Monday, June 23, 2014 3:30 PM-3:45 PM

Sperm and eggs that are broadcast into the sea face an uncertain fate because they might come into contact with too few or too many sperm, as either competitors or mates, or because the gametes they encounter are partially or fully incompatible. The selective forces generated by patterns of sperm availability might drive the rapid evolution of gamete recognition proteins. Here I examine how sperm and egg recognition proteins in the sea urchin Strongylocentrotus franciscanus have co-evolved over several hundred years associated with the extirpation of predatory sea otters from the Pacific Northwest and the resulting explosion of sea urchin abundances, and thus sperm availability, along this coast. Over this time-span, allele frequencies in the sperm bindin protein has shifted from one common allele that performs best at low densities to the emergence of a second common allele that is resistant to polyspermy at high densities. This pattern is mirrored by changes in allele frequencies in the egg receptor for sperm bindin and also results in the contemporary development of linkage-disequilibrium between these sperm and egg proteins driven by assortative mating. These results suggest that gamete recognition can evolve rapidly with shifts in abundance allowing individuals to successfully reproduce under changing demographic conditions.

Sexual selection in a wild insect population

Ummat Somjee, Christine Miller, Allen Moore

3D_306C-Reproductive Traits
Monday, June 23, 2014 3:45 PM-4:00 PM
Sexual selection is a potent evolutionary force that results in some of the most exaggerated and variable traits in nature. The strong and consistent action of sexual selection should quickly deplete genetic variation in such traits, however this variation persists. How can such variation be sustained despite strong directional selection? One resolution to this problem is that selection is not consistent but fluctuates in strength and direction in response to environmental changes. Indeed, a vast majority of studies that measure selection in nature do so at one space or time, resulting in a static perception of selection. In this study, we use a sexually dimorphic insect species to investigate the influence of changing environments on sexual selection. The life history of the insect Leptoscelis tricolor (Hemiptera: Coreidae) is closely tied to its host plant, a resource that varies considerably over space and time. Mating, egg laying and development occur on host plants. In addition, males use their enlarged hind femurs as weapons while defending territories on distinct species of host plant. To understand if selection is responsive to temporal and environmental changes we measure selection as it occurs in nature, over time and across two distinct host plant species. Our results reveal that selection is likely weak but dynamic . In conclusion, our results suggest that environmental changes lead to dynamic patterns of selection on body and weapon size in L. tricolor.

Diet affects ejaculate traits in a lizard with condition-dependent fertilization success

Ariel Kahrl, Robert Cox

3D_306C-Reproductive Traits
Monday, June 23, 2014 4:00 PM-4:15 PM
Sexual selection is predicted to deplete genetic variation in fitness-related traits, but condition-dependence can maintain phenotypic variation in the face of strong selection. Characteristics of the male ejaculate, such as the quantity or quality of sperm, can be both condition-dependent and subject to strong sexual selection. Because sperm production can be energetically costly, males are predicted to respond to limited resources by reducing the quantity or quality of their sperm. We tested the condition-dependence of ejaculate traits by experimentally altering body condition through food restriction in the lizard Anolis sagrei, which has condition-dependent fertilization success. As predicted, food restriction reduced male body condition and decreased total sperm production relative to males fed ad libitum. Additionally, sperm morphology within individuals was more variable in food-restricted males, suggesting that energy limitation detrimentally impacted both the quality and quantity of sperm. Food restriction also increased the size of the sperm midpiece, suggesting a possible tradeoff between sperm quality and quantity under energy limitation. Because these ejaculate traits are potentially related to sperm competitive ability and fertilization success our results suggest that condition-dependence may be important for male fitness and the evolution of sperm morphology.

The effect of plasticity and viability costs of proteins on the evolution of seminal fluid composition

Sumit Dhole, Maria Servedio

3D_306C-Reproductive Traits
Monday, June 23, 2014 4:15 PM-4:30 PM
Seminal fluid proteins (Sfps) of many internally fertilizing species are some of the fastest evolving molecules in animals. The influence of these proteins on male success in sperm competition and their role in sexual conflict contribute to the strong positive selection acting on these proteins. Production of Sfps has been shown to be energetically expensive and time consuming. The evolution of male investment of resources in different kinds of Sfps, however, has only recently received empirical attention, and has not yet been addressed with formal theory. Here we present analysis of a model of evolution of seminal fluid composition. In spite of their diverse functions, Sfps involved in sperm competition increase male fitness in one of three ways -– 1) “avoidance” proteins help males avoid direct sperm competition; e.g. by delaying female remating, 2) “defense” proteins help males defend their sperm from displacement by the female’s subsequent mate, and 3) “offense” proteins aid males in displacing sperm of preceding males. We studied how male investment in these three categories of Sfps evolves in the light of sperm competition. Our previous results indicate the evolution of a single optimal strategy in seminal fluid composition based on the efficiencies of these proteins. Here we present an analysis of the effects of plasticity in male investment in Sfps and different viability costs of Sfps on the evolutions of seminal fluid composition. We incorporate plasticity in the model by allowing males to alter their seminal fluid composition prior to mating based on the mating status of the female. Males mating with virgin females reallocate resources towards avoidance and defense proteins, whereas males mating with females that have previously mated reallocate resources towards offense proteins. We find that plasticity in male investment has a complex set of unintuitive effects on the evolution of seminal fluid composition. In contrast with scenarios without plasticity, plasticity allows the existence of multiple optimal seminal fluid compositions at the genotypic level. Our results indicate that across populations, plasticity can facilitate the maintenance of not only phenotypic, but also genetic variation in seminal fluid composition. The level of plasticity also alters the seminal fluid composition that evolves in a population. At high levels of plasticity males evolve to invest only in avoidance and lose investment in defense. We also find that if Sfps incur a viability cost on males, males evolve to make smaller investments in the costlier proteins.

Parallel evolution during local adaptation

Graham Coop, Peter Ralph

3D_402-ASN Vice Presidential Symposium:Modern approaches to local adaptation
Monday, June 23, 2014 3:15 PM-3:45 PM
Models for detecting the effect of adaptation on population genomic diversity are often predicated on a single newly arisen mutation sweeping rapidly to fixation. However, populations can also adapt to a new environment by multiple mutations of similar

phenotypic effect that arise in parallel, at the same locus or different loci. In this talk I will discuss models of parallel evolution during local adaptation, and how parallel evolution can confound population genomic signals of adaptation.

Clinal variation in adaptation to elevation in Boechera stricta (Brassicaceae), a perennial forb native to the Rocky Mountains

Jill Anderson, Tom Mitchell-Olds

3D_402-ASN Vice Presidential Symposium:Modern approaches to local adaptation
Monday, June 23, 2014 3:45 PM-4:15 PM
Natural populations evolve in response to a complex suite of abiotic and biotic conditions that often vary substantially across the landscape. Strongly divergent selection can result in adaptive population differentiation, especially when gene flow is minimal. In the evolutionary literature, local adaptation studies have focused primarily on testing home site advantage of genotypes from two distinct habitats (e.g., wetland vs. upland) reciprocally transplanted into both environments. Nevertheless, most species do not inhabit only two contrasting environments, but rather encounter a gradient of environmental conditions across their range. For most species, we know little about clinal variation in fitness, phenotypes and local adaptation across complex gradients. Is divergent selection at fine spatial scales strong enough to counteract the homogenizing forces of gene flow?

Here, we use a provenance trial approach to examine clinal variation in local adaptation in Boechera stricta (Brassicaceae), a perennial forb native to the US Rocky Mountains. We conducted this study in both the southern (Colorado) and northern (Montana) portions of the range of B. stricta. In Colorado, we planted seeds and seedlings of 24 local maternal families from populations spanning a broad elevational gradient (2869-3682m) into two test gardens (2884 m and 3133m). In 2012 and 2013, we recorded fitness (survival, probability of flowering, fruit number, seed set), life history traits (flowering time, size at flowering), and damage from insect herbivores. In Montana, we planted a separate set of 24 local families (elevation of origin: 2414-2884m) into one mid-elevation garden at 2534m, and quantified fitness over 2 growing seasons.

We find clear clinal variation in fitness and traits. In Montana, genotypes from greater geographic distances and lower elevation are poorly adapted to the garden. In Colorado, in the higher elevation garden, germination success followed a predicted quadratic pattern with highest fitness for seeds from elevations similar to the garden. At the lower garden, survivorship declines by 142% for every 100m increase in provenance elevation. Foliar herbivory is positively correlated with elevation of origin in both Colorado gardens, indicating limited herbivore resistance in high elevation families. Short growing seasons and cool temperatures could limit herbivore populations and reduce selection for resistance at high elevations. High elevation families flower earliest at the smallest sizes, likely reflecting an evolutionary response to short growing seasons. The poor performance of high elevation families in the low garden foreshadows future maladaptation in their home sites in the context of climate change.

Genomics of local adaptation in evolving populations of microbes

Rees Kassen, Susan Bailey, Alana Schick

3D_402-ASN Vice Presidential Symposium:Modern approaches to local adaptation
Monday, June 23, 2014 4:15 PM-4:45 PM
The outcome of divergent selection is expected to be the evolution of specialization and, so, local adaptation. Although local adaptation is fairly common at the phenotypic level, the genomic changes contributing to its evolution are far less well understood. In a previous experiment we selected the Gram-negative microbe Pseudomonas fluorescens in environments that differed in the number and spatial arrangement of three distinct carbon sources for 1000 generations. Trade-offs in fitness characterstic of local adaptation evolved following divergent selection on single resources, as expected. We have now reconstructed the sequence of mutations substituted in each lineage and have estimated their fitness effects both in the environment of selection and in all other environments used in the experiment. I will report on these and related results from other microbial experiments that together provide a first glimpse into the genomic evolution of local adaptation.

Identifying ancient polyploid events in angiosperms: a phylogenomic approach

Michael McKain, Haibao Tang, Alex Harkess, Saravanaraj Ayyapalayam, Jeff J. Doyle, Steven Cannon

3D_BalC-SSB Symposium: Phylogenomics, transcriptomics, and the evolution of gene expression
Monday, June 23, 2014 3:15 PM-3:45 PM
Polyploidy is a pervasive phenomenon in eukaryotes, especially angiosperms. Understanding the long-term ramifications of polyploidy on the evolution of organisms requires knowing when these events occurred on the phylogeny. Here, we demonstrate the utility of transcriptomics for the identification and phylogenetic placement of polyploid events. Though incomplete in nature, transcriptomes provide large collections of exomic data from numerous species using smaller investments of time and money compared to traditional PCR-based approaches and full genome sequencing. This deeper taxonomic sampling allows for more precise identification of the timing of polyploid events within a phylogeny. The depth of genomic sequencing for each species also allows for the identification of lineage specific polyploid events and, at times, extremely ancient events that my evade full genomic analyses using synteny. Additionally, transcriptomes provide a number of low copy genes that are useful in the reconstruction of species trees. Furthermore, transcriptomes provide the basis for more exact target enrichment approaches that can answer more specific questions regarding genome composition, molecular evolution, and phylogeny. By looking at various lineages throughout the angiosperms, we show that gene trees made from transcriptomes can be used to identify both well-known and novel polyploid events, create a species tree for sampled taxa, place the

polyploidy events in the context of the tree, and provide some precursory insight into the composition of polyploid genomes over time.

The Butterfly Plant Arms-Race Escalated via Gene and Genome Duplications

Patrick Edger, H.M. Heidel-Fischer, Michael Bekaert, Adrian Platts, Gavin Conant, Michael Barker, Michelle Tang, Eric Wafula, Josh Der, Claude dePamphilis, Stephen Wright, Thomas Bureau, Mathieu Blanchette, Jocelyn Hall, Ann Smithson, Johannes Hofberger, Eric Schranz, H

3D_BalC-SSB Symposium: Phylogenomics, transcriptomics, and the evolution of gene expression
Monday, June 23, 2014 3:45 PM-4:15 PM
Diffuse coevolutionary interactions are thought to have driven the diversification of much of the life on Earth (Darwin 1854) and involve the evolution of key innovations (Ehrlich and Raven 1964) that may escalate in their complexity over time due to 'arms-race' dynamics between the interacting parties. However, the genetic basis of key innovations is poorly understood, and the tempo and mode of their evolution is unstudied on a genomic scale. Here we present evidence of escalation on a genomic scale for both sides of an ancient coevolutionary interaction, finding that interactions were facilitated by both local (i.e. tandem) and whole genome duplication events.

Increases in Plant Diversity Associated with Changes in Genome Composition and WGDs

Michael Barker, Emily Sessa

3D_BalC-SSB Symposium: Phylogenomics, transcriptomics, and the evolution of gene expression
Monday, June 23, 2014 4:15 PM-4:45 PM
Polyploidy, or whole genome duplication, is a prominent feature of plant evolution. Nearly 1/3 of flowering plant species are of recent polyploid origin and all have some polyploid ancestry. Recent analyses have found that although most polyploid species go extinct at relatively high rates, the rarely successful lineages are associated with more than half of the significant increases in flowering plant net diversification rates. We sought to further explore the nature of these highly successful polyploids and test if they have left a different genomic legacy than other events in flowering plant history. Our analyses of a broad collection of plant genomic and transcriptomic data find evidence that significant shifts in genome composition are highly correlated with increases in the net diversification rate. We also find that many of these shifts, but not all, are associated with WGDs. In contrast, ancient WGDs that are not associated with an increase in diversity have left behind little legacy in plant genomes. Overall our results suggest that plant diversification is associated with significant changes in genomic composition and that the long-term fates of genes following polyploidy are associated with the success of their lineage.

Social selection and the evolution of color patterns

Trevor Price

3E_BalC-ASN Presidential Address
Monday, June 23, 2014 -
The reasons why animals vary so much in color are only understood at the broadest level. Why is one bird species blue and a close relative of the species red, one sexually dimorphic and its close relative monomorphic? Models of sexual selection suggest that such differences could be arbitrary, whereas other investigations relate differences to features of the environment. Focusing on our work on birds (Old World and New World warblers) which differ in color in striking ways both within and between groups, I will specifically (1) expand sexual selection to consider a role for mate stimulation in the evolution of color patterns, (2) describe mechanistic approaches towards understanding how species differ in perception of color, and (3) consider how condition dependence of sexually selected traits impacts their evolution.

Evolution of the tissue specificity of inherited predispositions to cancer

Brian Muir, Leonard Nunney

4A_301A-Gene Expression
Tuesday, June 24, 2014 8:30 AM-8:45 AM
Studies of familial cancers have found that only a small subset of tissues are affected by inherited mutations in a given tumor suppressor (TSG) or proto-oncogene (POG), even though the mutation is present in all tissues. The tissue specificity of these genes suggests that each gene is acting as a critical regulator of cell division in the predisposed tissues but not in those tissues with no elevated risk of hereditary cancer. This suggestion, however, has been difficult to support. Studies investigating the presence vs. absence of gene and protein expression have found that TSGs and POGs are expressed in nearly every type of normal human tissue. Recent work, however, suggests that it is a high vs. low level of TSG or POG expression that may predict the importance of each gene across different tissue types. In this study, we test the hypothesis that TSGs and POGs have higher constitutive expression in the normal (non-cancerous) tissues where they are implicated in familial cancers, relative to those tissues where they are not. We examined microarray expression levels of 15 TSGs and 8 POGs across 12 human tissue types and found a significant difference between expression levels in susceptible vs. non-susceptible tissues. We found the target gene to have its highest expression level in the corresponding susceptible tissue(s) for 5 (33%) of the TSGs ($p=0.02$) and 5 (62.5%) of the POGs ($p=0.0004$) examined. This is the first study to report such findings in gene expression data. We conclude by discussing possible explanations as to why this pattern is not detected in a greater proportion of the genes and suggest new research directions that can be explored using this approach.

Regulatory adaptation is linked to global gene expression changes in human evolution

Courtney Babbitt

4A_301A-Gene Expression
Tuesday, June 24, 2014 8:45 AM-9:00 AM

Courtney C. Babbitt1,2, Ralph Haygood1, Lisa W. Pfefferle1, Olivier Fedrigo1,2, and Gregory A. Wray1,2,3

1. Department of Biology, Duke University

2. Institute for Genome Sciences & Policy, Duke University

3. Department of Evolutionary Anthropology, Duke University

There are many dramatic phenotypic differences between humans and non-human primates distributed across many tissue types. In order to understand the ways in which gene expression has required trade-offs across multiple tissues we used RNA-Seq to assay gene expression between humans, chimpanzees, and macaques in matched samples from frontal cortex, cerebellum, liver, white adipose, and skeletal muscle. We found a slightly negative correlation with evidence of adaptation in coding regions and changes in gene expression. However, we found a significant correlation between categories of genes that show evidence of adaptation in regulatory regions (including both promoters and distal enhancers) and differential gene expression between humans and chimpanzees. There is also evidence that many genes are not under significant constraint across tissues, thereby allowing the expression of these genes to evolve rapidly. Across all tissues, the gene ontology categories that are highly differentially expressed include neural processes, metabolism, development, and signaling, and many of these changes are specific to the human lineage. Significant gene expression changes between humans and chimpanzees are also enriched for genes associated with late onset diseases prevalent in humans such as insulin signaling and epithelial cancers. Collectively, these results suggest that regulatory adaptations that changed gene expression during human evolution may have also had knock-on effects that increase our susceptibility to certain late onset diseases.

Genomic imprints of freshwater transitions in the alewife (Alosa pseudoharengus)

Jonathan Velotta

4A_301A-Gene Expression
Tuesday, June 24, 2014 9:00 AM-9:15 AM

Among fishes, ecological transitions into freshwater environments are often associated with episodes of diversification and adaptive radiation. We know little about the genomic modifications that underlie these shifts. Alewives are found in ancestrally anadromous migratory populations and in multiple, independently evolved landlocked populations, allowing us to test for parallel genomic responses to freshwater transitions. In this study, we sequenced gill transcriptomes from two landlocked populations and one anadromous population of alewives, which were experimentally challenged with freshwater and seawater in the laboratory. We then characterized divergence in gene expression between alewife life history forms. We detected divergence in expression of genes with osmoregulatory functions, several of which have diverged in parallel between independently evolved landlocked populations and an anadromous one. However, most genes showing parallel divergence between life history forms were not osmoregulatory, suggesting that a variety of molecular pathways may be under selection in the transition to freshwater. Our analysis identifies osmoregulatory loci and other candidate genes that are implicated in adaptation to exclusively freshwater habitats.

SNP differentiation and differential gene expression in endemic Epischura baikalensis from Lake Baikal

Lev Yampolsky, Larry Bowman

4A_301A-Gene Expression
Tuesday, June 24, 2014 9:15 AM-9:30 AM

Lake Baikal, extremely diverse in benthic life, has a remarkably uniform zooplankton, with over 95% of biomass represented by just one species of an endemic calanoid copepod, Epischura baikalensis Sars. This species, arguably the most abundant of all freshwater multicellular animals, due to Baikal's volume, is a pivotal primary consumer of pelagic algal production. Despite a significant current mixing, it is excluded form Baikal's shallow, warmer bays, populated by cosmopolitan zooplankton, which is, in turn, until recently was very rare in the open Baikal. We obtained a partial transcriptome of E. baikalensis and investigated genetic differentiation of SNP frequencies and gene expression profiles between samples taken in different parts of Baikal. The first two principle components describing both SNP differentiation and differential expression are correlated with the latitudinal gradient and with the distinction between Maloe More straight and the main body of the lake. Genes that are most differentiated at SNPs also tend to have the most divergent expression profile. We discuss these findings in the light of plastic and selection response of Baikal Epischura to current and future increases of surface temperatures in Baikal.

Detecting changes in gene expression by high-dimensional analysis of codon usage bias

David McCandlish, Premal Shah, Joshua Plotkin

4A_301A-Gene Expression
Tuesday, June 24, 2014 9:30 AM-9:45 AM

One difficulty in understanding the evolution of codon usage bias is that the space of codon frequencies is high-dimensional. This has led to the proposal of several univariate summaries of codon usage (e.g. CAI, tAI, etc.). However, additional insight may be gained by considering information that is discarded when computing these univariate summaries.

Here we analyze the high-dimensional geometry of expected codon usage under a mutation-selection-drift model where the strength of selection on translational efficiency is determined by gene expression level. Taking account of amino acid usage results in a 40-dimensional codon usage space; but at equilibrium the expected codon usage of a gene whose expression level is constant over evolutionary time must lie on a one-dimensional curve. Surprisingly, even genes whose expression levels are allowed to change arbitrarily through evolutionary time have expected frequencies that are restricted to a tiny fraction of codon usage space.

We apply this geometric analysis to understand patterns of codon usage across the yeast genome. In particular, we sort all genes into three sets: genes whose codon usage is well-explained by a constant expression level, genes whose codon usage is well-explained by an expression level that changes over evolutionary time, and genes whose codon usage cannot be explained by arbitrary time-varying selection on translational efficiency.

Ecological constraints on sensory systems: Compound eye size in Daphnia is reduced by resource limitation.

Christopher Brandon, *Jeff Dudycha*

4A_301B-Trait Evolution
Tuesday, June 24, 2014 8:30 AM-8:45 AM
Eye size is an indicator of visual capability, and macroevolutionary patterns reveal that taxa inhabiting dim environments have larger eyes than taxa from bright environments. This suggests that the light environment is a key driver of variation in eye size. Yet other factors not directly linked with visual tasks (i.e., non-sensory factors) may influence eye size. We sought to jointly investigate the roles of sensory (light) and non-sensory factors (food) in determining eye size and ask whether non-sensory factors could constrain visual capabilities. We tested environmental influences on eye size in four species of the freshwater crustacean Daphnia, crossing bright and dim light levels with high and low resource levels. We measured absolute eye size and eye size relative to body size in early and late adulthood. In general, Daphnia reared on low resources had smaller eyes, both absolutely and relatively. In contrast to the dominant macroevolutionary pattern, phenotypic plasticity in response to light was rarely significant. These patterns of phenotypic plasticity were true for overall diameter of the eye and the width of individual facets. We conclude that non-sensory environmental factors can influence sensory systems, and in particular, that resource availability may be an important constraint on visual capability.

Functional traits, biomes, and diversification rates in Rhamnaceae

Renske Onstein, *Peter Linder*

4A_301B-Trait Evolution
Tuesday, June 24, 2014 8:45 AM-9:00 AM
Species diversification is inextricably linked to a lineage's intrinsic innovations and the extrinsic events it is exposed to over evolutionary time. However, the temporal sequence of these diversification 'triggers', and their additive or interactive effects on speciation and extinction rates is unclear. 'Adaptations' are traits which evolve during or just after movement to new environments, whereas 'exaptations' have evolved prior to the transition to the new environment, thereby facilitating this shift. In this study we investigate if functional trait syndromes evolved as adaptations or exaptations to certain biomes, and if those lineages possessing the trait syndrome in the associated biome diversify faster than lineages lacking the traits or not occurring in the particular biome. We test this in the Rhamnaceae, which occur as lianas or large trees with big leaves in tropical rainforests, as woody shrubs with small, sclerophyllous leaves and revolute margins in Mediterranean shrublands, and as spiny shrubs in deserts. We assembled trait and biome data for 759 Rhamnaceae species (70% of total species) and use a dated phylogeny (280 species) to define trait syndromes positively associated with the biomes, to test for correlated evolution between them, to reconstruct ancestral states to evaluate the temporal sequence of innovation and extrinsic opportunity, and to test for differential diversification rates between adapted and non-adapted lineages. Results indicate correlated evolution between trait syndromes and biomes, and generally higher diversification rates of adapted compared to non-adapted lineages. The sequence of evolutionary events (i.e. adaptation or exaptation) in rainforests and deserts remains unclear, but we find strong evidence that the Mediterranean trait syndrome evolved as an adaptation to Mediterranean shrublands. Although both the Mediterranean biome and the trait syndrome individually increase diversification rates, a decreased speciation rate was detected for the interaction between the two, suggesting that well adapted, specialised lineages in Mediterranean shrublands may reach evolutionary dead ends.

Optimal Predator Learning and the Evolution of Mimicry

David Kikuchi, *Thomas Sherratt*

4A_301B-Trait Evolution
Tuesday, June 24, 2014 9:00 AM-9:15 AM
A major question in animal communication is why signals are often complex, involving multiple components, dimensions, or sensory modalities. One potential explanation is that signals evolve complexity because they face selection to be distinct from other signals. In Batesian mimicry, where undefended mimics evolve to resemble defended models, signals can evolve varying degrees of complexity. Models for Batesian mimics should experience selection to become distinct from their parasitic mimics, and respond by increasing the complexity of their signals. In support of this notion, models for Batesian mimics often evolve complex displays such as those found on noxious tropical butterflies. The conditions required for selection to favor the evolution of signal complexity remain underexplored, however.

We hypothesize that the strength of selection to be distinct, and hence the subsequent degree of signal elaboration (increasing complexity), should be inversely proportional to the cost:benefit ratio of attacking defended models versus undefended mimics. This is because a higher cost:benefit ratio makes sampling defended mimics more costly. Therefore, predators should be less willing to pay the price of learning about more complex, distinctive signals, resulting in reduced selection for signal elaboration. To formalize this hypothesis, we present the results of a Bayesian model that employs stochastic dynamic programming to arrive at an optimal solution for predator behavior. This model illustrates ecological scenarios under which selection for convergence in signal evolution is highest.

Small dog, hairy dog, big dog, scary dog: understanding the genetics of morphological traits in the domestic dog

Jessica Hayward, Marta Castelhano, Kyle Oliveira, Liz Corey, Sara Kalla, Rory Todhunter

4A_301B-Trait Evolution
Tuesday, June 24, 2014 9:15 AM-9:30 AM

The domestic dog (Canis lupus familiaris) displays extreme diversity of morphological traits, primarily due to intensive artificial selection during breed formation. This unique history makes the dog an excellent model species for studying morphological phenotypes. Since many of these phenotypes (such as fur length, body size, and ear flop) are fixed within breeds, breed-mapping approaches to genome-wide association studies (GWAS) have been used to successfully identify underlying quantitative trait loci (QTLs). In contrast to humans, a few QTLs of large effect account for the majority of variation among dog breeds.

To further investigate the genetic basis of body size, and several fur phenotypes, we genotyped a diverse panel of 4000 dogs, representing over 150 breeds and 350 village dogs, at more than 180,000 SNP markers. GWAS revealed additional novel loci, including a missense mutation in the gene MC5R that is associated with both the degree of fur shedding and medium versus short length fur.

Our genotyped panel also contained individual body size measurements for over 2000 dogs. GWAS of individual and breed-average body size measures yielded similar results, with the identification of seventeen key QTLs, accounting for 80 to 85 % of variation in weight and height. Using a linear model, we estimate the effect sizes of each QTL on numerous body size measurements within and among breeds, as well as in village dogs. Furthermore, we test for non-additive and epistatic effects between loci, providing the most complete understanding to date of the genetic architecture of size variation in this model system.

Testing traits associated with low nutrient adaptation in Helianthus

Lisa Donovan, Shu-Mei Chang, Kelly Bettinger

4A_301B-Trait Evolution
Tuesday, June 24, 2014 9:30 AM-9:45 AM

Plants associated from nutrient poor habitats generally have slower growth rates, delayed flowering, and more conservative resource traits, all of which have been hypothesized to be adaptations to low nutrients. However, phenotypic selection and artificial selection experiments generally do not support these adaptive hypotheses. We conducted a simulated natural selection experiment on interspecific hybrids of Helianthus annuus x H. petiolaris under very low N conditions in order to experimentally test for traits associated with low nutrient adaptation in an herbaceous annual. The experimental design included six breeding populations that were initially started from same 18 maternal families but cross-pollinated only within each population after that. Three populations served as our control populations and, for each, a random plant from each maternal family contributed progeny to the next generation. For each of the remaining 3 selected populations, the plant from each maternal family with the highest seed production contributed progeny to the next generation. After several generations, plants in the selected populations have significantly higher fitness (estimated as total seed production per plant) than plants in the control populations. The plants in the selected populations also have later budding and flowering, smaller seeds, larger stem diameter at first flower and lower leaf water content. The analyses of additional traits (biomass allocation and leaf resource-use related traits) are still pending. Taken as a whole, the results will provide a robust test of traits associated with low nutrient adaptation in an herbaceous annual.

The role of extinction in the assembly of large-scale biodiversity patterns

Cristina Isabel Pokorny Montero, Ricarda Riina, Mario Mairal, Andrea Briega, Jon Cendoya, Isabel Sanmartín

4A_302A-Macroevolution
Tuesday, June 24, 2014 8:30 AM-8:45 AM

Understanding how transoceanic disjunct distributions (closely related organisms scattered across continents) came to be has shaped biogeography as a science from the old vicariance paradigm, where a once continuous biota was fragmented by Earth tectonic events, to a more recent molecular-based hypotheses of long-distance dispersal across oceanic barriers. Compared to these disjunctions, large-scale continental disjunctions (closely related taxa scattered within a continent), have received less attention. The barriers in this case are not so much geographical (e.g., an ocean basin) but ecological: the existence of stretches of inhospitable land that are outside the ancestral climatic tolerance of a given organism. One of the best examples of this distribution is the African "Rand Flora" (aka, "Rim Flora"), a floristic pattern that relates plant species disjunctly distributed in the continental margins of Africa (i.e., Macaronesia-NW Africa, Horn of Africa-South Arabia, Eastern Africa, and South Africa), separated by the tropical lowlands of Central Africa and the arid terrains of the Sahara Desert in the north and the Kalahari Desert in the south. Traditionally, this disjunction has been explained by fragmentation of an ancient widespread African flora by aridification-driven vicariance events, leaving relict taxa in "climatic refuges" in the eastern and western margins of Africa, but recent molecular studies point to independent dispersal events from neighboring regions. The molecular revolution and the possibility of integrating time into biogeographic reconstructions have enabled testing these alternative hypotheses within a spatio-temporal framework. Continental disjunctions are especially interesting for understanding the role of extinction in the assembly of global biodiversity patterns because, as with the Rand Flora, they are often attributed to large-scale climatic events that would have extirpated intermediate populations from a once continuous distribution, leaving relicts on either side of the disjunction. Unlike lineage extinction that is clade-specific, these extinction events are clade-wide, affecting unrelated lineages that may differ in their ecological requirements, dispersal mode, or age. In here, we show results from our Rand Flora project in which we attempt to estimate extinction rates across unrelated flowering plant lineages.

Species selection and evolving traits can and do interact

Carl Simpson

4A_302A-Macroevolution
Tuesday, June 24, 2014 8:45 AM-9:00 AM

Species selection is a higher-level version of natural selection, where speciation and extinction rates covary with phenotypic or macroecological properties of species. Species selection acts on species' properties without regard for how those properties are produced or how the species containing those properties are related. In contrast, the macroevolutionary response to selection, depends on the structure of the properties' phylogenetic variation among species in the clade and on how that variation is produced over species' lifetimes. This means that the response to species selection is governed by both microevolutionary phyletic and phylogenetic change. For species selection to generate large-scale trends, both species selection and the macroevolutionary response to species selection must align in a concordant way. But the interaction between selection and the response to selection can be complex. For example, if species selection is strong but orthogonal to microevolutionary change, the resultant is an equilibrium non-trend, where the average trait values among species are stable over time. Non-trends are interesting because if selection or the response to selection are considered only in isolation, strong directional trends are expected. What matters for any given selection and response regime is the resultant vector produced by the vector of selection and the vector of response to selection.This framework lends itself to studying the evolution of a wide variety of trait distributions. Many traits often change over the lifetime of species and also show highly variable phylogenetic signal. For example, geographic range size is consistently associated with extinction selectivity, yet range size changes dramatically over the lifetimes of species as well as over phylogeny. What this framework provides is a means to understand how changes to trait distributions are made. How much change is due to selectivity or due to phyletic change? How do these inferred changes interact with each other to produce the total change in the distributions of traits? The answers to these questions show how macroevolution is more than microevolution scaled up over deep-time. Cladogenesis and extinction together add new levels evolutionary processes that make up the major features of macroevolution.

A permutation-based framework for detecting genus-level selection

Kenneth Hoehn, Paul Harnik, V. Louise Roth

4A_302A-Macroevolution
Tuesday, June 24, 2014 9:00 AM-9:15 AM

The ability of higher-level taxonomic units to be acted upon by natural selection has a long history as a contentious issue in evolutionary theory. Despite extensive theoretical discussion, the topic has largely evaded empirical resolution. Given the recent development of large, publicly-available databases, a simple and robust hypothesis-testing framework for detecting higher-level selection could facilitate significant strides to resolving this question. We introduce a permutation-based approach, implemented in the R package perspectev. This method allows for an explicit test of whether empirical patterns of covariance between genus-level geographic range and survivorship are reducible to lower levels. We applied this approach to five different paleontological data sets of varying taxonomic breadth, geological timing, extinction magnitude, and geographic extent, including a previously identified interval of higher level selection during the Cretaceous-Paleogene (K-Pg) mass extinction event. Through simulation studies, we demonstrate that this method is a reliable means of detecting genus-level selection for geographic range size, confirm previous findings of genus-level selection in North American K-Pg molluscs, and identify two other instances of potential genus-level selection during Cenozoic background extinction events. Ultimately, we conclude that some higher taxa have, at certain points in history and within certain geographic regions, behaved as coherent evolutionary individuals. We show that evidence implicating higher-level selection has varied across taxa and extinction events, and we release our method as a simple-to-use R package in the hope that others will help determine the relative frequency of this macroevolutionary phenomenon.

Massive horizontal gene transfer of a chimeric photoreceptor in ferns

Fay-Wei Li, Kathleen M. Pryer

4A_302A-Macroevolution
Tuesday, June 24, 2014 9:15 AM-9:30 AM

Ferns are well known for their shade-dwelling habits. Their ability to thrive under such low-light conditions has been linked to the evolution of a novel chimeric photoreceptor—neochrome—which fuses red-sensing phytochrome and blue-sensing phototropin modules into a single gene, thereby optimizing phototropic responses. Despite its potential importance in conferring a distinct evolutionary advantage to ferns living under dense canopies, the origin of neochrome has remained a mystery. We recently traced the origin of neochrome to hornworts, and showed that ferns acquired neochrome from hornworts via horizontal gene transfer (HGT). Subsequent phylogenetic analyses further revealed a large-scale discordance-- between the fern neochrome gene tree and the fern species tree, suggesting additional HGT occurred among ferns. Here we present new genomic evidence supporting that fern-to-fern neochrome HGT is present and likely rampant. Our finding not only provides the first evidence that a plant-to-plant HGT can have a profound evolutionary impact, but also has implications for the evolution of photosensory systems in plants.

Tempo and mode of anti-bat ultrasound production and sonar jamming in the diverse hawkmoth radiation

Akito Kawahara, Jesse Barber

4A_302A-Macroevolution
Tuesday, June 24, 2014 9:30 AM-9:45 AM

Bat-insect interactions date back millions of years, and the shared evolutionary history between echolocating bats and nocturnal insects have resulted in a suite of unique defensive strategies. Ultrasound production and hearing are two of the most fundamental strategies that nocturnal insects use as protection against bats. However, no research has comprehensively combined behavioral and phylogenetic data to examine how anti-bat ultrasound production, hearing, and jamming have evolved. We recently discovered that large, charismatic hawkmoths produce ultrasound using their genitalia. Here we tested ultrasound production in over 100 species (623 total specimens), and resolve the evolutionary history of hawkmoths by conducting a comprehensive molecular phylogenetic analysis of all subfamilies, tribes, and subtribes. We show for the first time, that ultrasound production in hawkmoths serves to jam bat echolocation, and that jamming has evolved at least two independent times in the family. Divergence time analyses that used multiple calibration points, reveals that anti-bat ultrasound is a relatively new behavior in large moths that first evolved in the mid-late Paleogene, ~30 Mya, after the radiation of insectivorous bats. Ears in hawkmoths evolved secondarily in at least two lineages that have developed the ability to produce ultrasound, implying that sound production might serve to startle predators. Our combined proximate and ultimate analysis of hawkmoths sheds light on the macroevolution of anti-bat ultrasound production in the insect-bat arms race.

The evolution and transcriptional connectivity of genes underlying ant division of labor

Tim Linksvayer

4A_302B-Social Behavior
Tuesday, June 24, 2014 8:30 AM-8:45 AM

Division of labor is a defining feature of eusocial organisms that is thought to underlie their ecological and evolutionary success. Hypotheses for the evolutionary genetic basis of social insect division of labor focus mainly on the simple modification of highly conserved gene networks that directly influence an individual’s physiology and behavior. We studied the degree to which the transcriptional architecture underlying worker age-based division of labor in the pharaoh ant Monomorium pharaonis includes highly conserved genes and tightly connected gene modules. We identified genes and modules of co-regulated genes underlying age-based division of labor among workers, and then estimated rates of molecular evolution at these genes. Altogether, our results suggest that the evolutionary genetic basis of worker division of labor involves combinations of conserved genes and highly connected gene modules, as well as less well-connected modules and more rapidly evolving genes.

Information flow through dominance network in social insect colonies

Anjan Nandi, Annagiri Sumana, Kunal Bhattacharya

4A_302B-Social Behavior
Tuesday, June 24, 2014 8:45 AM-9:00 AM

Social insect colonies are known for their fascinatingly successful social organizations which could be achieved by an effective flow of information through the complex connectivity patterns among the colony members. Network representation of such behavioural interactions offers a powerful tool for structural as well as dynamical analysis of the underlying regulatory systems. In search of the structural design principles that are fundamental to such regulatory systems, we analyze the dominance interaction networks in the tropical social wasp Ropalidia marginata - a species where behavioural observations indicate that such interactions are principally responsible for the transfer of information between individuals about their colony needs, resulting in a regulation of their own activities. Our research reveals that the dominance networks of R. marginata are structurally similar to a class of naturally evolved information processing networks, a fact confirmed also by the predominance of a specific substructure - the 'feed-forward loop' - a key functional component in many other information transfer networks. Further analysis confirms that the networks are sufficiently stable under small fluctuations and yet capable of more efficient information transfer compared to their randomized counterparts. Our results suggest the involvement of a common structural design principle in different biological regulatory systems and a possible similarity with respect to the effect of selection on the organization levels of such systems. The findings are also consistent with the hypothesis that dominance behaviour has been shaped by natural selection to co-opt the information transfer process in such social insect species, in addition to its primal function of mediation of reproductive competition in the colony.

Gene to brain to behavior to fitness: maintaining variation in sociality through avpr1a and OXTR polymorphism in bank voles

Mikael Mokkonen, Esa Koskela, Eija Lönn, Tapio Mappes, Angela Sims, Phill Watts

4A_302B-Social Behavior
Tuesday, June 24, 2014 9:00 AM-9:15 AM

The neuropeptide hormones vasopressin and oxytocin modulate a range of socio-reproductive behaviors important for mammalian evolution. In Microtus voles, the length of the microsatellite locus situated in the arginine vasopressin receptor (avpr1a) 5’ promoter region regulates expression of this gene, but a comparable regulatory system has not been reported for the oxytocin receptor (OXTR), despite the presence of a microsatellite. We initially characterized polymorphic allelic variation in the promoter microsatellites of both OXTR and avpr1a genes on gene expression in the bank vole (Myodes glareolus). By genotyping wild-caught individuals, we artificially bred males and females based on the length of the avpr1a and OXTR microsatellites. We measured their reproductive success and survival in two separate field enclosure experiments (focusing on avpr1a and OXTR respectively), where the social environment was manipulated (density and operational sex ratio, OSR). Our results indicate that the fitness of OXTR and avpr1a genotypes is dependent on the sex and social environment of bank voles. We will discuss how sexually antagonistic selection and density-dependent selection can maintain allelic variation in avpr1a and OXTR by focusing on the gene-to-brain-to-behavior model of sociality in evolution.

The co-evolution of altruism and collective movement

Jaideep Joshi, Vishwesha Guttal

4A_302B-Social Behavior
Tuesday, June 24, 2014 9:15 AM-9:30 AM

Altruism is one of the most puzzling phenomena in evolutionary ecology, because a group of altruists is susceptible to invasion by cheaters. However, altruists can sustain if they interact more often among themselves than with defectors. This condition, called positive assortment, is typically thought to arise due to mechanisms such as kin recognition, limited dispersal, and/or reciprocity.

Even in the absence of the above mechanisms, structured populations of multiple groups/demes may facilitate positive assortment. Across many taxa, collectively moving animals spontaneously form groups that merge and split. Such groups are typically driven by local flocking interactions (such as tendencies to be attracted to and orient with neighbors). In this context, we explore whether dynamic group formation of animal groups can provide a mechanism for positive assortment.

Here, we present an agent-based co-evolutionary model of altruism and collective movement, where each individual possesses two evolvable traits: local flocking tendency, and cooperative/defective tendency. We show that starting from purely solitary defectors, strong altruism can co-evolve with collective movement, resulting in a polymorphic population of altruists and defectors. We find that positive assortment is achieved through differences in the evolved local flocking tendencies of altruists and defectors. The groups exhibit spontaneous self-sorting, as individuals with larger flocking tendency move together more than others.

Beyond aggression: antiandrogen treatment of subordinate males modifies social behavior in wild meerkats

Christine Drea, Javier delBarco-Trillo, Lydia Greene

4A_302B-Social Behavior
Tuesday, June 24, 2014 9:30 AM-9:45 AM

Androgen function is best understood in the context of mediating male reproductive and aggressive behavior, often at the cost of male involvement in parenting or prosocial activity. Among members of social species, testosterone is typically invoked to explain rank-related differences; however, its role within a rank, particularly among subordinates, is underappreciated. We explored the actions of testosterone in subordinate, male members of a cooperatively breeding species, the meerkat (Suricata suricatta). No rank-related testosterone differences have been observed in male meerkats, yet subordinate helpers rarely reproduce and, relative to dominant breeders, perform more infant care. We manipulated testosterone, in the field, by treating well-habituated, subordinate males, in multiple groups, with an antiandrogen (21-day release flutamide pellets, s.c.). During a month of the breeding season in the Kalahari, we monitored androgen concentrations (via baseline serum and time-sequential fecal sampling) and recorded behavior using a focal observation protocol. Relative to controls, flutamide-treated animals initiated less and received more high-intensity aggression (biting, threatening, feeding competition), initiated more prosocial behavior (social sniffing, grooming, huddling), and less frequently assumed the 'dominant' role during social play (pinning while wrestling, play mounting, chasing). Although interfering with the actions of testosterone produced the anticipated depressive effects on aggression, while enhancing prosociality, treatment also revealed rare evidence of testosterone's activational effects on adult play. Despite a focus on 'low-profile' males, our findings show a more pervasive role for androgens in adult social behavior than is traditionally recognized, with possible relevance for understanding tradeoffs in the evolution of cooperative systems. Funded by NSF IOS-1021633.

Convergent evolution of a rare trait: the history of red flowers in Solanaceae

Julienne Ng, Stacey Smith

4A_302C-Plant Evolution
Tuesday, June 24, 2014 8:30 AM-8:45 AM

Angiosperms are known not only for their diversity of flower colors and forms, but also the widespread convergence of independent lineages on similar floral phenotypes. Despite this apparent evolutionary lability, some traits remain exceptionally rare. Using the tomato family (Solanaceae) as a model system, we examine the evolution of one such rarity: red flower coloration. This color is generally rare in angiosperms and accounts for just 1% of Solanaceae species. Using model-based methods that account for branch length, the stochastic nature of evolution, and potential state-dependent diversification, we trace the history of red flowers in Solanaceae and estimate the number of independent transitions. Our results indicate multiple independent origins of red flower coloration via at least three distinct developmental mechanisms. Given the repeated convergent transitions to red flowers via different developmental mechanisms, we suggest that the present day rarity of red-flowered taxa may not reflect evolutionary constraint but instead reduced diversification rates, possibly associated with ecological specialization.

Genome-wide analysis reveals rapid genetic changes in natural Brassica rapa populations following drought

Steve Franks, Nolan Kane, Niamh O'Hara, Silas Tittes, Joshua Rest

4A_302C-Plant Evolution
Tuesday, June 24, 2014 8:45 AM-9:00 AM

Determining the genetic basis of adaptive evolution is a major goal in biology. We analyzed genome-wide genetic differences between ancestors and descendants of natural populations of Brassica rapa that previously evolved changes in multiple phenotypic traits following drought. Site frequency spectrum analyses revealed several locations in the genome with evidence of recent soft selective sweeps in descendants. We found many genes with outlier FST values between ancestors and descendants. Several of these genes have functions related to traits like stress response and flowering time that make them particularly likely targets of recent selection by drought. The changes in allele frequencies that we found at many loci provide definitive evidence of genetically-based rapid evolution in these natural populations. Our results suggest that these evolutionary changes were driven by selection acting on standing variation in multiple genes underlying traits of adaptive significance.

LARGE-SCALE ADAPTIVE DIVERGENCE IN BOECHERA FECUNDA, AN ENDANGERED WILD RELATIVE OF ARABIDOPSIS

Bao-Hua Song, Larry Leamy, Cheng-Rui Lee, Vanessa Cousins, Ibro Mujacic, Antonio Manzaneda

4A_302C-Plant Evolution
Tuesday, June 24, 2014 9:00 AM-9:15 AM
Many biological species are threatened with extinction because of a number of factors such as habitat loss, and their preservation depends on an accurate understanding of the extent of their genetic variability within and among populations. In this study we assessed the quantitative genetic divergence in 10 populations of an endangered cruciferous species, Boechera fecunda, restricted to two geographical regions (WEST and EAST) in western Montana. Heritabilities estimated from nested ANOVAs were generally high for leaf and rosette traits, but quite low and non-significant for water use efficiency (WUE). Genetic coefficients of variation were high for all traits, indicating ample existing genetic variability. Measures of quantitative genetic differentiation, QST, were calculated for each trait from each pair of populations. For four traits, these values were significantly higher for populations between regions compared to those within regions (even after adjustment for neutral genetic variation), supporting that natural selection has acted to produce regional divergence in this species. Our analysis also revealed that the B. fecunda populations are locally adapted to specific environmental conditions in the EAST and WEST regions, especially measures of precipitation. Conservation efforts for B. fecunda therefore should be directed to the preservation of populations in each of these two regions without attempting transplantation between regions.

Evolution of Crassulacean acid metabolism in the Agavoideae

Karolina Heyduk, Michael McKain, Jim Leebens-Mack

4A_302C-Plant Evolution
Tuesday, June 24, 2014 9:15 AM-9:30 AM
Crassulacean acid metabolism (CAM) is an adaptive mode of photosynthesis that has evolved at least 35 times independently across flowering plants. Plants which exhibit CAM are largely found in arid or water-stressed habitats, where high transpiration rates during the day result in stomatal closure and a drop in carbon uptake. To accommodate their arid lifestyle, CAM plants have a temporal regulation of gas exchange, whereby they open their stomata for carbon uptake a night, when transpiration rates are lowest. Carbon is stored as malic acid in leaves until the daytime, when stomata close and CO2 is released around RuBisCO, increasing the carboxylation efficiency of the enzyme while conserving water. Understanding the evolution of CAM as a modified photosynthetic process will shed light on the causes and consequences of CAM evolution on speciation rates and biogeography. Here, we examine the repeated evolution of CAM in the subfamily Agavoideae (Asparagaceae, Asparagales). This subfamily consists of familiar genera like Agave and Yucca, and shows evidence of at least three gains and/or losses of CAM. Using a sequence capture approach that estimates evolutionary histories from nearly 100 genes, we created a robust phylogeny of the subfamily using more than 60 species. Photosynthetic pathway was mapped onto the phylogeny and was used to find relationships between CAM, biogeography, and rates of evolution. Molecular evolutionary analyses were performed on key genes for CAM functionality to assess whether repeated CAM evolution shows parallel molecular and functional changes in gene sequences. By pairing novel phylogenomic methods with character trait assessment, we have a better sense of the impacts of this novel trait on the evolutionary history of Agavoideae species.

Shoot development, life history trade-offs, and perenniality in Arabidopsis lyrata

David Remington

4A_302C-Plant Evolution
Tuesday, June 24, 2014 9:30 AM-9:45 AM
Perenniality in plants can be interpreted in terms of the balance between production and consumption of meristems or other resources. Among perennials, this balance is manifest as trade-offs between growth and reproduction. The perennial Arabidopsis lyrata is an ideal system for studying these processes due to its wide genetic variation in resource allocation and its close relationship to the annual A. thaliana. We previously found that resource allocation differences between divergent Norway and North Carolina populations result from cascading effects of QTLs affecting early development, and do not involve direct costs of reproduction. To investigate these developmental differences in more detail, we collected shoot-development data on plants from both populations growing under controlled conditions. We hypothesized that trade-offs occur under a simple model in which pre-reproductive vegetative development of lateral meristems precluded reproductive transition during the same growing season. Instead, our results showed that individual shoots underwent vegetative-to-reproductive transitions, but Norway plants produced more rosette leaves per shoot before the reproductive transition than North Carolina plants. Plants producing more rosette leaves per shoot produced fewer inflorescences, and these effects were sufficient to explain the reduced reproductive output in Norway plants. These data suggest that trade-offs result largely from delays in reproductive transition at the individual shoot level, involving allocation of limited growing-season time rather than meristem fates per se. Implications for understanding local adaptation to climatic conditions will be discussed.

Does religion or education matter more when predicting university students' understanding of evolution?

Leslie Rissler, Sarah Duncan, Nicholas Caruso

4A_303-Education
Tuesday, June 24, 2014 8:30 AM-8:45 AM
There is much opposition to evolution in the public sphere, especially in America. The strong and negative correlation between belief in a god and acceptance of evolution across the world suggests that religiosity may drive some of the resistance to evolution. There is also clear evidence that as scientific education increases, acceptance of evolution increases and religiosity decreases; this has been shown at the individual, state, and country levels. However, little is know about college students' views on evolution. We used a 34-question survey of 2,999 students at a major research institution in the Deep South to assess

how education and religion impact knowledge and acceptance of evolution. Using Structural Equation Modeling (SEM) we show that religiosity is strongly and negatively correlated with the Measure of Acceptance of the Theory of Evolution (MATE) scores. Academic level, major (science vs. non-science), and high school education are positively correlated with the MATE scores but much less important in the overall model than religion. We also find that if students were taught creationism or creationism and evolution in high school, their MATE scores as seniors are significantly lower than those students who were taught nothing. We also surveyed three different biology courses to determine Pre- and Post-class MATE scores, and we find that MATE scores do improve with instruction but that improvement depends on the degree of religiosity. Students who seldom/never attend church were the ones that had the highest MATE scores and the most improvement. We discuss these results in relation to other studies and geographic regions, and we reflect on what this means for improving science education.

Forest vs. trees: does it matter whether the MATE measures student acceptance of, rather than understanding about, evolutionary theory?

Matthew Rowe, Marcus Gillespie, Li-Jen Shannon, Steven Koether, Lori Rose

4A_303-Education
Tuesday, June 24, 2014 8:45 AM-9:00 AM
The tool most often used to determine whether students accept the explanatory power of the Theory of Evolution is the 20-question Likert-scale Measures of the Acceptance of Evolutionary Theory, or MATE. This survey has recently been criticized, in part because it may not be a valid assessment for all populations, but more centrally because it may measure how well students understand the theory of evolution, rather than accepting it as the best explanation for the diversity of life. Numerous studies, including our own, have demonstrated the ineffectiveness of general education science courses at improving student critical thinking (CT) skills in general, and their understanding of basic explanatory theories in the sciences, including evolution, in particular. We have previously reported how a novel experimental approach to teaching a gen-ed science course can help students improve their CT skills while also demonstrating improved scores on the MATE. We here update those results. Specifically, we show that it simply does not matter how many gen-ed science courses a student takes in terms of their performance on the MATE. That is, students who have completed a one, two, three, or four “typical” gen-ed science courses show absolutely no improvement in their MATE scores, underscoring a pedagogical weakness of such courses. A class designed, however, to help students understand the Nature of Science leads to significant improvements in both their CT skills and their performance on the MATE. We argue that such improvements are the forest, while arguing about the semantics of “acceptance” vs. “understanding” are the trees; if we hope to generate a cohort of scientifically literate college graduates, citizens who will fight to prevent the teaching of pseudoscientific nonsense in their public schools, it would be unfortunate if we abandon the MATE because it measures changes in understanding rather than in attitude.

Assessing student perceptions and explanations of microbial evolution

Alita Burmeister, Richard Lenski, Jim Smith

4A_303-Education
Tuesday, June 24, 2014 9:00 AM-9:15 AM
Evolution is a core concept for biological literacy at the undergraduate level. However, evolution is often overlooked in microbiology classrooms. Evolution instruction especially lags in laboratory-based courses where the inertia is strong due to efforts involved in revising curricula. We used a theme of antibiotic resistance and evolutionary applications in an upper-level undergraduate microbial genetics laboratory course with the goals of (1) increasing students’ ability to explain the details of evolutionary microbial genetics and (2) increasing students’ acceptance and value of microbial evolution. We presented core concepts and applications of microbial evolution during the course’s weekly lecture. One half of the class also completed a three-week E. coli evolution experiment (“treatment” group) while the other half completed only the traditional exercises (“control” group). We assessed the effectiveness of these activities using pre and post attitude surveys and open-ended content questions about microbial variation, inheritance, and selection. Students in both groups highly accepted and valued microbial evolution at the beginning of the semester and had slight, but generally nonsignificant, positive attitude gains at the end of the semester. Surprisingly, scores on the content questions did not improve by the end of the semester for either group. We attribute this in part to a lack of grade-based incentives and students’ seemingly less earnest attempts on the post assessment. Of greater interest to microbial evolution curricula and assessment, we also observed the potential for traditional microbiological instruction to inadvertently reinforce misconceptions and confound definitions of the key terms “variation” and “selection.” To develop suggestions for teachers to avoid these issues, we continue to investigate subdiscipline-specific definitions and language use. This study highlights the persistent need for microbial evolution education tools.**What is this gorilla doing in my gene pool? Using trans-specific polymorphisms as a case study in evolution education.**

Norman Johnson, James Smith, Ryan Gregory

4A_303-Education
Tuesday, June 24, 2014 9:15 AM-9:30 AM
Some genes exhibit an unusual pattern in which alleles from one species (e.g., human) may be more closely related to alleles from another species (e.g., chimpanzees or gorillas) than they are to other alleles of the same species. This phenomenon, called trans-specific polymorphism (TSP), is counter-intuitive, even shocking - what is a gorilla allele doing in our gene pool? Nevertheless, TSPs arise from evolutionary processes.

Indeed, we argue here that using TSPs as a case study can be an effective tool in teaching evolutionary genetics, as this phenomenon ties together many concepts from the subfields of from population genetics, phylogenetics, and molecular genetics into a single interesting and coherent story. Such a case study of TSPs can also be used as an example of how we answer questions and test alternative hypotheses in evolutionary biology. As a bonus, using TSPs as a case example deepens and reinforces students' appreciation for the evidence for evolution – how else could polymorphisms that extend beyond species' boundaries be explained but as the result of shared ancestry?

Here, we begin with the case of TSPs in the MHC loci. We explore and work through alternative hypotheses that could explain the phenomenon, explaining the evidence and logic that would cause us to accept or reject alternative hypotheses. Along the way, we cover the main concepts relevant to explain the evolutionary principles that underlie this unusual pattern. Among the concepts are those of phylogenetics and tree thinking, the processes behind how polymorphisms arise and are lost (mutation, random genetic drift and effective population size, and the different types of natural selection), and hybridization and gene transfer between species.

Teaching teachers to teach evolution: An idiot's guide

Becky Fuller

4A_303-Education
Tuesday, June 24, 2014 9:30 AM-9:45 AM
Recent polls indicate that less than half of the U.S. population accepts evolution as scientific fact. Studies also indicate that teacher training in science and evolution can potentially increase teacher effectiveness in teaching evolution in the K-12 classroom. At the University of Illinois, we have implemented a 3-day summer teacher workshop in evolutionary biology. Our workshop has three main goals. Our first goal is to increase teacher knowledge and confidence in evolution. To do this, we discuss the book 'Why Evolution is True' by Jerry Coyne as well as the Discovery Institute's response 'Why Darwinism is False' by Jonathan Wells. The goal with these readings is to make teachers aware of the fallaciousness of the arguments posed against evolution. Our second goal is to equip teachers with activities that they can use in their classrooms. To achieve this goal, we do a number of activities with the teachers including the toilet paper timeline of evolution, the great clade race, the Guppy Game, and a BLAST activity using hemoglobin. Our third goal is to provide teachers with examples of current research in evolutionary biology. To do this, we employ a number of lunchtime speakers that present results from their ongoing research.

While our teacher workshop is very successful in many ways, there are things that can be done to increase its effectiveness. In this talk, I will present results from teacher surveys relating to (a) the strengths and weaknesses of our workshop and (b) the extent to which our activities were implemented into the K-12 curriculum. I will also present results on what teachers want and what education experts tell us we need to do to increase the efficacy of our outreach efforts.

Origin and biogeographic relationships of the Southern Appalachian Flora

Paul Manos, Jose Eduardo Meireles

4A_305A-Phylogenetics and Diversification
Tuesday, June 24, 2014 8:30 AM-8:45 AM
The rich flora of the Southern Appalachian provides a natural experiment for understanding how one of the major refuges of temperate biota has evolved over the last 60 million years. We investigated the biogeographic origins and patterns of whole-flora assembly for 252 woody species representing 157 North American seed plant clades. We tested the hypothesis that intercontinental disjunctions occurred during two main periods of geologic history. A literature survey was used to build a phylogenetically-informed database to identify patterns of biogeography and diversification. We generated a list of area connections for all clades, and derived graphic representations of the dynamic of changing area connections and contributions at increasing phylogenetic depth. Species diversity within clades was estimated and plotted relative the number of clades that contain disjunctions to Eurasia, and divergence time data were plotted for key nodes between North American and Eurasian sister clades, and between areas within North America. Southern Appalachian species share equal numbers of sister area connections between Eastern North America and Eastern Asia. Quantification of the overall pattern of diversity across North American clades showed that less than 25% of these clades contribute significantly to adjacent regional floras. At increasing phylogenetic depth, sister clades relationships with Eurasia dominate the biogeographic pattern, with connections to the component area of Europe increasing in contribution. Divergence time data for 60 clades showed that Eastern North America and Eurasian disjunctions occurred continuously throughout the Cenozoic.

Resolving the phylogenetic relationships of the carnivorous plant genus Sarracenia using gene target enrichment

Jessica Stephens, Willie Rogers, Karolina Heyduk, Ron Determann, Jenny Cruse-Sanders, Russell Malmberg

4A_305A-Phylogenetics and Diversification
Tuesday, June 24, 2014 8:45 AM-9:00 AM
The adaptation of plant carnivory to survive in nutrient poor habitats has evolved at least six times in flowering plants. While phylogenies currently exist for many of these groups, the evolutionary relationships of one of the more well studied carnivorous plants, Sarracenia, remain largely unclear. Previous attempts at constructing a phylogeny for the genus have been unable to resolve polytomies, most likely due to a recent adaptive radiation compounded with frequent ongoing hybridization between species. Together these processes can result in high levels of gene tree discordance more frequently than expected. Multilocus data can mitigate these issues; increasing the numbers of loci sequenced is expected to lead to more precise model parameters and therefore increase nodal support values in phylogenetic analyses. Here, we used target enrichment of 287 genes across 71 accessions of the genus, representing the 11 species listed in Mellichamp and Case (2009), and a combination of 10 putative infraspecific taxa listed by Mellichamp and Case (2009) and McPherson and Schnell (2011), and 2 outgroups within the family Sarraceniaceae on an Illumina HiSeq platform. Species tree

estimations were conducted using multiple phylogenetic analyses (e.g. MP-EST, STEM-hy, *BEAST). Results from these coalescent approaches show support for many of the relationships within the genus with high resolution. Specifically, the genus consists of two subclades. The first subclade comprises S. purpurea, S. rosea, S. minor, S. psittacina, and S. flava, with the last two as sister taxa which supports previous results. Sarracenia oreophila, S. alata, S. leucophylla, S. alabamensis, S. jonesii, and S. rubra comprise the second subclade. The Sarracenia purpurea complex is monophyletic, while many accessions of the Sarracenia rubra complex (i.e. S. rubra ssp. gulfensis and S. rubra ssp. wherryi resulted in a polytomy with S. alata this may be due to hybridization or possibly incomplete lineage sorting within the S. rubra complex. Understanding these relationships can better facilitate future research on the evolution of carnivory. In addition, this study highlights the use of multilocus data and multiple accessions in elucidating evolutionary relationships among recently radiated or hybridizing taxa.

Museum specimens illuminate paraphyly within the Asiatic striped squirrels (genus Tamiops).

Melissa Hawkins, Jennifer A. Leonard, Kristofer M. Helgen, Gavin Perri, Jesus E. Maldonado

4A_305A-Phylogenetics and Diversification
Tuesday, June 24, 2014 9:00 AM-9:15 AM

The Asiatic striped squirrels of the genus Tamiops belong to a highly diverse group of sciurids in the subfamily Nannosciurinae with over 60 recognized species. This genus is composed of small striped arboreal squirrels that are widely distributed across SE Asia and occupy a diversity of habitats from lowland to montane forests (up to 4,000 meters in the Himalayan mountains). Four species are currently recognized in the genus (T. mcclellandii, T. rodolphii, T. swinhoei and T. maritimus), although recent molecular work revealed that six populations within the T. swinhoei-maritimus species complex were highly differentiated and may represent different species. In this study, we generated a phylogeny using whole mitochondrial genomes for representative populations from all four species of Tamiops from museum specimens. Our results revealed that the remaining two species (T. mcclellandii and T. rodolphii) were also paraphyletic in our analyses. No currently recognized species in the genus formed a monophyletic group. This is in agreement with previous research that found incongruent phylogenies generated from autosomal versus mitochondrial genes. Our data is thus compatible with the hypothesis that historical mitochondrial introgression events generated this pattern throughout the genus. However, the timing of these events remained unresolved and in this study we combined both mitogenomic and morphological data to attempt to clarify the species boundaries in all species of Tamiops. We used the program BEAST to date the mitochondrial divergence between and within species. Additionally, morphological measurements and pelage characteristics were studied in 140 museum specimens to evaluate if intermediate phenotypes occur, or if the incongruent mitochondrial lineages represent ancient introgression events.

Our results indicate that the speciation process in this genus involved ancient mitochondrial capture/introgression resulting in the pattern observed today. Additionally, nuclear DNA will be necessary to more clearly delineate species of Tamiops, drawing on a large number of samples from across each species' range.

RNA-seq reveals strong evidence of positive selection and gene expression differences over 20 million years of evolution in Heteromyid rodents

Nicholas Marra, J. Andrew DeWoody

4A_305A-Phylogenetics and Diversification
Tuesday, June 24, 2014 9:15 AM-9:30 AM

When populations evolve under disparate environmental conditions, they experience different selective pressures that shape patterns of sequence evolution and gene expression. These, in turn, may be manifested in genetic and phenotypic differences between species. For instance, water scarcity may drive adaptations for efficient osmoregulation in desert species that are relaxed or absent in related species from mesic habitats. Desert rodents have been shown to have an extraordinary ability to retain water during waste production. Although much is known regarding the unique kidney physiology of kangaroo rats (Dipodomys spp.) and their ability to retain water during waste production, the genetic basis of these physiological adaptations to desert life is relatively unknown. Here, we utilized RNA-seq data to conduct a comparative study to identify osmoregulatory genes expressed in Heteromyid rodents. We sequenced kidney tissue from two temperate desert species (Dipodomys spectabilis and Chaetodipus baileyi) from two separate subfamilies of the Heteromyidae and compared these transcriptomes to a tropical mesic species (Heteromys desmarestianus) from a third subfamily. The evolutionary history of these subfamilies provided a robust phylogenetic control that allowed us to separate shared evolutionary history from convergence. Using two methods to detect differential expression (DE), we identified 1,890 genes that showed consistent patterns of DE between the arid and mesic species. A three-species, reciprocal BLAST analysis revealed 3,511 sets of putative orthologues that, upon comparison to known Mus musculus sequences, identified 323 annotated and full-length genic regions. Selection tests displayed evidence of positive selection (dn/ds >1) on 6 genes in the two desert species and remained significant for one of these genes after correction for multiple testing. Additionally, we took advantage of the geographic distribution of these species to explore whether species from tropical latitudes have a more diverse immunogenetic repertoire due to exposure to greater parasite burden. To test this idea we compared the spleen transcriptomes of the tropical species (H. desmarestianus) to the two temperate species. In this comparison we identified 632 genes that were consistently upregulated in H. desmarestianus and 492 genes that were consistently downregulated in H. desmarestianus. Additionally, we found some evidence of immune related gene ontology terms that were overrepresented in H. desmarestianus. Thus we find consistent differences in evolution of genes expressed in two tissues. Due to strong natural selection in disparate environments, these genes have evolved differently in related species in terms of expression levels and/or nucleotide sequence.

Phylogeography and speciation of Pitcairnia flammea (Bromeliaceae) adapted to Neotropical rock outcrops

Clarisse Palma-Silva, Carla Sardelli, Mateus Ribeiro Mota, Carolina da Silva Carvalho, Juliana Santin, Felipe Aoki-Gonçalves

4A_305A-Phylogenetics and Diversification
Tuesday, June 24, 2014 9:30 AM-9:45 AM

In Neotropics the isolation and ancient age of the rock outcrops is reflected in the high number of endemic species. Because of their fragmented nature, species adapted to rock outcrops are interesting models for studying the evolutionary consequences of limited gene flow among disjoint populations. Pitcairnia flammea (Bromeliaceae) is adapted to rock outcrops (inselbergs), within the Atlantic rainforest. This wide-range species possess huge morphological variability with at least seven recognized varieties occurring in allopatry and/or sympatry. The divergence time of these lineages; demographic events that shaped the contemporary genetic structure; and patterns of gene flow among the naturally fragmented populations, were investigated by characterizing the population genetic structure revealed by uni and biparental molecular markers. We observed a latitudinal gradient in genetic diversity from south to north of the species distribution. This pattern is in opposite to observed for dwelling-forest species in the same geographical region. P. flammea populations are genetically structured, suggesting restricted pollen and seed dispersal, and consequently strong role of drift in evolutionary history of these naturally fragmented populations. We identified bottlenecks in recent past for all populations studied. These results indicate the Neotropics has a mosaic of patterns pointing to highly complex processes responsible for its astonishing species diversity. Financial Support: FAPESP, CNPq, CAPES

Climate change driven vicariance of Appalachian Trees

Jose Eduardo Meireles, Paul Manos

4A_305B-Phylogeography
Tuesday, June 24, 2014 8:30 AM-8:45 AM

Although the shared history between Eastern North American and Eastern Asian forests is one of the most striking biogeographic patterns of the Northern Hemisphere, its origins remain poorly understood. Most previous studies have focused on distinguishing between different connection routes and were based on either relatively few clades or taxonomic information from floristic surveys. The increasing availability of time calibrated trees along with species geographic distribution and global paleoclimatic data presents a unique opportunity to dissect not only the timing of these disjunctions, but also which factors influence the biogeographic dynamics of Northern temperate forests. Here we integrate time-calibrated phylogenies of 60 flowering plant clades, current species niches and paleoclimatic data to draw inferences on the drivers of the biogeographic history of the Appalachian woody flora. We show that historic climate change was the main factor of the biogeographic dynamics, and that clades with different temperature niches responded differently to the same paleoclimatic changes. Using a survival Bayesian model we determined that departures from a clades' inferred 'temperature optimum' increased its risk of undergoing vicariance. Our work highlights the importance of taking organismal ecology into account in order to estimate meaningful biogeographic dynamics.

Does dispersal ability affect the spatial organization of geographic ranges?

Dominic Evangelista, Jessica Ware

4A_305B-Phylogeography
Tuesday, June 24, 2014 8:45 AM-9:00 AM

Speciation patterns, habitat selection, and inheritance of range features all contribute to how closely related species are organized in space. Another biological trait, dispersal ability, is indeed important to individuals but its effect on large scale patterns of biodiversity is contentious. We examined how dispersal ability correlated with range clustering in insect and vertebrate taxa of the Guiana Shield. The Guiana Shield is a region where large waterways have been shown to be important boundaries for animal dispersal, but the degree to which these boundaries are effective at determining animal distributions should vary by a taxon's ability to disperse across it. Therefore, we predicted that, among closely related species, weakly dispersing taxa will show spatially clustered distributions more often than in strongly dispersing taxa. We tested this by comparing actual distributions to random Poisson distributions and comparing aggregate results. Our two major findings are that: (1) levels of spatial clustering vary significantly among taxa with different dispersal paradigms, and (2) dispersal ability does not correlate with differences in spatial clustering of taxa. Given these findings, we believe that organismal specific traits (e.g. niche, evolutionary history) are more important in determining these patterns because of a disparity in relavent temporal scales and an inability to standardize definitions of dispersal ability.

Phylogenetic and environmental controls on the geographic range dynamics of woody plants since the Last Glacial Maximum

Paul Harnik, Hafiz Maherali, Paul Manos, Joshua Miller

4A_305B-Phylogeography
Tuesday, June 24, 2014 9:00 AM-9:15 AM

The size and location of a taxon's geographic range is dynamic - contracting, expanding, or shifting in location over time in response to changes in suitable environmental and ecological conditions. Despite this lability, some previous comparisons across lineages have found that range sizes are conserved, or more similar among closely-related than distantly-related taxa. Such similarities are unexpected under an allopatric model of speciation which predicts asymmetric range sizes between sister taxa at least early in their histories. However, conservatism in life history traits may counteract such asymmetry, particularly if closely-related taxa share dispersal traits which make them either "rapid expanders" or "slow movers". Here we assess whether geographic range is conserved by focusing on the phylogenetic structure of geographic range shifts among woody plants in eastern North America following the Last Glacial Maximum using a molecular phylogeny and geographic data from the pollen fossil record. We find that the velocities with which woody plant genera shifted their range limits between 16-10 ka were positively correlated over time - i.e., lineages that moved further in one interval also tended to move further in subsequent intervals – with the strength of this correlation weakening towards the present-day (16 ka) intervals of time. Lastly, we assess the phylogenetic structure of life history traits and their correlation with biotic velocities.

Molecular phylogeny and historical biogeographic reconstructions onto shifting continents in the cockles and giant clams (Bivalvia: Cardiidae)

Nathanael Herrera, Jan Johan ter Poorten, Paula Mikkelsen, Rüdiger Bieler, David Jablonski, Scott Steppan

4A_305B-Phylogeography
Tuesday, June 24, 2014 9:15 AM-9:30 AM

Reconstructing historical biogeography of the marine realm is complicated by indistinct barriers and over the deeper time scales relevant to major clades, a dynamic landscape due to plate tectonics. Here we report a large-scale synoptic phylogeny for the marine bivalve family Cardiidae (cockles and giant clams) and an examination of patterns of diversification across the marine realm. We analyzed nuclear Histone 3 and 28S and mitochondrial 16S for 110 species representing 37 of the 44 recognized genera and all eight extant subfamilies. Lineage divergence times were estimated using a Bayesian approach and 13 well documented fossil calibrations. Ancestral geographic ranges and range expansions/dispersals were reconstructed using the dispersal-extinction-cladegenesis (DEC) method with a stratified paleogeographic model in which dispersal rates were scaled according to area connectivity, with this connectivity varying according to shifting tectonics across three time slices. The resulting topologies are compared to previous anatomical and molecular findings. We confirm the monophyly of only two subfamilies, Tridacninae (giant clams) and Clinocardiinae, and found rampant paraphyly/polyphyly in the other six subfamilies. The Cardiidae seem to have originated in the tropical Indo-Pacific some time in the early Cretaceous and diversified within the tropical Pacific. The extant diversity seen in the Atlantic is derived from species that dispersed from the tropical Indo-Mediterranean region during the Cenozoic via the Tethys Sea. Contrary to some other clades, the western Atlantic fauna are derived from Indo-Pacific clades rather than western Atlantic, despite a narrower Atlantic during the dispersal events. Finally, we test the accuracy of DEC biogeographic reconstructions with the extensive fossil record of these clades.

Resolving Intralocus Sexual Conflict: results of a long-term selection experiment in Drosophila melanogaster.

Andrew Stewart

4A_306A-Sex and Evolution
Tuesday, June 24, 2014 8:30 AM-8:45 AM

Intralocus sexual conflict (IASC) occurs due to the expression of sexually antagonistic alleles: those that increase fitness when expressed in one sex, but decrease fitness when expressed in the other sex. This genetic conflict is expected whenever the sexes are selected toward differing phenotypic optima for a trait that has a positive genetic correlation between the sexes. IASC can be resolved, when the intersexual genetic correlation for the trait in question is reduced or eliminated. While IASC has been documented in a wide variety of traits among many taxa, there is little extant data indicating whether this conflict is rapidly resolved, or persists for long periods of evolutionary time. Here we report the results of long-term selection experiment in Drosophila melanogaster, where the sexes were antagonistically selected on for body-size (males=larger; females=smaller). Despite ample genetic variation for body-size in both sexes, no IASC resolution was observed after 100 generations of selection, indicating that IASC can act as a long-term impediment to adaptation. However, after an additional 50 generations of selection, substantial resolution was observed in both the selection lines (although to differing degrees), confirming that resolution was, in fact, possible for this trait.

Evolutionary capacitance in sex determination

Paul Sequeira, Yen-Shan Chen, Joseph Racca, Nelson Phillips, Michael Weiss

4A_306A-Sex and Evolution
Tuesday, June 24, 2014 8:45 AM-9:00 AM

The heterogametic XY sex chromosome pair determines male development in therian mammals. A Y-chromosome linked gene, Sry, encoding an architectural transcription factor, initiates the male-specific gene-regulatory network leading to the male phenotype. Reduced transcriptional activity of human SRY below a critical threshold causes 46, XY gonadal dysgenesis and in turn somatic sex reversal. Atypical Sry genes found in the rodent superfamily Muroidea possess a microsatellite-encoded tail domain that functions to buffer variation in the rest of the protein. The DNA microsatellite is analogous to a capacitor as it stores charge (genetic variation) in an electrical circuit. Loss of the tail domain through microsatellite instability (discharge of the capacitor) can reduce the tail length below its functional threshold and thereby unmask accumulated variation in the Sry protein—engendering developmental chaos in gonadogenesis. A model for studies of this evolutionary mechanism is provided by the grass mice of genus Akodon, whose species-specific Sry variant contains a foreshortened tail associated with reduced transcriptional activity. Notably, several Akodon species have a high proportion of fertile XY females in wild populations. We propose that Akodon Sry offers a snapshot of rapid evolution following discharge of this microsatellite-derived genetic capacitor. We envisage that more extreme divergence of sex-determination systems in Muroidea, including loss of Sry and even the entire Y chromosome, is a direct consequence of microsatellite instability unique to this taxon of mammals.

Fight fire with fire: Redirected meiotic drive in Drosophila affinis subgroup

Spencer Koury, Ryan Mulqueen

4A_306A-Sex and Evolution
Tuesday, June 24, 2014 9:00 AM-9:15 AM

Fisherian sex ratios are the general rule in biology. Fisher proposed that independent of the mating system or sex determination system, strong frequency dependent selection will always favor even sex ratios in panmictic populations. Thus, any genetic tendency towards producing one sex will not be advantageous in the long run. However, sex chromosome meiotic drive, where males carrying the sex-ratio locus on the X chromosome (XD) have predominately female offspring, is commonly observed in the Drosophila obscura group. The persistence of XD chromosomes causes long-term intragenomic conflict favoring the evolution of suppressors to restore even transmission of X and Y bearing gametes. The Drosophila affinis subgroup is particularly notable for its multiple XD chromosomes and suppression associated Y chromosome polymorphism. Even more surprising is the phenomenon of redirected drive, where males carrying the XD chromosome with a particular genetic background have predominately male offspring, reversing the phenotypic effect of the sex-ratio locus. Redirected drive has only been documented in D. affinis and was previously shown to be the result of another anomaly in this species, XO male fertility. I present evidence for redirected drive in the closely related species D. athabasca where XO males are sterile. Experimental crosses are consistent with an autosomal recessive gene interacting with the XD chromosome to cause redirection of the sex chromosome drive. Using population genetic models I evaluate the conditions for selective maintenance of polymorphism at this autosomal locus. This work demonstrates that even though Fisher's Principle may predict long-term evolutionarily stable states, transient phases of sex ratio distortion can have major impact on maintenance of genetic polymorphism and genome evolution.

Neo-sex chromosomes in Habronattus jumping spiders: fusions, chiasma localization, and sexual conflict

Wayne Maddison, Geneviève Leduc-Robert

4A_306A-Sex and Evolution
Tuesday, June 24, 2014 9:15 AM-9:30 AM

Chromosome fusions are rarely found in entelegyne spiders, a pattern which has been attributed to an evolutionary constraint caused by their proximal chiasma localization. However, some Habronattus species deviate from this pattern by having neo-Ys produced by fusions between an X chromosome and an autosome. Among the 72 species of Habronattus studied, 47 have XX0 sex chromosomes in males (the ancestral state for the family), 10 have XXY, and 15 have XXXY. The phylogeny indicates that neo-Ys (XXY or XXXY) have evolved 8-15 times in this group, a remarkable number for a clade this size. The origin of the neo-Y in Habronattus is correlated with more distal chiasmata, representing the release of the hypothesized proximal chiasma localization constraint. Although the release of this constraint would permit these fusions to occur, it does not explain why X-autosome fusions are favored while autosome-autosome fusions remain rare. Sexual conflict between alleles of the same locus may favor fusions that isolate male-favored alleles on the neo-Y. This intralocus sexual conflict hypothesis could explain both the many X-autosome fusions, and the stunning complexity of male Habronattus courtship displays.

Intragenomic conflict over sex ratio in a moss

Stuart McDaniel, Jose Miguel Ponciano, Adam Payton

4A_306A-Sex and Evolution
Tuesday, June 24, 2014 9:30 AM-9:45 AM

Population genetic theory is built on a foundation of Mendelian segregation. The success of this theory tells us that, in general, each allele at a heterozygous locus has an equal chance of being transmitted from one generation to the next. Striking exceptions to this generality are well known, in which nearly all of the offspring inherit a distorter allele, but these cases are seldom expected to be polymorphic. In contrast to this expectation, a few recent studies report subtle but persistent deviations from 1:1 meiotic segregation ratios in natural populations, suggesting that our knowledge of the distribution of segregation distortion may be biased toward strong drivers with major fitness effects. Here we generated meiotic sex ratio estimates for two populations of the dioecious moss Ceratodon purpureus. Using a general hierarchical likelihood model we found an overall male-biased sex ratio and significant genetic variation for offspring sex ratio in both populations. Furthermore, we found a positive association between a male-biased sex ratio and total spore production, pointing to a previously unexplored genetic correlation between meiotic sex ratio and resource allocation between maternal gametophytes and their nutritionally dependent offspring sporophytes. If frequent across the genome, weak distorters such as these could make a major contribution to the maintenance of polymorphism for fitness, the genomic architecture of recombination, and the evolution of reproductive isolation.

Convergent evolution of alternative developmental trajectories associated with diapause in African and South American killifish

Andrew Furness, David Reznick, Mark Springer, Robert Meredith

4A_306B-Evolution and Development
Tuesday, June 24, 2014 8:30 AM-8:45 AM

There are several contrasting views of conservation during vertebrate embryology. One view is that early development is conserved because it cannot readily be changed without disrupting later development. In contrast, Darwin argued that all stages of development are potentially subject to adaptive diversification, but early development tends to be conserved because embryos reside in an egg or their mother's womb and hence are not exposed to strong selection. Raff's hourglass model represents a sort of compromise between these views; it accommodates known diversity in early development owing to different egg types and starting material, but retains the notion of developmental constraint and hence conservatism with respect to a mid-embryogenesis phylotypic period, characterized by the patterning of the main features of the adult body plan. Short-lived annual killifish enable us to contrast these different models, and support Darwin's view of embryology. Annual killifish are adapted to life in seasonally ephemeral water-bodies and persist through the production of desiccation resistant eggs that undergo long periods of diapause, or developmental arrest, enabling them to traverse the inhospitable dry season. Environmental cues that indicate the season govern whether eggs enter a stage of diapause mid-way through development or skip this diapause and are 'direct-developing'. We report, based on construction of a supermatrix phylogenetic tree of the order Cyprinodontiformes and a battery of comparative analyses, that the ability to produce diapause eggs evolved independently at least six times within African and South American killifish. We then show that in species representative of these lineages, embryos destined to enter diapause display significant reduction in development of the cranial region and circulatory system relative to direct-developing embryos. This divergence along alternative developmental pathways begins mid-way through development, well before diapause is entered, during a period of purported maximum developmental constraint (the phylotypic period). Finally, we show that entering diapause is accompanied by a dramatic reduction in metabolic rate and concomitant increase in long-term embryo survival. Morphological divergence during the phylotypic period thus allows embryos undergoing diapause to conserve energy by shunting resources away from energetically costly organs (brain and heart) thereby increasing survival chances in an environment that necessitates remaining dormant, buried in the soil, and surrounded by an egg shell for much of the year. Our results indicate that adaptation to seasonal aquatic environments in annual killifish imposes strong selection during the embryo stage leading to marked diversification during this otherwise conserved period of vertebrate development.

Shifts in the Expression of Developmental Regulatory Genes Involved in the Evolution of a Novel Life History Difference

Jennifer Wygoda, David McClay, Greg Wray

4A_306B-Evolution and Development
Tuesday, June 24, 2014 8:45 AM-9:00 AM

Developmental mode can influence dispersal, gene flow, speciation and extinction rates in marine taxa and thus can have important consequences for micro- and macroevolutionary processes. While the ancestral developmental mode of sea urchins is indirect through a feeding larval stage (planktotrophic), non-feeding development (lecithotrophic) has evolved independently multiple times. In order to identify evolutionary changes in gene expression underlying this ecologically significant shift in life history, we used Illumina RNA-seq to measure expression dynamics across 6 developmental stages in three sea urchin species: the lecithotroph Heliocidaris erythrogramma, the closely related planktotroph Heliocidaris tuberculata, and an out-group planktotroph Lytechinus variegatus. Our analyses draw on a well-characterized developmental gene regulatory network (GRN) in sea urchins to understand how the ancestral developmental program was altered during the evolution of lecithotrophic development. Our results suggest that changes in gene expression profiles were more numerous during the evolution of lecithotrophy than during the persistence of planktotrophy, and this contrast is even stronger when only GRN genes are considered. We found evidence for both conservation and divergence of GRN linkages in H. erythrogramma, as well as significant changes in the expression of genes with known roles in patterning the larval skeleton and gut, which are greatly modified in lecithotrophs. Collectively, these results indicate that the transition from planktotrohpic to lecithotrophic development involved numerous changes to key developmental processes.

A Dictionary of Genetic Effects for the Drosophila Wing

David Houle, Eladio J. Marquez, Rosa Moscarella

4A_306B-Evolution and Development
Tuesday, June 24, 2014 9:00 AM-9:15 AM

Traditional studies of development have emphasized 'the break it and show a picture the resulting mess' approach to genetics. Such experiments are not terribly relevant to evolution, as mutations with major effects usually drastically reduce fitness. Furthermore, they do not address the origins of variation in quantitative traits. We have constructed a Dictionary of Genetic Effects by quantitatively down-regulated the expression of over 100 genes during Drosophila melanogaster development using RNAi, and measured the effects of these manipulations on wing shape. Approximately 40% percent of these knockdowns have a quantitative effect on shape, 20% are lethal during development, and in the remaining 40% the evidence for an effect is ambiguous. Of those with effects, the majority have a linear effect on wing shape with degree of knockdown, but a few are strongly non-linear in some way. Several genes show threshold effects, and others give a curved trajectory through shape space. The linear effects of these genes fall within a 6 dimensional space that is approximately the first six dimensions of genetic variation within natural populations of D. melanogaster. The major pathways that genes have been assigned is somewhat predictive of the nature of the phenotypic response, however vectors do not closely match effects inferred from a genome-wide association study. We are able to predict some of the effects using our model of wing development. While our Dictionary contains only a few simple entries, a Dictionary of Genetic Effects would ultimately provide the foundation for studying the genotype-phenotype (GP) map. Understanding the GP map is necessary to understand the effects of mutation, the nature of standing genetic variation, the relative impact of natural selection in phenotype space, and the genetics of species differences.

Linking dynamic gene expression in a cichlid key innovation to adaptive molecular evolution

Sharon Clemmensen, Darrin Hulsey

4A_306B-Evolution and Development
Tuesday, June 24, 2014 9:15 AM-9:30 AM

Trophic divergence in cichlid fishes is linked to shifts in pharyngeal jaw morphology. The changes in the genetic and developmental architecture underlying this key innovation are largely unknown. Gene expression plasticity, or the differences in gene expression in response to changes in environment, may have large effects on the rate of gene evolution. Using next-gen whole transcriptome sequencing, we measured shifts in gene expression in the muscular sling of the cichlid pharyngeal jaw in response to a diet shift in lab-reared cichlids. We examined the relationship between changes in gene expression and the rate of sequence evolution (dN/dS) among genes to determine if genes with high differential expression showed more adaptive divergence than did genes with low differential expression.

The role of ontogeny in homology statements: case studies from morphology and phylogenomics of pancrustaceans

Joanna Wolfe

4A_306B-Evolution and Development
Tuesday, June 24, 2014 9:30 AM-9:45 AM

The study of ontogeny as an integral part of understanding the pattern of evolution dates back over 150 years, but only recently have ontogenetic data been explicitly incorporated into phylogenetic homology statements. I developed approaches to incorporate data both from fossils and development, providing proof-of-concept that ontogeny does affect morphological phylogenetic reconstructions. This work focused on the Pancrustacea (crustaceans + hexapods), a clade with remarkable morphological disparity, comprising over half the world's described species (over 800,000 in total). Many possible sister-group relationships have been proposed, diverging in the Cambrian. The only (and therefore oldest) likely Cambrian crown-group pancrustacean fossils are known from spectacular three-dimensionally phosphatized larvae from 'Orsten' type faunas, with impressively complete developmental sequences (but without unequivocal adult stages). These fossils have spurious placements in a traditional morphological analysis. Conserved synapomorphies in larvae may be overprinted later in development, obscuring phylogenetic signal. Therefore, each semaphoront (discrete larval or adult stage) is considered separately. Increased informativeness from larvae may apply to expressed genes, which promise to resolve deep phylogenetic questions, yet are susceptible to duplication and loss throughout evolution, resulting in trees potentially built from non-homologous genes. These alternative genes are expressed at different times in ontogeny, as they frequently play a role in development. Current work extends the semaphoront approach to phylogenomics, by sequencing transcriptomes of multiple semaphoronts of Decapoda, representing a broad sample of both species and metamorphic stages. Preliminary results suggest >50% of genes are differentially expressed between larval and adult semaphoronts within species, supporting the hypothesis of additional homologies in larval expression, which will provide synapomorphies allowing the reconstruction of the correct tree. Inclusion of data from multiple semaphoronts may have broader applications to other phylogenetic problems which may rely on ontogenetically variable homology statements.

Adaptive models of speciation: testing a role of sexual selection

Rebecca Safran, Elizabeth Scordato, Laurel Symes, Rafael Rodriguez, Tamra Mendelson

4A_BalC-SSE Symposium: The role of sexual selection in speciation: an integration of theoretical and empirical perspectives
Tuesday, June 24, 2014 8:25 AM-8:45 AM

Speciation by divergent natural selection is well supported. However, the role of sexual selection in speciation less well understood due to disagreement about whether sexual selection is a mechanism of evolution separate from natural selection, as well as confusion about various models and tests of sexual selection. We outline how sexual selection and natural selection are different mechanisms of evolutionary change, and suggest this distinction as critical when analyzing the role of sexual selection in speciation. Further, we clarify models of sexual selection with respect to their interaction with ecology and natural selection. In doing so, we outline a research agenda for testing hypotheses about the relative significance of divergent sexual and natural selection in the evolution of reproductive isolation.

The interaction of ecology and sexual selection in speciation

Laurel Symes, Elizabeth Scordato, Rebecca Safran, Tamra Mendelson

4A_BalC-SSE Symposium: The role of sexual selection in speciation: an integration of theoretical and empirical perspectives
Tuesday, June 24, 2014 8:45 AM-9:05 AM

Ecological context may be a critical component of speciation by sexual selection. However, the relative importance of ecological differences to this process remains poorly understood. To determine how sexual selection interacts with the environment during population divergence, and the relative importance of these interactions, we conducted a review of the empirical literature. We find that when both ecological context and sexual selection are studied, interactions between them are the norm, rather than the exception, and that natural and sexual selection appear to contribute jointly to population divergence. We categorize and assess the frequency of different types of interactions and present data on traits that diverge in tandem with specific ecological factors. In addition, we highlight which taxa, traits, and ecological variables are best understood and which represent promising but understudied areas.

The contrasting roles of sexual selection during speciation with gene flow

Maria Servedio, Reinhard Bürger

4A_BalC-SSE Symposium: The role of sexual selection in speciation: an integration of theoretical and empirical perspectives
Tuesday, June 24, 2014 9:05 AM-9:25 AM

The elaborate displays that often differ between closely related animal species cause many researchers to assume that sexual selection is a major driving force in speciation. While mate choice can certainly be an important component of speciation, recent theoretical studies suggest that the sexual selection that it generates can often inhibit the speciation process. We examine the ability of Fisherian sexual selection to contribute to lasting species differentiation, by using a population genetic model to isolate its effects after the onset of gene flow between allopatric populations. We show that even in the situation most favorable to speciation, when sexually selected traits are under ecologically divergent selection, mating preferences tend to introgress faster than trait alleles, causing sexual selection to counter the effects of local adaptation. The net amount of trait divergence thus often drops with stronger Fisherian sexual selection. The effects of pure Fisherian sexual selection on species maintenance are therefore much more inhibitory than previously assumed.

Speciation in darters: a potential example of mutation-order divergence by sexual selection

Tamra Mendelson

4A_BalC-SSE Symposium: The role of sexual selection in speciation: an integration of theoretical and empirical perspectives
Tuesday, June 24, 2014 9:25 AM-9:45 AM

Secondary sexual traits can be elaborate and strikingly diverse. Yet, the mechanisms that initiate this diversification are often a mystery. Diversification in secondary sexual traits is typically explained by local adaptation or drift, but many cases of divergence in sexual ornaments have no clear ecological explanations, and random drift is difficult to demonstrate. Here I present empirical data on aspects of speciation in darters, a diverse and colorful group of North American freshwater fishes. Data address the relative rate of evolution of different reproductive barriers, female preferences for male color variants within and between species, species differences in male aggressive behavior, and ecological divergence across the clade. I then present an alternative explanation for diversification in sexual ornaments that may better explain diversification in darters than current hypotheses. Mutation-order divergence by sexual selection contrasts with ecological speciation in that populations diverge in response to similar (global) rather than different (local) selective agents. Sexual selection may be particularly prone to a mutation-order process, as the sexual environment (pool of potential mates or competitors) can be similar in early stages of divergence. Quantitative simulations demonstrate that divergence by a mutation-order process in secondary sexual traits and preferences is stable in the face of some gene flow. I conclude by highlighting aspects of darter speciation that are consistent with mutation-order divergence by sexual selection.

Genome-wide analysis of wild-type Epstein-Barr virus genomes derived from healthy individuals of the 1000 Genomes Project

Arcadi Navarro, Gabriel Santpere, Fleur Darre, Soledad Blanco, Antonio Alcamí, M.Mar Albà

4B_301A-Genome Evolution
Tuesday, June 24, 2014 10:15 AM-10:30 AM

Most people in the world (~90%) are infected by the Epstein-Barr virus (EBV), which establishes itself permanently in B-cells. Infection by EBV is related to a number of diseases including infectious mononucleosis, multiple sclerosis and different types of cancer. So far, only seven complete EBV strains have been described, all of them coming from donors presenting EBV-related diseases.

To perform a detailed comparative genomics analysis of EBV including, for the first time, EBV strains derived from healthy individuals we reconstructed EBV sequences infecting lymphoblastoid cell lines (LCLs) from the 1000 Genomes Project. Since strain B95-8 was used to transform B-cells to obtain LCLs, it is always present, but a specific deletion in its genome sets it apart from natural EBV strains. After studying hundreds of individuals, we determined the presence of natural EBV in at least 10 of them and obtained a set of variants specific to wild-type EBV. By mapping the natural EBV reads into the EBV reference genome (NC007605) we constructed wild-type viral genomes from three individuals.

Analysis of all the available sequences reveals a complex history of recombination among EBV strains and that latency genes harbor more nucleotide diversity than lytic genes. Six out of nine latency-related genes present the molecular signature of positive selection, suggesting rapid host-parasite co-evolution.

The evolutionary dynamics of endogenous retroviruses by computer simulations

Fabricia Nascimento, Allen Rodrigo

4B_301A-Genome Evolution
Tuesday, June 24, 2014 10:30 AM-10:45 AM

Endogenous retroviruses (ERVs) are viewed as ancient retroviral infections in vertebrate genomes and are commonly referred to as viral “fossils”, accounting for approximately 8% of the human genome. They are retroviruses that have infected and colonized germ cells and are passed to the offspring. Because proviruses have the potential to disrupt genes and to change the host gene expression, which might lead to diseases, they are negatively selected and end up losing their viral function, becoming unable to re-infect. However, some ERVs are still able to re-infect because they still have intact viral genes. They are therefore theoretically able to form viral particles, even after millions of years within the host genome, yet the reason for this remains elusive. In this study we developed algorithms to understand the evolutionary dynamics of full-length ERVs (genome size = 10,000 bp) in host genomes by expanding described transposable element (TE) models known as the “strict master” and “transposon” models. The first model assumes that only one element of a given family is capable of producing a copy, while the second model assumes that all elements of a given family are equally like to produce a new copy in the host genome. By simulating both phylogenetic trees and DNA sequences, we tested how viral inactivity and ongoing activity for retrotranposition or reinfection of an ERV family influences phylogeny shape. We tested additional parameters such as virus mutation rate and the rate of an ERV to generate a new copy in the host genome. Current results show that phylogenetic programs do not always recover the “true” phylogenetic tree topology when DNA sequences are used to reconstruct the phylogeny. These results show promise with respect to our understanding of activity and inactivity of ERVs in vertebrate host genomes. It suggests that although ERV tree topologies are commonly referred to as following a “strict master” or “transposon” models by visual inspection, we should be careful in doing so. Results suggest that there are regions in the tree topology space where we cannot distinguish between the different models. A way of sorting this problem out would be to combine information of the tree branch lengths to the tree topology in order to better distinguish these different models.

Determination of complete mitochondrial genome sequences of cartilaginous fishes using next generation sequencing

Lei Yang, Gavin Naylor

4B_301A-Genome Evolution
Tuesday, June 24, 2014 10:45 AM-11:00 AM

Cartilaginous fishes (chondrichthyes) include sharks, skates, rays, and chimaeras. Currently, there are around 1300 extant species of cartilaginous fishes. The mitochondrial genome is a commonly used molecular marker for the studying of systematics and population genetics of these fishes. However, to sequence whole mitogenome sequences for all chondrichthyans using traditional methods is expensive, time-consuming, and sometimes not feasible, e.g. for dried museum specimens. In this study, over 100 mitogenomes of cartilaginous fishes were sequenced using short-PCR based Sanger sequencing or long-PCR based next generation sequencing methods. These sequences plus mitogenome sequences downloaded from the GenBank will be used to design RNA baits. These baits will then be employed to capture mitogenome sequences for more chondrichthyes. We expected to use this method to obtain whole mitogenome sequences for all chondrichthyan species we can get. These data will contribute significantly to the reconstruction of the Chondrichtyan Tree of Life. Studies on population genetics of chondrichthyes using mitogenomes will also be greatly facilitated.

Chloroplast genome sequencing of extinct and endangered Hawaiian mints and their New World relatives (Lamiaceae)

Andreanna Welch, Katherine Collins, Aakrosh Ratan, Daniela Drautz, Stephan Schuster, Charlotte Lindqvist

4B_301A-Genome Evolution
Tuesday, June 24, 2014 11:00 AM-11:15 AM

The endemic mints represent one of the largest plant lineages in the Hawaiian Islands. Since their divergence from New World mints ~4 million years ago they have diversified into a group of 60 species in three genera and represent a remarkable array of eco- and phenotypes. Today, many members of this group are endangered or already extinct and therefore primarily known and available only from herbarium samples collected during the last century. Phylogenetic analyses have been utilized with a gene-by-gene approach to investigate evolution in this lineage, but its recent diversification means that sequence divergence, and hence phylogenetic resolution, is low. Therefore, a genomic approach is necessary to gain a better understanding of the rapid diversification of this lineage, but genetic resources are limited and no genome-wide analyses have been generated for close relatives of the Hawaiian mints. We used a next-generation sequencing approach to obtain a high-quality (50x coverage), complete plastid genome (~150Kb) from an extinct Hawaiian mint species, Stenogyne haliakalae. By resequencing of close relatives, we have generated 10 additional complete genomes and up to 86% genomic coverage for four other species, including from 100-year old herbarium material. Although high-throughput technologies allow for sequencing of multiple, complete chloroplast genomes it may not be a cost-effective approach in closely related, recently diverged species where use of historical material is necessary and genetic differentiation at even the genome-scale is limited. In order to target hypervariable regions, we targeted ~100 SNPs from throughout the chloroplast genome in 96 mint species using a next-generation amplicon sequencing approach. This approach generated ~20Kb sequence data per individual and increased the total number of variable sites among the sequenced species to ~1,000. Amplification of even more distant relatives was successful and analysis of such hypervariable regions using high-throughput sequencing demonstrate the potential of such an approach in rapidly evolved lineages.

Genome size evolution in North American fireflies

Sarah Sander, J. Spencer Johnston, Shawn Hanrahan, David Hall

4B_301A-Genome Evolution
Tuesday, June 24, 2014 11:15 AM-11:30 AM

Genome size varies dramatically across the tree of life. Certain taxonomic groups have received more attention than others. Here we document variation in genome size across 22 species of firefly (Coleoptera: Lampyridae). We find considerable differences in genome size within a genus and up to 5-fold across genera. Further, we investigate genetic and physiological correlates with genome size expansion/contraction.

Modular color evolution facilitated by a complex nanostructure

Chad Eliason, Rafael Maia, Matthew Shawkey

4B_301B-Trait Evolution
Tuesday, June 24, 2014 10:15 AM-10:30 AM

Understanding how complex traits diversify remains an important question in evolutionary biology. Extensive evidence suggests that the genetic and developmental architecture of complex traits can channel evolutionary change. However, in many cases selection acts on functional properties of complex traits rather than directly on morphology. Thus, with functional traits, the way that form maps to function can be crucial in understanding how such traits respond to selection. Feather colors in birds are among the most diverse phenotypes in nature and can be produced either by selective light absorption by pigments (pigment-based colors), or light scattering from nanoscale structures varying in refractive index (structural colors). Based on the deterministic association between structural color and its producing components, an increase in the number of tunable morphological parameters may increase the number of free optical parameters. Such innovations have been shown to result in accelerated color diversification and the opportunity to occupy novel areas of colorspace. However, the mechanisms by which these flexible templates might favor or channel the evolution of colors relies on understanding i) how added morphological complexity enables the evolution of multiple, independent evolutionary modules and ii) how these structural modules map to color attributes, both of which remain unknown in an evolutionary context. Many species of dabbling ducks (Anatini) have a remarkably conspicuous patch of colorful plumage in their wings (the speculum), which is often momomorphic (found in both males and females) and in most species is iridescent. These gaudy plumage patches vary considerably in color and have been shown in some species to be sexually-selected and used as visual signals in mate attraction and male-male competition signals. The structure responsible for producing these iridescent speculum colors is a 2-dimensional photonic crystal formed by the arrangement of small (100-200 nm) melanin granules (melanosomes) into a hexagonal pattern. Here, we ask how this complex template affects the independent variation (evolvability) of color attributes. Using a combination of electron microscopy, reflectance spectrophotometry, and multivariate comparative methods, we show that morphological complexity causes functional decoupling among color variables, allowing them to evolve independently and at different rates. By explicitly studying evolutionary trends in both form and function, our results demonstrate that color evolvability is facilitated by the functional architecture of the system rather than covariation among morphological traits (e.g., due to shared genetic or developmental pathways). These results are important because they show how internal features of organisms (e.g., innovations in the form-function map) relate to macroevolutionary patterns of phenotypic diversity and therefore might help explain why some clades are more color-diverse than others.

Competition kernels and coexistence

Richard FitzJohn

4B_301B-Trait Evolution
Tuesday, June 24, 2014 10:30 AM-10:45 AM

Modelling interspecific competition, and how it varies with species traits, is central to theory about coexistence and diversity. In many models, the competitive effect of one species on another is calculated directly from traits, using simple functional forms (e.g., gaussian, sigmoidal), increasing linearly with species abundance. This approach is disconnected from empirical studies of competition, where such quantities are extremely difficult to measure. We aim to bridge this gap using models where competition emerges implicitly via the use of common resources; both simple phenomenological models and more complex mechanistic models. Our results suggest that even in simple models with implicit competition, simple functional forms are often insufficient to capture ecological or evolutionary dynamics and thus question the widespread use of such functions in current theory

---

Evolution of secondary woodiness in Hedyotis-Oldenlandia complex (Rubiaceae) in Asia and the Pacific

Suman Neupane, Paul Lewis

4B_301B-Trait Evolution
Tuesday, June 24, 2014 10:45 AM-11:00 AM

Hedyotis-Oldenlandia complex (ca. 600 spp.) lies within a primarily herbaceous tribe Spermacoceae of the fourth largest plant family, Rubiaceae. However, some of the members (eg. genera Hedyotis and Kadua etc) in the complex are characterized by their uniquely derived secondary woody habit. These secondary woody clades also exhibit high endemicity, a montane distribution with narrow altitudinal range and high species diversity compared to their wide-ranging herbaceous sister lineages. This presentation will discuss the correlates of the secondary woodiness and differential rate of evolution and diversification between herbaceous and woody groups within Hedyotis-Oldenlandia complex.

Linking gene flow to changes in traits, fitness, and population dynamics in the wild

Sarah Fitzpatrick, Chris Funk, Lisa Angeloni

4B_301B-Trait Evolution
Tuesday, June 24, 2014 11:00 AM-11:15 AM

A fundamental, yet still unresolved question in evolutionary and conservation biology is how gene flow affects local adaptation, fitness, and population dynamics. Gene flow can break down local adaptation by introducing maladaptive alleles, or wipe out local distinctiveness, especially if generalist genotypes dominate. Inbred recipient populations are especially vulnerable to genomic sweeps following gene flow, where the majority of the population's genes originate from immigrants. Alternatively, gene flow may speed up adaptive evolution (e.g., to a changing climate) by increasing the 'working surface' of natural selection.

We took advantage of recent introduction experiments using Trinidadian guppies to test the effects of gene flow from adaptively divergent immigrants on traits, individual fitness, and population dynamics in native, genetically depauperate, recipient populations. We monitored gene flow, survival, and population dynamics for 3 months pre- and 26 months post-introduction using mark-recapture techniques. A suite of known fitness-related phenotypic traits (coloration, morphology, life history) were quantified for each individual from the wild populations. In addition, common garden assays were carried out pre- and post-gene flow in order to determine whether changes in traits had a genetic basis. To evaluate reproductive success we reconstructed a wild pedigree for the monitored populations. Individual survival and population growth rate were evaluated with mark-recapture data in Program MARK.

We documented extensive gene flow from initially maladapted, translocated guppies into native recipient populations. Levels of heterozygosity, allelic richness, and effective population size increased after the onset of gene flow. In addition, results from common garden assays revealed genetically based changes in traits caused by gene flow. Despite seasonal variation, gene flow ultimately resulted in steep increases in individual fitness (defined by survival and reproductive success) and overall population size. In general, our results suggest that gene flow provided major fitness benefits to recipient populations, likely caused by genetic rescue. But, these benefits may have come at the cost of losing the native genetic signature.

Dobzhansky-Muller incompatibilities and the evolution of reproductive isolation

Ata Kalirad

4B_302A-Speciation
Tuesday, June 24, 2014 10:15 AM-10:30 AM

One of the most alluring topics in evolution and ecology is the question of speciation. The Dobzhansky-Muller (DM) model of genetic incompatibilities has been the major theoretical framework in our understanding of speciation. Although DM incompatibilities have been observed in nature, a detailed study of their general properties such as the average probability of incompatibility using a biological system is missing.

In the DM model, an ancestral population splits into two populations that evolve independently with no gene flow between them. While evolving, new mutations arise and fix in both populations. Upon contact between these populations, mutations that arose in each population, while compatible with their own genetic background, can be incompatible with alleles in the other population. The negative epistasis between this alleles can lead to inviability/sterility of the hybrids. Orr expanded this model to allow incompatibilities to include more than two loci.

RNA molecules are perfect for studying the DM model because they have been extensively used to study epistatic interactions. Furthermore, they are crucial to many biological functions at the cellular level, e.g. regulating gene expression. Considering their biological importance, DM incompatibilities in RNAs can contribute to reproductive isolation in nature.

Our results, using diverging RNA complex in silico, have helped us to determine the average probability of DM incompatibilities and their average contribution to the overall reproductive isolation.

Life history selection drives the early evolution of reproductive barriers in Mimulus guttatus

Megan Peterson, Amy Angert, Kathleen Kay

4B_302A-Speciation
Tuesday, June 24, 2014 10:30 AM-10:45 AM
A major goal of ecological speciation is to understand how divergent selection on individual traits contributes to the evolution of reproductive barriers. Although many studies have demonstrated the evolution of ecological barriers in response to discrete niche shifts, empirical tests of ecological speciation along continuous ecological gradients remain scarce. We quantified early reproductive barriers among 11 populations of monkeyflower (Mimulus guttatus, Phrymaceae) spanning continuous life-history variation along elevation gradients in California. We examined the pattern and strength of life-history selection across two years in a montane habitat to test the hypothesis that traits under divergent selection underlie incipient barriers. We find that montane habitats favor perennial phenotypes, including later flowering, larger flowers, and increased investment in vegetative reproduction. In turn, these traits contribute to temporal and mating system isolation that increases with life-history divergence. Together, this work provides a mechanistic link between life history selection and the early evolution of ecological barriers.

First passage time to allopatric speciation and species creation rate

Ryo Yamaguchi, Yoh Iwasa

4B_302A-Speciation
Tuesday, June 24, 2014 10:45 AM-11:00 AM
Allopatric speciation is a mechanism to evolve reproductive isolation; it is caused by the accumulation of genetic differences between populations while they are geographically isolated. We study the rate of allopatric speciation for a species in multiple islands between which migration occurs only infrequently. We assumed that mating incompatibility is controlled by a number of loci that behave as neutral characters in the accumulation of novel mutations within each population. Genetic distance between populations was defined as the number of incompatibility-controlling loci that differ between them. Genetic distance increases through the separate accumulation of mutations in different populations, but drops after a successful migration event followed by genetic mixing between migrants and residents. We calculated the time to allopatric speciation, which occurs when the genetic distance exceeds a specified threshold. The diffusion approximation, stochastic differential equation, and the direct computer simulation of individual-based model are all similar. There is an intermediate optimal rate of migration that maximises the rate of species creation by recurrent invasion and diversification. We also discuss waiting time to allopatric speciation and its geographic patterns of a species forming metapopulation.

A simple biophysical model of protein binding DNA predicts higher rates of allopatric speciation in small populations

Bhavin Khatri, Richard Goldstein

4B_302A-Speciation
Tuesday, June 24, 2014 11:00 AM-11:15 AM
Speciation is fundamental to understanding the huge diversity of life on Earth. Evidence suggests reproductive isolation arises most commonly in allopatry with an increasing rate of speciation for small populations. Current theory does not address how the speciation rate varies with population size in the important weak mutation regime of evolution. In addition, increasing data suggest that many species differences involve a divergence in the regulation of gene expression and that a number of speciation genes involve transcription factors. Here, we address the underlying biophysical basis of speciation by using a simple model of transcription factor-DNA binding and how their co-evolution in two allopatric lines leads to incompatibilities. Surprisingly, we find this simple consideration leads to a new prediction for the monomorphic regime of evolution, that smaller populations should develop incompatibilities more quickly. We show this arises due to two factors; 1) smaller populations have a greater initial fixed genetic load, due to the effect of sequence entropy, and so are closer to incompatible regions of phenotype space; 2) for larger populations substitutions are no longer nearly-neutral and the divergence between lineages slows down. These predictions are consistent with observations of large species diversity in small habitats such as Cichlids in the East African lakes, contrasted with the lower diversity of marine animals, which have large ranges and population sizes.

Strong premating reproductive isolation contributes to incipient speciation in Mimulus aurantiacus

James Sobel, Matt Streisfeld

4B_302A-Speciation
Tuesday, June 24, 2014 11:15 AM-11:30 AM
Determining which forms of reproductive isolation have the biggest impact on the process of divergence is a major goal of speciation research. These barriers are often divided into those that affect the potential for hybridization (premating isolation), and those that occur after mating has occurred (postmating isolation), and much debate has surrounded the relative importance of these categories.

Within the species Mimulus aurantiacus, red- and yellow-flowered ecotypes occur in the southwest corner of California. We show that these two taxa are largely separated by ecogeographic isolation, with the red-flowered ecotype occupying relatively benign habitats near the coast, and the yellow-flowered ecotype inhabiting harsher inland environments. Along a narrow zone of contact, additional reproductive barriers have the potential to limit gene flow, and in these locations, differential visitation by pollinators provides strong but incomplete isolation. We show that postmating forms of reproductive isolation have little or no impact on gene flow; therefore, premating barriers are solely responsible for divergence. Structure analysis reveals that these premating barriers are sufficient to delineate taxa genetically; however, analysis of molecular variation across thousands of RAD-seq markers shows that the genomes of these taxa are largely undifferentiated. These data suggest that two forms of ecologically-based divergent selection are contributing to incipient speciation in these taxa, and the interaction between these two independent agents may be necessary to maintain stable phenotypic differentiation in the face of ongoing gene flow.

Sexual selection and species recognition in Calopteryx damselflies

Idelle Cooper, Oumar Sacko, Tom Getty

4B_302B-Sexual Dimorphism
Tuesday, June 24, 2014 10:15 AM-10:30 AM

Traits used in species recognition and traits used in mate choice are thought to be under contrasting selection pressures, as traits under sexual selection within a species should not interfere with signals of species identity. Conflict between these roles can be avoided if different traits act as signals in each case, but here we consider how a single trait may be under selection in both cases. We examined how damselfly wing pigmentation may be used in species recognition in sympatric populations of C. maculata and C. aequabilis, and how it may also be under sexual selection during mate choice within C. maculata. In a mark-recapture study of C. maculata, we found that successfully mated males had darker wings, which may be favored in mate choice by females. In caged mating experiments using both species, we tested the role of wing pigmentation in species recognition, using damselflies from allopatric and sympatric populations that show variation in wing pigmentation. We found that wing pigmentation also functioned in species recognition, but in courtship by males. Wing pigmentation is under sexual selection in males and under selection for species recognition in females. A single character, therefore, may be under contrasting selection pressures but not conflict due to sexual dimorphism of that trait.

Character displacement in the wing color patterns of rubyspot damselflies: An experimental test of multiple character displacement hypotheses

Jonathan Drury, Gregory Grether

4B_302B-Sexual Dimorphism
Tuesday, June 24, 2014 10:30 AM-10:45 AM

Social interactions between closely related species have largely been studied in reproductive contexts, under the rubric of reproductive character displacement (RCD) theory. Nevertheless, aggressive interactions between species are also very common, yet agonistic character displacement (ACD), a process wherein natural selection acts on traits that mediate the occurrence or outcome of interspecific aggression, is an understudied evolutionary phenomenon. Previous research suggests that patterns of geographic variation in wing color patterns and competitor recognition of male rubyspot damselflies (Hetaerina spp.) have resulted from ACD. However, RCD may also have acted to produce the same geographic patterns, and recent theoretical work has shown that RCD dominates ACD when mate recognition and competitor recognition are based on the same traits. To determine whether female mate recognition in Hetaerina is based, in part, on male wing color patterns, we carried out a phenotype manipulation experiment in the field. Compared to control males, male H. americana that we manipulated to have wing coloration resembling a sympatric congener (H. titia) suffered no reduction in mating success with conspecific females. Thus, in H. americana, female mate recognition is not based on male wing coloration. Moreover, experimental males experienced increased interspecific fighting rates. These results strengthen the case for ACD as the process responsible for the character displacement pattern in Hetaerina wing coloration.

Adaptation and the tempo of phenotypic change during radiation in the Hawaiian damselflies (Coenagrionidae: Megalagrion)

Jonathan Brown, Idelle Cooper, Sam Sherwood, Madeline Cloud, Mark McPeek

4B_302B-Sexual Dimorphism
Tuesday, June 24, 2014 10:45 AM-11:00 AM

The endemic Hawaiian damselflies (Coenagrionidae: Megalagrion spp.) are a single radiation whose species have diversified over 11 my, in the process differentiating into a unusually broad array of larval habitats, from permanent streams to seeps and puddles, and even to damp terrestrial habitats. They are also extremely variable in adult coloration (including both female and sexual dimorphism); variation in color traits and dimorphisms are generally assumed to be due to sexual selection, though we propose that in this system they function as an adaptation. Here, we address the interaction between geographic isolation and adaptation to larval and adult habitats in the speciation process, including the development of mating barriers between species.

First, we provide evidence from phylogenetic comparative analysis that adult color evolution can be rapid and is likely due to ecological selection. Aside from reflecting light to produce color, pigments can also act as protective antioxidants against the harmful effects of solar radiation. We show that variation in light habitats (as measured by canopy cover) significantly explains body color variation within sexes (female dimorphism), between sexes (sexual dimorphism), and among populations and species. Surprisingly, the degree of habitat difference between sexes also determines the degree of sexual dimorphism in body color, a trait usually attributed to sexual selection.

Second, we evaluate how these strong adaptive pressures on larvae and adults have interacted with non-adaptive mechanisms -- geographic isolation and sexual selection. At the level of the entire Hawaiian radiation, we find strong differences in the tempo of morphological evolution of male clasper shape (a mate recognition character), compared to continental coenagrionid radiations driven primarily by non-adaptive speciation. We also predicted that as species spread geographically, they should encounter both new larval and new adult light environments and rapidly differentiate in characters involved in adaptation and in neutral markers, if accompanied by evolution in mate recognition characters. Using microsatellite variation in one widely distributed and color variable species, M. calliphya, we find strong genetic differences associated with geographic isolation, especially between island complexes; in addition, clasper shape varies significantly between island complex populations. A synergistic effect of isolation and ecological selection on multiple traits across steep ecological gradients may explain the rapid tempo of change in morphology and color in this high island archipelago.

Evolution of Body Size and Sexual Size Dimorphism in Two Replicated Lizards Radiations

James Schulte, Joshua Lavelle, Daniel Pincheira-Donoso

4B_302B-Sexual Dimorphism
Tuesday, June 24, 2014 11:00 AM-11:15 AM

The iguanian lizard clades Phrynosomatinae in North America and Liolaemini from southern South America share many similarities in their ecological, physiological, and morphological diversity. Specifically, both groups occupy a variety of microhabitats on their respective continents, but without the predictable ecomorphological relationships demonstrated by Caribbean Anolis or extreme size variation found in monitor lizards (Varanus). However, both groups contain multiple independent origins of viviparity and within Liolaemini over half of the more than 270 species have live birth. This study will explore evolutionary patterns of male and female body size and sexual size dimorphism (SSD) to identify whether particular lineages within each of those groups have exhibited exceptional rate shifts in body size or SSD. If such shifts are identified, we will then determine if they are associated with changes in other phenotypic traits, such as reproductive mode or occupation of a specific microhabitat. We also will evaluate whether the use of two alternative treatments of body size (maximum size vs. mean size) has a significant impact on inferences made using these methods.

Endocrine disrupting chemicals lead to higher order behavioral effects when they alter interacting phenotypes in guppies, Poecilia reticulata

Bronwyn Bleakley, Roberto Rosa, Johnny Joseph

4B_302B-Sexual Dimorphism
Tuesday, June 24, 2014 11:15 AM-11:30 AM

Endocrine disrupting chemicals (EDCs) are a class of common environmental contaminants known to alter individual physiology and behavior. EDC exposure has many effects on the physiology of animals but one of the most striking is male feminization. Feminization of physiology is often accompanied by feminization of behavior, including reductions in boldness and/or aggression and loss of mating displays. These behaviors place crucial roles in structuring social interactions among many animals. When social behaviors are influenced by interactions among conspecifics, they are termed "interacting phenotypes." Interacting phenotypes, traits that at least in part reflect an interaction with social partners, often result from indirect genetic effects, or the influences of genes carried in social partners on the behavior of a focal individual. These effects are mediated through the phenotype of the social partner. We hypothesized that exposure to endocrine disruptors could generate higher order behavioral effects, altering the behavior of untreated individuals through interactions with exposed individuals and/or altering the social organization of whole groups. We measured the effects of EDC exposure in guppies, Poecilia reticulata, because guppies exhibit complex social behavior influenced by indirect genetic effects. In one experiment, social partners were exposed to one of two common EDCs: vinclozolin or bisphenol-A and then allowed to interact with untreated focal individuals in the presence of a predator model. Focal behavior changes in response to treated partners compared to untreated partners for many aspects of cooperative antipredator behavior. In a second experiment, whole groups were exposed to vinclozolin and changes in social network structure were measured. Taken together, these data suggest that impacts of endocrine disrupting chemicals at low and environmentally relevant doses can have far reaching effects, even on individuals that were unexposed, via the influence of social partners.

A History of High Latitude Adaptation in Holarctic Ground Squirrels (Urocitellus)

Bryan McLean, Joseph Cook

4B_302C-Adaptation
Tuesday, June 24, 2014 10:15 AM-10:30 AM

The evolution of squirrels has been strongly influenced by global climatic and tectonic changes. However, the general "adaptability" of squirrels may be best investigated within the context of their response to selective pressures in the most extreme environments. To address this, we analyzed the phylogeny, biogeographic history and morphological adaptation of Holarctic ground squirrels (Urocitellus), a genus that includes multiple high latitude species as well as the northernmost ground squirrel species in the world, the Arctic ground squirrel (U. parryii). We inferred phylogenetic relationships and past distributional shifts in Urocitellus using multilocus Bayesian methods and ancestral range reconstructions. In addition, we employed geometric morphometric data and comparative analyses to examine the evolution of body size and cranial shape along the Urocitellus phylogeny as well as the association of both these traits with life at high latitudes. Preliminary results suggest that colonization of the arctic occurred early in the diversification of Urocitellus, and that increased body size - one adaptation to such habitats - has generated strong allometric changes in cranial shape among these species.

Evaluating the immediate capacity for ongoing adaptation

Ruth Shaw, Charles Geyer, Julie Etterson, Stuart Wagenius

4B_302C-Adaptation
Tuesday, June 24, 2014 10:30 AM-10:45 AM
Adaptation of natural populations has been assessed almost exclusively retrospectively, but insight into the capacity for ongoing adaptation is also valuable, both to ground understanding of the dynamics of the adaptive process and to inform management of populations as environment changes. A population's capacity for immediate adaptation is set by its additive genetic variance for lifetime fitness [Va(W)], as RA Fisher showed. Estimates of Va(W) and the distribution of additive genetic effects on fitness for populations of the annual plant, Chamaecrista fasciculata, and the long-lived perennial, Echinacea angustifolia, will be presented, and their implications will be considered.

Inferential Evolution and the Reflection Principle

Christopher J. Ellison, Jessca Flack, David Krakauer

4B_302C-Adaptation
Tuesday, June 24, 2014 10:45 AM-11:00 AM
In this talk, we introduce an information-theoretic framework for investigating the limits of adaptive inference. The framework is designed to work with a range of adaptive dynamics, including learning and selection.

We treat organisms as regularity extracting machines which build efficient models of the environment. Here, "efficient" depends on both the ability of an organism to predict future environmental conditions and on model complexity. The environment is represented by a stochastic dynamical system known as a hidden Markov model. At each interval, organisms make observations about the environment and use them to predict the future.

Organisms use their observations to update a model (also a hidden Markov model) of the environment. Thus, we consider a discrete-time evolutionary model, similar to the replicator equation, but with selection acting on an continuous space of probability density functions---this is Bayesian inference. An information-theoretic measure of complexity known as the statistical complexity describes the minimum number of bits an observer of the organism would need in order to predict its future behavior optimally. This complexity measure is used to compare organismal complexity in time to the complexity of the environment.

We find that the complexity of the environment typically places an upper bound on the complexity of organisms. We call this "the reflection principle". We explore violations of this principle through the effects of: (1) transients; (2) encoding constraints; and (3) hierarchical or ecological networks.

Preadaptation to human environmental impacts: Deforestation filters species and facilitates geographic reshuffling in an anthropogenic world

Luke Frishkoff

4B_302C-Adaptation
Tuesday, June 24, 2014 11:00 AM-11:15 AM
Habitat conversion is reshaping biological communities, yet it remains unclear why some species suffer while others prosper after environmental changes. Given that the majority of large-scale human impacts are quite recent, most traits that confer survival ability in evolutionarily novel anthropogenic habitats are likely preadaptations. To identify which species characteristics promote survival after habitat conversion, we examined two closely related species of Neotropical leaf litter frogs with contrasting affinities for deforested habitats. We show that a species' thermal niche corresponds with deforestation tolerance, with the more deforestation-affiliated species (Craugastor fitzingeri) occurring warmer climate zones, occupying warmer microclimates within landscapes, and possessing optimal performance abilities at warmer temperatures than the more forest-affiliated species (Craugastor crassidigitus). We verified the generality of the role of thermal niche in deforestation tolerance by expanding our analysis to a community of 33 reptile and amphibian species in southern Costa Rica. Mean annual temperature across a species' range better predicted a species' presence in deforested habitat than commonly used traits, such as body size. Because temperature (rather than just vegetative structure) determines affiliation with deforested habitats, changing local temperature regimes as a result of land-use conversion may allow species to expand into colder climate zones. We tested for such recent range expansion by assessing the population genetic structure of the two focal Craugastor species. We find evidence for upslope range expansion, of C. fitzingeri into middle elevation landscapes. By understanding how habitat conversion interacts with species' niches we can gain insight into lasting human signature on the evolutionary trajectory of Earth's biota.

Geographic mosaics of phenology, host preference, adult size and microhabitat choice predict butterfly resilience to climate warming

Nichole Bennett, Camille Parmesan, Michael C. Singer, Paul Severns

4B_302C-Adaptation
Tuesday, June 24, 2014 11:15 AM-11:30 AM
The climate-sensitive butterfly Euphydryas editha exhibited interpopulation variation in egg placement and phenology. This should expose individuals to diverse thermal environments, which we investigated by measuring "eggspace" temperatures adjacent to natural egg clutches in populations distributed across a range of latitudes (36.8-44.6°) and altitudes (213-3171 m). Eggs laid >50 cm above the ground averaged 3.1°C cooler than ambient air at 1 m height, while those at

Interpopulation variation in phenology also strongly influenced thermal environment and buffered exposure to thermal stress. At sites with hotter July temperatures, the single annual flight/oviposition period was advanced such that eggs were laid on earlier dates, with cooler ambient temperatures. The insects possessed two mechanisms for advancing egg phenology; they could advance timing of larval diapause-breaking and/or shorten the life cycle by becoming smaller adults. The mean weight of newly-eclosed females varied among populations by more than a factor of two, suggesting that variable size did influence phenology.

Possible options for in situ mitigation of thermal stress include further advancing phenology and raising egg height. We argue that these options still remain, as evidenced by current patterns of variation and by failure of E. editha to meet expected biogeographic relationships, such as the expectation that populations at equatorial and poleward range limits be restricted to higher and lower elevations, respectively. This optimistic example shows how complex local adaptation can generate resilience to climate warming.

Inquiry-based learning in the Evolution classroom

Ajna Rivera, Lisa Wrischnik

4B_303-Education
Tuesday, June 24, 2014 10:15 AM-10:30 AM
Teaching a subject perceived as not useful or as uninteresting is a perennial problem for the educator. Over the last three semesters, I have used my upper-level majors Evolution course as a testing ground for novel approaches to engaging a population of primarily pre-health students in a subject that they do not perceive as relevant. In this talk I will present different techniques that have increased student satisfaction and conceptual learning, as assessed by their ability to explain difficult concepts and to apply facts and ideas in novel situations. In general, I used a variety of in class and out of class group and individual activities that both required to the student to use in-class and textbook information or techniques in novel situations and introduced new material. These included critical reading of a journal article, replying to critics of evolution, testing mating strategies, and performing basic phylogenetic techniques. The capstone project used the Quaardvark portal to first asses correlation of two traits in Aves species and then to use real data to map the evolution of both of these traits on a phylogenetic tree. Quaardvark is a database that provides flexible structured natural history data for a variety of animals. It is run through The Animal Diversity Web, which also provides undergraduate-level activities designed to help students explore relationships between animal traits.

New assessment tools to capture student thinking about evolution and provide them with timely feedback

Denise Pope, Kerry Kim, Jody Clarke-Midura, Susan Maruca, Eli Meir

4B_303-Education
Tuesday, June 24, 2014 10:30 AM-10:45 AM
Teaching evolution to undergraduates comes with many challenges, one of which is uncovering student thinking that may be impeding their understanding of evolutionary concepts. A further challenge is providing them with feedback that will help them overcome these misconceptions. Multiple-choice questions are limited in their ability to capture students' thinking, whereas short answer or essay questions ("open response" questions) are difficult to implement in large classes in a way that allows instructors to provide specific and timely feedback. SimBio is developing assessment tools that will bridge this gap between multiple-choice and open response questions, to use in computer-based activities, such as our virtual labs and tutorials. We have developed two tools, "LabLibs" and "WordBytes," that provide more structure and constraint than open response, but allow for more flexible and complex answers than multiple-choice. In LabLibs, students complete answers by selecting from multiple drop-down menus; in WordBytes, students construct answers from a pool of words and phrases. The more constrained nature of LabLibs makes it relatively straightforward to categorize all possible answers and write feedback for them. The greater freedom for constructing answers afforded by WordBytes makes scoring and feedback more complicated, but still less labor-intensive than grading short answer questions.

We tested these tools through student interviews in Spring 2013 to assess their ability to capture student thinking, and found good agreement between student responses in open response format and using the LabLibs and WordBytes tools. We then implemented LabLibs and WordBytes questions in two SimBio virtual labs on evolution ("Darwinian Snails" and "Mendelian Pigs") in Fall 2013 and Spring 2014 semesters. We have data from over 1,000 students at multiple schools each semester. To test the effectiveness of LabLibs and WordBytes in aiding student learning, we compared student answers before and after receiving feedback. Results suggest that the majority of students learn effectively from these tools, but they prove challenging for about 5-10% of students. Additionally, grading and feedback for LabLibs was accurate over 90% of the time, and could be specified by an instructor in about an hour. Unlike traditional computer grading of short answer questions, WordBytes grading could be specified without collecting a large number of student answers, though the accuracy improved when student answers were used to refine the grading rules. Taken together, we find WordBytes and LabLibs offer a reasonable tradeoff between student expression and ease of grading and feedback.

National Experiment in Undergraduate Science Education (NEXUS) - teaching and assessing a competency-based life science curriculum with case studies

Jane Indorf, Michael Gaines

4B_303-Education
Tuesday, June 24, 2014 10:45 AM-11:00 AM
The Howard Hughes Medical Institute (HHMI)-funded National Experiment in Undergraduate Science Education (NEXUS) is a pedagogical experiment to create and evaluate new competency-based teaching modules for undergraduate life science education. NEXUS is a collaborative effort among Purdue University, University of Maryland Baltimore County, University of Maryland College Park, and the University of Miami (UM) with each institution designing a unique part of this innovative curriculum. While encapsulating principles set forth in the BIO 2010: Transforming Undergraduate Education for Future Research Biologists (2003) and Vision and Change in Undergraduate Biology Education (2011) reports, NEXUS was motivated by the Association of American Medical Colleges (AAMC)-HHMI Scientific Foundations for Future Physicians (SFFP) report (2009) outlining eight science competencies that premedical students should master during their undergraduate career, which are applicable to all life science students. These competencies integrate biological concepts with

principles of chemistry, mathematics, and physics. The NEXUS curriculum is designed for students to achieve mastery of these scientific competencies and gain an interdisciplinary perspective of biology.

At UM we have developed case studies that present real world situations through narratives. As students read through the story, they answer associated questions in which they apply their scientific knowledge and integrative understanding of scientific concepts. We have developed a library of eight case studies which have been piloted in UM's Advanced Program for Integrated Science and Math (PRISM). PRISM is a science curriculum for undergraduates who are specifically interested in pursuing a research career. PRISM courses focus on integration of the sciences. All NEXUS case studies are tightly aligned to course objectives and SFFP competencies. We use student performance on case studies and their feedback on surveys to gauge student mastery of the competencies. Students are assessed pre- and post-case study to evaluate their effectiveness.

This presentation will focus on an evolution case study to demonstrate how they engage students and to highlight the results of our NEXUS evaluation. Data indicate that UM faculty and students are open to this new way of teaching, and even prefer teaching and learning with case studies. Students like the integration of the sciences and application to real life issues. They also appreciate the challenge of critical thinking. NEXUS case studies are helping students relate complex biological topics they learn in class to real world situations and are enabling them to make connections among their different science courses.

Hit the Road, Chuck! Evolution Education Goes Mobile With The Darwin Day Roadshow

Jory Weintraub

4B_303-Education
Tuesday, June 24, 2014 11:00 AM-11:15 AM

To celebrate Charles Darwin's birthday each year, the scientists and educators of NESCent (The National Evolutionary Synthesis Center) hit the road to bring evolutionary science to schools, museums and town halls in communities around the country, via a program called The Darwin Day Roadshow. We are particularly interested in reaching out to small rural communities which would not otherwise have a Darwin Day celebration, as well as communities with high numbers of under-represented minority students. Our teams talk to students, teachers and the general public about their research in evolutionary science and discuss the rewards and challenges of science careers. Prior to hitting the road, all of our scientists participate in professional development workshops focused on effectively communicating evolution to the public. The host teachers take an active role in working with us to plan the visits, and in return each host teacher receives a large collection of evolution teaching resources to support their continued teaching of evolution in engaging, dynamic ways. To date, we have visited thousands of students and teachers in twenty-two states. The Darwin Day Roadshow not only exposes students, teachers and the general public to cutting edge evolutionary science (and valuable information on science careers), but provides novel outreach experiences and professional development opportunities for NESCent scientists.

Visualizing cooperation theory in the non-majors evolution classroom: free tools for teaching the evolutionary dynamics of the Prisoner's Dilemma

Christopher Jensen

4B_303-Education
Tuesday, June 24, 2014 11:15 AM-11:30 AM

The Prisoner's Dilemma (PD) is a game theory construct that has become one of the standard models employed by theorists seeking to understand how cooperation evolves. Because the PD effectively captures the dynamics of social dilemmas in which the temptation to cheat is greatest, it has frequently been used as the fundamental building block of models that explore a myriad of potential mechanisms by which cooperation might evolve. For this reason, understanding the dynamics of the PD is a pre-requisite for understanding much of evolutionary theory that seeks to explain the basis for cooperative behaviors. Traditionally, model constructs like the PD have been taught by introducing the mathematical toolset of game theory. While this mathematical approach may be effective for most students majoring in evolutionary biology, it is far less effective for most non-majors. Does this mean that explaining how cooperation evolves is too advanced a task for the non-majors evolution course? I contend that the answer to this question is "no": using the right approaches, non-majors without significant mathematical skills can achieve understanding of the most important properties of the PD and therefore of basic theory explaining cooperation.

In this talk I will introduce a collection of free teaching tools that I have developed in collaboration with digital artists and graphic designers. These tools are designed to provide undergraduate non-majors with the opportunity to understand key game theory concepts without using any math. An interactive storybook introduces the PD and its four possible outcomes by allowing students to explore each outcome within a "choose your own adventure" structure. A series of infographic images allows students to visualize the most important properties of the PD, including how its potential outcomes compare to the outcomes of other archetypal game theory constructs. An interactive, inquiry-based simulator allows students to set up their own Iterated Prisoner's Dilemma tournaments and analyze their results using a variety of intuitive data visualizations. During my talk I will show how these tools work, discuss how I use them in my courses, and answer questions about incorporating visual and inquiry-based learning tools into the non-majors classroom.

Exploring the origins and diversification of ratsnakes using anchored hybrid enrichment to generate 100s of loci for species tree estimation

Xin Chen, *Alan Lemmon, Emily Lemmon, Frank Burbrink*

4B_305A-Phylogenetics and Diversification
Tuesday, June 24, 2014 10:15 AM-10:30 AM

Sampling a sufficient number of loci across the genome is paramount for estimating credible species trees with high nodal support. These trees with low topological and branch length error are important for use in downstream comparative approaches to properly understand species and morphological diversification. Here we produce a species tree phylogeny of all recognized global ratsnakes (~83 species) using 304 loci generated with anchored phylogenetic methods. We compare different techniques for estimating species trees from large data sets, but note that we obtain nearly 100% support at all nodes with these data. We demonstrate that the ratsnakes are monophyletic with origins in Asia and discuss processes of species diversification across continents.

The phylogenetic position of Indian coralsnakes provides insights into the evolutionary history of basal Elapids

Utpal Smart, Todd Castoe, Eric Smith, David Sanchez, Karthikeyan Vasudevan, Ramesh Aggarwal

4B_305A-Phylogenetics and Diversification
Tuesday, June 24, 2014 10:30 AM-10:45 AM
The Asian coralsnakes (Calliophis and Sinomicrurus) are an enigmatic assemblage of poorly known venomous snakes. A clear understanding of their radiation, including evolutionary relationships, temporal patterns of species diversification and biogeographic history has remained elusive. Using both mitochondrial and nuclear gene fragments and fossil data we estimate the most comprehensive phylogenetic relationships to-date among Asian coralsnakes and evaluate their position among the Elapidae. The phylogenetic signal in our data set is evaluated using concatenated methods (parsimony, bayesian and maximum likelihood) and species tree analyses, and we used multiple calibration points to assess bayesian divergence times in major elapid lineages. Our phylogenetic analysis refutes the monophyly of coralsnakes and reveals the presence of three cryptic, higher-level taxa in the Indian peninsula, two of which are endemic to the Western Ghats Biodiversity Hotspot. According to our divergence analysis, Indian Calliophis species are basal to all other elapids and split from them in the late Oligocene/early Miocene.

Gene Trees vs Species Trees: Piecing together the evolutionary history of the New Zealand cicada genus Kikihia

Sarah Banker, Chris Simon

4B_305A-Phylogenetics and Diversification
Tuesday, June 24, 2014 10:45 AM-11:00 AM
The genus Kikihia is endemic to New Zealand and contains 31 recognized species or subspecies. This genus is well distributed across the two islands of New Zealand and their low dispersal rates and rapid evolution makes Kikihia an ideal model for phylogenetic analysis. An intuitive tree (Dugdale and Fleming, unpublished data) complied from a combination of ecological, morphological and behavioral observations recognized four groups within the genus Kikihia., . The analysis of mitochondrial DNA recognized five groups, the newest of which (Westlandica Group) was composed of cicadas from three of Dugdale and Fleming's groups (Marshal et al. 2009). The goal of investigating nuclear genes is to determine if a nuclear-gene phylogeny supports the Westlandica group as independent, or not and to provide greater resolution to the close relationships within and among groups. The Westlandica group, if not independent, may be the product of past hybridization events and mitochondrial capture, which would be an interesting life history event to observe. The nuclear genes EF1a, Calmodulin, Period and ARD1 were sequenced for 60 specimens of Kikihia, and used to create Bayesian and Maximum Likelihood phylogenetic trees to compare to the mitochondrial phylogeny. These individual gene trees were then combined into a species tree using STEM and *BEAST.

Reconstructing the molecular phylogeny of giant sengis (genus Rhynchocyon) using museum samples

Elizabeth Carlen, Jack Dumbacher, Galen Rathbun

4B_305A-Phylogenetics and Diversification
Tuesday, June 24, 2014 11:00 AM-11:15 AM
Macroscelidea is the order of sengis also known as elephant-shrews. The 18 extant species vary in size and pelage coloration and are restricted to the African continent. Giant sengis (genus Rhynchocyon) have historically been classified using morphological characters, specifically pelage color and pattern. We are investigating whether the currently accepted morphologically distinct species represent phylogenetically distinct species, interbreeding populations with a high degree of variation within a single gene pool, or some other genetic construct. Moreover, previous phylogenetic studies of the Macroscelidea have failed to take into account the phenotypic variation and geographical distribution of Rhynchocyon. Using fresh tissue and historical samples we analyzed 5,800 nucleotide bases (3.4 kb of mitochondrial DNA and 2.4 kb of nuclear DNA) representing all described Rhynchocyon taxa. These data were used to reconstruct a phylogeny of giant sengis and confirm the taxonomic classifications. This research seeks to provide a better understanding of the giant sengi species complex, the biogeographical patterns, and the historical causes for such patterns.

A Complex History of Diversification, Dispersal, and Introgression in the Notropis rubellus (Teleostei: Cyprinidae) species group

Dominik Halas

4B_305A-Phylogenetics and Diversification
Tuesday, June 24, 2014 11:15 AM-11:30 AM
Mitochondrial and nuclear introgression result in incongruence among gene trees, and can greatly complicate the process of species tree reconstruction, which in turn makes it difficult to accurately reconstruct the history of dispersal and diversification within a group. In the Central Highlands of North America (the Appalachian, Ozark, and Ouachita Mountains) multiple clades of fishes have been diversifying extensively since the Miocene, resulting in the highest diversity of freshwater fishes to be found outside the tropics. Multi-locus phylogenies of the taxa which took part in this diversification are revealing new details of the temporal and geographical context of this diversification. One such taxon is the Notropis rubellus species group, a complex of eight distinct lineages within the highly diverse freshwater fish family Cyprinidae. It ranges throughout eastern North America, including the Central Highlands, and has also dispersed northward into formerly

glaciated regions. Though a mitochondrial phylogeny of the group exists, the basal relationships within the group are unresolved, hindering reconstruction of its history. In this talk, I present a new multi-locus species tree analysis of the group; with the addition of five nuclear loci, relationships between lineages within the group are fully resolved. Most of the diversification within the group is Pleistocene in age; this contrasts with considerably older divergence dates seen in many sympatric species. Further, the species tree analysis suggests that introgression, both mitochondrial and nuclear, has played a role in the diversification of the group, resulting in a reticulate history for the origin of some populations. The temporal incongruence and with the role of introgression in the diversification history of the Notropis rubellus species group hints at a high level of complexity in the history of dispersal and diversification in the fishes of the North American Central Highlands. Though introgression complicates the reconstruction of accurate species trees, it appears that species tree analyses, if interpreted correctly, may also be helpful in determining that introgression has occurred, and which lineages were involved.

An unusual colonization scenario among Galápagos organisms: Origin and diversification of endemic leaf-toed geckos (Phyllodactylidae: Phyllodactylus)

Omar Torres-Carvajal, Charlie Barnes, María Pozo-Andrade, Washington Tapia, Gabriela Nicholls

4B_305B-Divergence and Biogeography in the Tropics
Tuesday, June 24, 2014 10:15 AM-10:30 AM

In this study we re-examine the biogeography of leaf-toed geckos (Phyllodactylus) endemic to the Galápagos islands. We aim to (i) test the multiple colonization hypothesis against the single colonization scenario proposed for most organisms in the archipelago, (ii) estimate the age of colonization of Phyllodactylus, and (iii) evaluate the role of dispersal and vicariance in the evolution of these lizards.

We sequenced six nuclear and four mitochondrial genes for all recognized species (except P. gilberti from Wolf) of Phyllodactylus from the Galápagos and four species from South America. Phylogenetic relationships were evaluated with likelihood and Bayesian methods including estimation of divergence times and species trees. We used the inferred phylogeny to evaluate previous biogeographic hypotheses. Our results support a multiple colonization scenario as opposed to the single colonization scenario proposed for most terrestrial organisms in this archipelago. All but one species of Phyllodactylus in the Galápagos belong to a single radiation. Founders of this radiation colonized the archipelago 13.2 million years ago, when islands currently above water had not yet emerged. Ten million years later, ancestors of P. darwini representing the second radiation colonized San Cristóbal.

Similar to other Galápagos organisms, the Pacific coast of South America seems to be the source for founders leading to the oldest radiation of leaf-toed geckos. Unlike most Galápagos endemics, however, P. darwini might have its origins in the Andes. Our phylogenetic hypotheses and recent paleogeographic data support both dispersal and vicariance as mechanisms leading to the radiation of leaf-toed geckos in the Galápagos. Our results are in agreement with recent literature demonstrating that the Galápagos harbors high levels of unrecognized diversity.

Testing the roles of orogeny and habitat heterogeneity in driving allopatry in mid-elevation frogs (Aromobatidae: Rheobates) of the northern Andes

Astrid Muñoz-Ortiz, Álvaro Velásquez-Álvarez, Carlos E. Guarnizo, Andrew J. Crawford

4B_305B-Divergence and Biogeography in the Tropics
Tuesday, June 24, 2014 10:30 AM-10:45 AM

Orogenic processes and Pleistocene climate fluctuations have been proposed as some of the main mechanisms to explain the high diversity and endemism for animals and plants in the Northern Andes. In this study we investigate and evaluate the role of Andean high peaks and the low Magdalena Valley in creating barriers to dispersal and promoting vicariance within the mid-elevation Andean frog genus Rheobates (Anura: Aromobatidae), endemic to Colombia. The frogs of this genus inhabit the flanks of the Eastern Cordillera (eastern and western) and the eastern flank of the Central Cordillera at an altitudinal range of 350—2200 metres above sea level. The two Cordilleras are separated by the Magdalena River Valley, while a continuous string of high mountain peaks above 2500 metres separate the flanks of the Eastern Cordillera. The disjunct distribution of Rheobates suggests that gene flow is restricted between populations living on different Cordilleras and on opposite flanks within the Eastern Cordillera. We analysed mitochondrial and nuclear DNA sequences from 37 individuals of Rheobates (Anura: Aromobatidae) to infer phylogenetic relationships, divergence times and ancestral areas. Additionally, we tested the role of climatic variables in determining the present geographical boundaries of the species using species distribution models. We found that phylogeny of Rheobates is largely predicted by geography, with one population from the eastern flank of the Eastern Cordillera sharing a common ancestor with all other Rheobates 21 million years ago (Ma; 95% credible interval 31–10 Ma). Populations in the Cordillera Central were monophyletic, isolated across the Magdalena Valley with a divergence time estimated at 13 Ma (19–7 Ma). We also detected one recent crossing of the Eastern Cordillera, along with unanticipated latitudinal phylogeographic structure within the western flank of the Eastern Cordillera. Environmental niche tests indicated that the Magdalena Valley and the high peaks of the Eastern Cordillera are significant environmental barriers to Rheobates populations. Our study offers broad support for the classic mountain orogeny model of vicariant divergence, but suggests that lowland habitat heterogeneity may also have played a long-term role in promoting vicariance, despite a long history of palaeo-climatic fluctuations.

Key words: Andean uplift, Colombia, disjunct distribution, divergence times, molecular phylogenetics, phylogeography, Rheobates, vicariance.

Evolution and Biogeography of the Bignoniaceae: Insights into the origin of the Neotropical Flora

Lucia Lohmann

4B_305B-Divergence and Biogeography in the Tropics
Tuesday, June 24, 2014 10:45 AM-11:00 AM
The history of present-day patterns of species diversity has fascinated biogeographers and ecologists for a long time. Yet, the exact factors that have shaped current distribution patterns remain to be understood. The plant family Bignoniaceae represents a conspicuous component of Pantropical forests, being particularly diverse and abundant in the Neotropics. The Neotropical representatives of the Bignoniaceae are distributed across multiple lineages, providing important insights into the origin of Neotropical ecosystems. Representatives of the Bignoniaceae occur in most ecological zones and exhibit considerable diversity in reproductive and vegetative morphology. The ecological importance of this group, combined with its broad distribution and morphological diversity make this plant family an excellent model for investigating the history of Tropical ecosystems, in particular the Neotropics where this plant family is most abudant and diverse. Here, I use broad-scale molecular phylogenetic data to investigate patterns of diversity across the Tropics. I then use fine-scale phylogenetic data of selected lineages to investigate finer-scale patterns of diversity within the Neotropics. Insights gained from ecological, morphological, genetic, biogeographic, paleontologic, and geologic data suggest that patterns of modern diversity have complex evolutionary histories.

Diversification of Malagasy ectotherms Part II: an exploration of patterns and processes

Brice Noonan, Anne Yoder, Miguel Vences, Achille Raselimaninana, Brian Fisher

4B_305B-Divergence and Biogeography in the Tropics
Tuesday, June 24, 2014 11:00 AM-11:15 AM
The tropical regions of the world house a disproportionately high amount of the world’s biodiversity. Though the reasons for this are not well understood, a number of hypotheses have sought to explain these high rates of speciation; most focusing on the well-studied biota of the Neotropics. The goal of this research project is to better understand biotic diversification in the tropics by focusing on Madagascar, a natural laboratory for such work. Due to its isolation it is well suited to exploring how organisms diverge (speciate) and persist in fragmented habitats without the confounding influence of migration to/from adjacent areas.

Ectotherms represent an ideal model with which to explore these hypotheses as the influence of abiotic changes (e.g. glaciation associated cooling) ties them more directly to the causal factors invoked. Examination of genetic patterns across the Malagasy landscape reveal a highly complex system of unrecognized diversity, unexpected patterns and fine-(geographic)-scale diversification that greatly enhances our understanding of evolution here and elsewhere in the tropics.

Phylogeny and biogeography of the spiny ant genus Polyrhachis (Hymenoptera: Formicidae)

Dirk Mezger, Corrie Moreau

4B_305B-Divergence and Biogeography in the Tropics
Tuesday, June 24, 2014 11:15 AM-11:30 AM
In terrestrial ecosystems, ants are one of the most widespread and dominant arthropod groups. Polyrhachis (spiny ants) is a very species rich genus which is widely distributed with more than 700 species over most of the Old World tropics. Based on seven nuclear and mitochondrial genes, we reconstruct the phylogeny of these ants and explain their current geographic distribution. We discuss whether their evolution started in South-East Asia or Australia.

Adaptation and Muller's ratchet in sympatric populations of sexual and apomictic Boechera spatifolia (Brassicaceae)

John Lovell, John McKay, Stephen Wright, Timothy Sharbel

4B_306A-Sex and Evolution
Tuesday, June 24, 2014 10:15 AM-10:30 AM
Asexuality holds several advantages over sexual reproduction, including increased genetic contributions to subsequent generations and reduced resource investment in reproduction. Despite this “2-fold” advantage, obligately asexual lineages are rare among multi-cellular organisms. “Muller’s Ratchet”, the sequential and irreversible fixation of deleterious mutations in asexual populations, is one explanation for the overwhelming prevalence of sexual reproduction in animals and vascular plants. Here, we use the atlas of non-coding genomic sequences that are conserved across the Brassicaceae plant family to characterize the extent and nature of mutations in seven sympatric pairs of sexual and apomictic (asexual) genotypes of Boechera spatifolia. In each of the seven comparisons, the ratio of mutations at conserved to neutral sites is significantly elevated in apomictic lineages relative to sexuals. Additionally, apomictic populations show signatures of reduced adaptation to local conditions across the landscape. These data provide evidence that asexual lineages harbor an increased level of mutations at sites under positive selection, and invoke Muller’s Ratchet as a powerful force in the evolution of asexual lineages.

The role of genetic drift in the maintenance of sexual reproduction in an artificial gene network model

Amanda Whitlock, Christina Burch, Kayla Peck

4B_306A-Sex and Evolution
Tuesday, June 24, 2014 10:30 AM-10:45 AM
Though sexual reproduction is nearly ubiquitous in nature, its costs are substantial. Foremost among these costs are the twofold cost of males and the cost of destroying successful genetic associations. Understanding the persistence of sex despite these detriments is a central question in evolutionary biology. Recent theoretical investigations of the benefits of sex have focussed on scenarios in which recombination eliminates linkage disequilibrium that accumulates due to genetic drift. Drift increases the probability that the fit, unmutated genotype will be stochastically lost and that deleterious mutations will become fixed in the population. By destroying linkage disequilibrium, sex hastens the removal of deleterious mutations from the population and prevents loss of the fit ancestral genotype. Previous computational investigations have supported this hypothesis, demonstrating greater than twofold benefits of sex arising from genetic drift in structured populations. However, these models did not incorporate interactions between

mutations, so sexual populations did not experience one of the major costs of sex--the cost of destroying successful genetic combinations.

Here we examine the consequences of genetic interactions for the evolution of sex in structured populations. We use a computational model of a regulatory gene network in which each gene regulates other genes, and these interactions determine a phenotype. These gene networks exist as individuals which undergo mutation, selection and reproduction in an evolving population. Previous work has shown the distribution of mutational effects evolves in this model due to changes in the genetic architecture, which evolves differently in sexual and asexual populations. In this work, we simulate evolution towards a target phenotype in a subdivided population, under conditions which will cause varying degrees of genetic drift and thus, linkage disequilibrium.

We find that fitness evolves in both sexual and asexual populations, reaching an equilibrium after an initial period of rapid evolution. Increased levels of genetic drift decrease the maximum fitness an evolving population reaches in both populations. However, we find no evidence under any conditions that sexual populations evolve to have a higher fitness than asexual populations. The recombination load experienced by sexual populations in our experiments was not sufficient to explain the complete absence of an advantage to sex in our experiments. Rather, an unanticipated impact of genetic interactions on drift load seems to explain this major difference between our experiments and those of Hartfield et al (2010; 2012). Our results emphasize the need to consider genetic interactions in investigations of the evolution of sex.

Unisexual whiptail lizards find a loophole: how meiosis progresses in a species created through hybridization

Aracely Newton, Diana Baumann, Peter Baumann

4B_306A-Sex and Evolution
Tuesday, June 24, 2014 10:45 AM-11:00 AM

Although sexual reproduction is the most prevalent form of proliferation among vertebrates, some organisms instead employ parthenogenesis and reproduce without contribution from males. The genus Aspidoscelis – commonly known as whiptail lizards – includes bisexual and unisexual species, with the latter having arisen by inter-specific hybridization between bisexual species.

We have previously shown that late oocyte nuclei from unisexual Aspidoscelis species contain twice as much DNA (8C) as their bisexual relatives, despite similar genome sizes and identical ploidy in somatic cells. We surmised that an additional doubling of chromosomes followed by normal meiosis allows for the formation of diploid oocytes. Using homolog specific probes, we further demonstrated that pairing occurs between identical, rather than homologous, chromosomes, an important deviation from sexual species which is pivotal for the maintenance of heterozygosity over many generations of parthenogenetic reproduction.

We have now characterized events preceding diplotene. Surprisingly, most oocyte nuclei in unisexuals harbor no more DNA than those in bisexuals, indicating that the additional doubling either occurs after initiation of meiosis or is restricted to a small subset of cells. Oocytes in adult bisexuals are predominantly diplotene, confirming successful progression through meiotic prophase. In contrast, unisexuals display a majority of oocytes in the pairing stage known as zygotene, suggesting that oocytes are stalled due to an inability to pair homologous chromosomes properly. Importantly, unisexual diplotene oocytes appear to be exclusively 8C, consistent with the existence of a checkpoint that prevents 4C oocytes from proceeding through pachytene and into diplotene. Strikingly, the small percentage of oocytes that progress to diplotene is sufficient to allow unisexual lizards to overcome the sterility that is commonly observed in inter-specific hybrids between species that are too divergent for complete homolog pairing during meiosis. Furthermore, the loss of over 95% of oocytes during oogenesis has no apparent effect on fecundity.

Germline mutation as an outcome of evolved and continually evolving biological processes

Adi Livnat

4B_306A-Sex and Evolution
Tuesday, June 24, 2014 11:00 AM-11:15 AM

In recent years it has become clear that germline mutation is affected by complex biological mechanisms and by DNA sequence and structure. Can this new empirical knowledge tell us something about how evolution works? Indeed, I argue that opening up the black box of the nature of mutation affects fundamental concepts in our understanding of evolution. Specifically, the fact that genetic interactions affect the per-locus probability and nature of germline mutation means that information flows from multiple loci into the locus undergoing mutation. This in turn means that, although complex combinations of alleles across loci are not in and of themselves heritable because they are broken down by meiotic recombination, they have heritable effects through the mutations that are derived from them. Finally, it follows that selection acting on complex combinations of alleles across loci--i.e., selection acting on individuals as complex wholes, and not simply on single alleles as separate actors--can have heritable effects and drive adaptive evolution. Thus, our new empirical understanding of the nature of mutation offers a way of addressing multiple fundamental open questions in evolutionary biology from a unifying perspective, including how genetic interactions evolve and what the role of sex in evolution is. Namely, sex generates a vast number of different combinations of alleles, selection acts on these combinations, and mutation allows the transmission of information from these combinations to future generations.

The effects of clonal reproduction on the rate of evolution.

Maria Orive

4B_306A-Sex and Evolution
Tuesday, June 24, 2014 11:15 AM-11:30 AM

We develop a model that examines how clonal reproduction affects a population's rate of evolution and amount of evolutionary lag. The types of life history structure typical of ecologically important organisms such as reef-building corals and many clonal plant species include modular organization, indeterminate growth, and the existence of both asexual (clonal) and sexual reproduction.

Predicting how such organisms will respond to rapid environmental change necessitates an understanding of which specific life history parameters most directly determine the rate of evolution and the amount of maladaptation. We use an extension of a previous population genetic model for the fate of alleles in stage-structured diploid populations with clonal and sexual reproduction (Orive 1995, 2001) as well as recent theoretical results for evolution in stage-structured populations (Barfield et al. 2011), which only considered sexual reproduction. Important features of the model developed here include an explicit consideration of the effects of somatic mutations and of the difference between sexual and clonal offspring in the environmental component of phenotype.

Differential natural selection on codon usage among amino acids in Drosophila pseudoobscura.

Richard Kliman

4B_306B-Molecular/Protein Evolution
Tuesday, June 24, 2014 10:15 AM-10:30 AM

Like other species of Drosophila, D. pseudoobscura has a distinct bias toward the usage of C- and G-ending codons. Codon bias differs among amino acids (and other codon classes) in Drosophila, which may reflect differences in the intensity of selection on codon usage. Ongoing natural selection on synonymous codon usage should be reflected by shifts in the site frequency spectra of derived states at polymorphic positions, with more pronounced shifts when the intensity of natural selection is increased. 33,729 synonymous polymorphic sites on Chromosome 2 in D. pseudoobscura were analyzed, and shifts in the site frequency spectra are consistent with differential intensity of natural selection on codon usage. The shifts are more pronounced for polymorphic synonymous sites than for polymorphic intron sites, also consistent with natural selection.

Using disease data to inform models of protein evolution

Jeffrey Thorne, Alexander Griffing, Eric Stone, Liwen Zou

4B_306B-Molecular/Protein Evolution
Tuesday, June 24, 2014 10:30 AM-10:45 AM

A mutation that causes disease is likely to be selectively deleterious and is unlikely to persist over time. For some protein-coding human genes, a large number of selectively deleterious mutations have been identified. We are interested in combining this information from disease data with interspecific sequence data. One reason for doing this is to improve our probabilistic models of protein-coding DNA evolution. Another reason is to predict whether a mutation might cause disease. A modelling challenge arises when an amino acid type at a protein sequence position causes disease in one species but not in another. Two separate attempts to meet this challenge as well as some preliminary results will be discussed.

Microsatellites as Targets of Natural Selection

Bret Payseur, Ryan Haasl

4B_306B-Molecular/Protein Evolution
Tuesday, June 24, 2014 10:45 AM-11:00 AM

Microsatellites – short tandem repeats – are highly polymorphic loci routinely used as neutral markers in population genetics. Microsatellites also contribute to morphological and behavioral evolution, control variation in gene expression throughout the genome, and cause disease, suggesting they are often targeted by natural selection. Existing population genetic models of selection and methods for its characterization, which focus on variants with low mutation rates such as single nucleotide polymorphisms (SNPs), are not appropriate for microsatellites. We developed models that flexibly describe the microsatellite fitness surface, along with realistic models of mutation based on microsatellite characteristics. We implemented a statistical approach that uses approximate Bayesian computation (ABC) to choose the models and parameter values that best fit microsatellite polymorphism data. Cross-validation simulations revealed that our method offers high power and low false positive rates in distinguishing selection from neutrality. We applied our approach to microsatellite genotypes from an Italian population of humans. A collection of microsatellites chosen as a priori candidates for selection showed a range of selective regimes, whereas loci far from genes mostly displayed neutral patterns. Both microsatellites that affect gene expression (located in promoters) and those that change protein structure (located in exons) were inferred to be targeted by selection. Some microsatellites known to cause disease appeared to evolve neutrally. By providing an initial portrait of microsatellite fitness surfaces, our results underscore the significance of considering non-SNP variation for understanding the effects of natural selection across the genome.

Selection on position and context of nonsense codons in introns

Megan Behringer, David Hall

4B_306B-Molecular/Protein Evolution
Tuesday, June 24, 2014 11:00 AM-11:15 AM

Introns occasionally remain in mature mRNAs due to splicing errors. Resulting encoded proteins represent a metabolic cost and may also have deleterious function. The nonsense mediated decay pathway degrades aberrant mRNAs, which it recognizes by the presence of an in-frame premature stop codon. We investigated whether selection has shaped the location and context of premature termination codons in introns in order to facilitate nonsense mediated decay in seven model organisms. We conclude that both the location and context of premature termination codons are shaped by selection for efficient degradation of aberrant mRNAs.

A Cross---species Study of Probabilistic Measures for Protein Amino Acid/Codon Preference Given Structure Environment Using Residue Level Features

Kuangyu Wang, Xiang Ji, Clemens Lakner, Shuhui Yu, Jeffrey Thorne

4B_306B-Molecular/Protein Evolution
Tuesday, June 24, 2014 11:15 AM-11:30 AM

People have long been interested in studying the impact of protein structure on protein evolution. Here, we constructed probabilistic models for protein amino acid/codon preference using high-resolution protein structure data from humans and mice. We were interested in detecting differences between the models from these species because such differences could stem from differences in effective population size. In addition, we examined whether tertiary structure had correlations with codon preference beyond those that can be explained via the amino acid encoded by the codons.

Diversification under sexual selection by mate choice: role of mate preference strength and divergence

Rafael Rodriguez, Janette Boughman, David Gray, Eileen Hebets, Gerlinde Höbel, Laurel Symes

4B_BalC-SSE Symposium: The role of sexual selection in speciation: an integration of theoretical and empirical perspectives
Tuesday, June 24, 2014 10:15 AM-10:40 AM

After decades of research, biologists continue to debate the contribution of sexual selection to diversification. This may be in part because comparative studies of the role of sexual selection in speciation have focused mainly on the strength of sexual selection, which is one of the main features that distinguish it from natural selection, but may fail to capture the full scope of the action of selection --- by contrast, students of natural selection focus on environmental differences that help capture differences in fitness peaks across populations. To ask how this disparity in focus may affect the conclusions of studies on selection, we examined how the strength of sexual selection by mate choice and the extent of divergence in mate preferences relate to mating display diversification, with a survey of case studies of mate choice. We find that diversification is better predicted by differences in display values favored by preferences, rather than by preference strength alone, although both of these factors interact in complex ways. More broadly, the strength of selection influences the rate of evolution, but differences in the causes of selection determine how much divergence can occur. We suggest that keeping this distinction in mind will help compare the roles of ecological and sexual selection in speciation.

Sexual selection and the cycle of speciation in birds

Nathalie Seddon

4B_BalC-SSE Symposium: The role of sexual selection in speciation: an integration of theoretical and empirical perspectives
Tuesday, June 24, 2014 10:40 AM-11:05 AM

Whether sexual selection drives animal diversification has long been controversial, and the traditional approach of comparing patterns of species richness among higher taxa has failed to resolve the issue. Here, we apply a novel phylogenetic modeling approach to a large sample of recent speciation events in birds using plumage dichromatism as an index of sexual selection. We show that sexual selection increases net diversification, both in terms of the formation of new species and also the rate at which they come into coexistence after periods of isolation. Overall, our findings establish the importance of sexual selection for the build up of biodiversity.

Multimodal signal divergence and the genomics of speciation-with-gene-flow in an island bird

Al Uy, Rebecca Safran, Elizabeth Cooper

4B_BalC-SSE Symposium: The role of sexual selection in speciation: an integration of theoretical and empirical perspectives
Tuesday, June 24, 2014 11:05 AM-11:30 AM

Divergence in mating signals can lead to premating reproductive isolation. However, given that many taxa simultaneously divergence in multiple signals across different sensory modalities, it remains less clear how changes in multimodal signals affect conspecific recognition and reproductive isolation. In addition, given that multiple traits can be used in conspecific recognition, can divergence in multimodal signals facilitate speciation despite substantial gene flow? Here, we explore these two questions using a flycatcher species complex in the Solomon Archipelago with populations that have fixed differences in plumage color (visual) and song (acoustic) signals despite small geographic barriers. We find that divergent multimodal signals can be used sequentially in conspecific recognition, with song acting in long-range and color in short-range communication. Further, we find extremely low differentiation in the genomic background between populations with divergent color and song, but candidate genes for plumage color are fixed between populations. Our work, therefore, suggests that speciation-with-gene-flow can be mediated by multimodal signal divergence.

Highly variable recombinational landscape modulates efficacy of natural selection in birds

Toni Gossmann

4C_301A-Genome Evolution
Tuesday, June 24, 2014 1:30 PM-1:45 PM

Determining the rate of protein evolution and identifying the causes of its variation across the genome are powerful ways to understand forces that are important for genome evolution. By using a multi-tissue transcriptome data set from great tit (Parus major), we analysed patterns of molecular evolution between two passerine birds, great tit and zebra finch (Taeniopygia guttata), using the chicken genome (Gallus gallus) as an outgroup. We investigated whether a special feature of avian genomes, the highly variable recombinational landscape, modulates the efficacy of natural selection through the effects of Hill-Robertson interference, which predicts that selection should be more effective in removing deleterious mutations and incorporating beneficial mutations in high-recombination regions than in low-recombination regions. In agreement with these predictions, genes located in low-recombination regions tend to have a high proportion of neutrally evolving sites and relaxed selective constraint on sites subject to purifying selection, whereas genes that show strong support for past episodes of positive selection appear disproportionally in high-recombination regions. There is also evidence that genes located in high-recombination regions tend to have higher gene expression specificity than those located in low-recombination regions. Furthermore, more compact genes (i.e., those with fewer/shorter introns or shorter proteins) evolve faster than less compact ones. In sum, our results demonstrate that transcriptome sequencing is a powerful method to answer fundamental questions about genome evolution in non-model organisms.

Genome sequencing, assembly and analysis of the four cactus host populations of Drosophila mojavensis

Luciano Matzkin, Carson Allan

4C_301A-Genome Evolution
Tuesday, June 24, 2014 1:45 PM-2:00 PM

Understanding the genetic basis of adaptation is one of the fundamental questions in biology. A complete grasp of the genetic architecture of adaptation can best be attained by a multifaceted approach, which incorporates not only information of the local ecological environment of the organism but as well as an understanding of genome level variation and divergence. Here we examine genomic divergence across the four ecologically distinct cactus host populations of Drosophila mojavensis. This necrotic cactus breeding species inhabits the deserts of the US southwest and northwest Mexico. Each population utilizes a distinct cactus species, providing resident populations with a unique chemical environment. The recent divergence of these populations (

Illumina sequencing was performed on inbred lines from each of the three populations (Sonora Desert, Mojave Desert and Baja California) at an approximate coverage of about 65X. Reads were then template assembled to the previous sequenced genome of D. mojavensis (from Catalina Island). Per population, we were able to reconstitute 93-97% of the template genome's scaffolds. Using our analysis pipeline, 14,238 loci of the 14,581 loci in the template genome were obtained, of which we were able to obtain complete alignments across the four populations for 13,517 loci. Rates of protein evolution were determined for all loci using a several approaches. Genes with evidence of positive selection (422 after FDR correction) were linked to the local ecological environment and involved several biological functions including metabolism, reproduction, and response to stimuli. Genes with accelerated rate of evolution were overrepresented in the X and dot chromosomes. There was an association between expression level and rate of evolution, with the gene set composed of low expression transcripts overrepresented for the high dN/dS ratio class genes. Furthermore, we observed that genes that were transcriptionally regulated in response to cactus host shift were significantly more likely to have evolved under positive selection. Results of this study provides insight into local ecological adaptation and the early process of speciation.

Genomic signatures of selection in a classic fisheries harvest experiment

Nina Overgaard Therkildsen, Steve Munch, David Conover, Stephen Palumbi

4C_301A-Genome Evolution
Tuesday, June 24, 2014 2:00 PM-2:15 PM

By imposing high levels of mortality on particular size and age groups, intense fishing can cause rapid evolution. Overwhelming evidence suggests that fishing has driven widespread changes in life history traits such as growth rate and timing of maturation across the world's fish populations. In many cases, the changes appear to be at least partially genetic, making fishing one of the most pervasive, human-caused evolutionary impacts in the sea. Yet, so far almost nothing is known about the underlying genomic basis for these common changes in fish stocks: what types of genetic variation does fisheries-selection act on, how extensively does it impact the genome through direct and hitchhiking effects, and how reversible are the changes once fishing stops? To address these questions, we have returned to a seminal experiment that demonstrated substantial evolution in growth rates and a suite of correlated traits in response to size-selective fishing over just five generations in the Atlantic silverside (Menidia menidia). With RAD-tag sequencing of archived samples from the original experiment, we have begun to characterize the genomic response underlying the observed phenotypic divergence between selected lines (e.g. a nearly two-fold difference in adult size). A scan of 39,351 SNPs distributed genome-wide indicate that selection has caused large allele frequency differences at hundreds of unlinked loci and that in most cases, the genetic changes are highly localized to single SNPs, with limited hitchhiking effects. These widespread signatures of soft rather than hard sweeps indicate selection primarily on ancient polymorphisms at high frequency in the original source population rather than on a few new or initially rare mutations. In addition to shedding light on how fisheries-induced selection operates, the study therefore also contributes to our general understanding of selection on standing genetic variation in large highly polymorphic populations.

Genome wide congealing and the dynamics of speciation

Samuel Flaxman, Jeffrey Feder, Patrik Nosil

4C_301A-Genome Evolution
Tuesday, June 24, 2014 2:15 PM-2:30 PM

Our current understanding of speciation is still largely based on theory for small to moderate numbers of genes. We describe a possible emergent genome process involving the aggregate effect of large numbers of genes contributing to the evolution of reproductive isolation across the speciation continuum. When a threshold number of divergently selected mutations of modest to low fitness effect accumulate between populations diverging with gene flow, nonlinear transitions can occur in which levels of adaptive differentiation, linkage disequilibrium, and reproductive isolation dramatically increase. In effect, the genomes of the populations start to "congeal" into distinct entities representing different species. At this stage, reproductive isolation changes from being a characteristic of specific genes to a property of the genome. We examine conditions conducive to genome wide congealing (GWC) and how to empirically test for GWC with some putative empirical examples. We conclude with cautious optimism that models and concepts discussed here may provide a framework for integrating information from genome scans, selection experiments, QTL mapping, association studies and natural history to develop a deeper understanding of the genomics of speciation.

MAC-PRF: Inferring intragenic clusters of sites under natural selection from polymorphism and divergence

Ning Li, Zi-Ming Zhao, Zhang Zhang, Jeffrey Townsend

4C_301A-Genome Evolution
Tuesday, June 24, 2014 2:30 PM-2:45 PM
Inference of natural selection between recently diverged species often relies on comparison and contrast of polymorphism and divergence in DNA sequences. Typically, whole genes have been assessed, analyzed as a unit, and implicated as being under selection, because uniform intensity of selection is an implicit or explicit assumption of extant tests for selection based on polymorphism and divergence. However, site-specific analyses of molecular divergence as well as abundant indirect evidence imply that regions within genes experience diverse levels of natural selection. To quantify this variation in selection based on intragenic polymorphism and divergence, we present a novel approach combining Model Averaged Clustering with Poisson Random Field theory (MAC-PRF). We demonstrate that when selection varies across a linear sequence, our method provides greater accuracy and precision than intragenically homogeneous Poisson Random Field approaches in estimating selection intensities. Furthermore, our genomic analysis of genes across the wine yeast Saccharomyces cerevisiae genome demonstrates that although much of the coding sequence is under purifying rather than adaptive natural selection, nearly 50% of coding sequence overall is under an adaptive regime of selection, and adaptively evolving sites are distributed across about 80% of the genes in the whole genome. The presence of extensive regions of purifying selection explains the finding that few genes are significant under traditional tests of polymorphism and divergence, even though many critical sites or regions within individual genes are playing important adaptive roles in an evolutionary history of adaptive natural selection.

Evolution of weed phenotypes in radish

Amanda Charbonneau, Ian Dworkin, Jeffrey Conner

4C_301B-Trait Evolution
Tuesday, June 24, 2014 1:30 PM-1:45 PM
Agricultural fields are an atypical habitat for most plants, and adaptation to such an environment generally requires plants to grow, flower and set fruit quickly or risk being tilled under. We use the genus Raphanus (radish) to understand which traits influence the success of weedy populations, and how those traits have evolved. We analyzed multiple subspecies, crop cultivars and geographically distinct weeds from Raphanus ssp. populations from around the world at neutral genetic markers to determine population structure; and also performed several large common garden experiments. Our analysis suggests that weedy radish has evolved from non-weedy ancestors, which would have had extremely low fitness in an agricultural setting. We are now taking a genome scan approach to look for signatures of selection in several weed populations.

Rapid evolution at the edge: selection on life-history traits during experimental range expansions

Emanuel Fronhofer, Florian Altermatt

4C_301B-Trait Evolution
Tuesday, June 24, 2014 1:45 PM-2:00 PM
Species' ranges are rarely static. Shifts in species' ranges have been especially pronounced in the context of global climatic changes and other anthropogenic environmental modifications. However, understanding and predicting the dynamics of ranges, which is highly relevant to both basic and applied research, has proven to be difficult.

In principle, population spread can be described as a function of three basic processes, which can be linked by trade-offs: dispersal, reproduction and density-dependence. Empirical evidence and a growing number of theoretical studies suggest that these three processes are subject to rapid evolutionary changes during invasions. This may lead to an acceleration of the population's spread. Yet, experimental evidence that substantiates these claims remains scarce.

We here present experimental evidence for the concurrent evolution of dispersal and other life-history traits – such as growth rate, equilibrium density and morphological parameters – during replicated invasions in microcosms of the ciliate Tetrahymena sp. In accordance with previous empirical studies and theoretical predictions we found that invasions select for higher individual velocities and dispersal rates. This was accompanied by changes in morphology: individuals at expanding range fronts showed larger and slightly more elongated cells. In addition, experimental invasions also impacted growth rates and fundamentally changed density-regulation within replicated populations. We not only observed that growth rates were higher at expanding range fronts but also found an increase in equilibrium population size. Together, these findings underline that invasion and range expansion cannot exclusively be studied from an ecological perspective, but must include evolutionary dynamics.

Patterns of metabolic network evolution in plants

Seung Rhee, Lee Chae, Kate Dreher, Taehyong Kim, Ricardo Nilo-Poyanco, Chuan Wang

4C_301B-Trait Evolution
Tuesday, June 24, 2014 2:00 PM-2:15 PM
Flowering plants dominate earth’s terrestrial environment. How plants evolved to achieve this dominance is a major question in plant biology. Historically, investigations into plant evolution have usually focused on morphological characters, even though metabolism is critical for producing adaptive traits such as pollination, stress tolerance, and defense. Consequently, little is known about the organization, function, regulation, and evolution of plant metabolic networks. To better understand plant metabolism in light of evolution and enable systematic comparisons of metabolism across plant species, we developed a high-throughput computational infrastructure that combines machine-learning based prediction, automated-validation, and manual curation of enzymes and pathways. Using this infrastructure, we predicted the metabolic complements of 14 flowering plants (7 grasses, 7 eudicots), 1 moss, 1 early vascular plant, and 1 algal species. We compared the conservation and divergence of metabolic pathways across these species in terms of

metabolic domain, pathway topology, gene duplication history, and genomic organization of metabolic genes. We discovered a number of interesting and surprising findings, including greater proliferation of genes coding for specialized metabolic functions by mechanisms distinct from primary metabolic genes, extensive lineage-specific patterns of physical clustering within the genome and coexpression, equivalent gain and loss events of reactions leading to pathway divergence, and differential points of divergence in biosynthesis and degradation pathways.

Phenotypic variation and differential gene expression in Virginia opossum (Didelphis virginiana) populations inhabiting different environments.

Sergio Nigenda, Ryan Harrigan, Hugo Ruiz-Piña, James Beasley, David Valenzuela, Robert Wayne

4C_301B-Trait Evolution
Tuesday, June 24, 2014 2:15 PM-2:30 PM
Correlating environmental with genetic variation is important for understanding how the environment and evolutionary processes jointly shape populations' phenotypic and genetic variation. The Virginia opossum (Didelphis virginiana) is a marsupial species widely distributed through Central and North America, inhabits different environments and shows phenotypic variation across its geographic range. Combining phenotypic data from museum and live specimens, environmental data from satellite databases and transcriptome data generated with RNA-Sequencing (RNA-Seq), we attempted to identify environmental variables and differentially expressed genes that may play an important role in driving the phenotypic differences and adaptation in this species. We found that temperature seasonality and isothermality are the environmental variables explaining most of the variation (20 to 71%) in body size, skin pigmentation and coat color. The morphological data also indicates that drastic changes in these phenotypes occur between latitudes 27° and 30° N. In addition, the carbohydrate metabolism, skeletal muscle contraction and melanocyte development gene ontology terms were significantly enriched when comparing tropical versus temperate populations. Interestingly, the genes Peroxisome proliferator-activated receptor gamma coactivator 1-alpha (PPARGC1A) and Tyrosinase related protein 1 (Tyrp1), show differential expression between these populations. PPARGC1A and Tyrp1 have shown to be important in regulating energy metabolism and pigmentation in placental mammals. Our results suggest that different selective pressures related to temperature stability could be acting in opossum populations distributed north and south of 27-30° N, and Tyrp1 gene could be involved in the biological pathways affecting skin and coat color variation observed in opossum populations. These results contribute to our understanding on how natural selection causes genotypic and phenotypic variation in marsupial species inhabiting different environments.

Repeated cis-regulatory evolution underlies convergent phenotypic adaptation in butterflies.

Sean Mullen, Jason Gallant, Vance Imhoff, Arnaud Martin, Robert Reed, Marcus Kronforst

4C_301B-Trait Evolution
Tuesday, June 24, 2014 2:30 PM-2:45 PM
Convergent evolution provides a rare, natural experiment with which to test the predictability of adaptation at the molecular level. Little is known about the molecular basis of convergence over macro-evolutionary timescales. Using a combination of positional cloning, gene expression analyses, and developmental data, we demonstrate that parallel wing pattern variation in two distantly related butterflies is controlled by cis-regulatory variation in the same gene, WntA. Population genomic sequencing reveals the specific variants controlling convergent mimetic polymorphism across 65 million years of evolution. By pinpointing the repeated modulation of a core developmental process in the generation of an adaptive trait, our results reveal a strikingly predictable molecular basis for phenotypic convergence over deep evolutionary time.

Changes in gene regulation associated with reproductive isolation in house mice

Katya Mack, Polly Campbell, Matt Bomhoff, Michael Nachman

4C_302A-Speciation and Hybridization
Tuesday, June 24, 2014 1:30 PM-1:45 PM
Understanding the genetic basis of speciation lies at the heart of evolutionary biology. While the majority of research in this area has focused on identifying incompatibilities between protein coding genes, negative epistatic interactions between divergent regulatory elements may also contribute to reproductive isolation. Here we characterize regulatory divergence between the partially reproductively isolated house mouse subspecies, Mus musculus musculus and Mus musculus domesticus. One direction of a cross between these subspecies produces sterile F1 males, while the reciprocal cross produces fertile F1 males. Whole testis transcriptome data was used to quantify gene expression levels in wild-derived inbred lines of M. m. musculus, M. m. domesticus, fertile F1 males, and sterile F1 males. This allowed us to identify genes that were misexpressed in sterile hybrids. Expression divergence between the subspecies was categorized as cis-, trans-, or some combination based on differential expression between the parents and allele-specific expression in the fertile F1 hybrid. Genes with expression outside the range of the parents in the sterile hybrid were identified as misexpressed. Comparison of these data sets provides insight into how divergent regulatory machinery contributes to hybrid dysregulation.

Natural hybridization between lineages that diverged from each other over 50 million years ago

Carl Rothfels, Anne K. Johnson, Peter H. Hovenkamp, David L. Swofford, Harry C. Roskam, Christopher R. Fraser-Jenkins

4C_302A-Speciation and Hybridization
Tuesday, June 24, 2014 1:45 PM-2:00 PM
The pace at which populations become reproductively isolated from each other determines how quickly new species can form. Here we show that a fern from the French Pyrenees, ×Cystocarpium roskamianum, is a recently formed intergeneric hybrid between parental lineages that diverged approximately 60 million years ago [95% highest posterior density: 40.2–76.2 million years ago]. This is an extraordinarily deep hybridization event—

roughly akin to an elephant hybridizing with a manatee, or a human with a lemur. This finding, especially in the context of other reported "deep hybrids," suggests that populations of ferns and other plants that reproduce by spores may take longer to achieve complete genetic separation from each other because they lack the premating isolation mechanisms that characterize many other groups. This result implies that major features of Earth's biodiversity—such as the relatively small number of species of ferns compared to those of angiosperms—may be, in part, an indirect byproduct of this slower "speciation clock," rather than a direct consequence of adaptive innovations by more diverse lineages.

Islands as venues for homoploid hybrid speciation: A case for the endangered hawaiian duck

Philip Lavretsky, Andrew Engilis, John Eadie, Jeffrey Peters

4C_302A-Speciation and Hybridization
Tuesday, June 24, 2014 2:00 PM-2:15 PM

Speciation is regarded primarily as a bifurcation from an ancestral species resulting in two distinct taxonomic units. Although hybrid speciation is known to occur, such events have been regarded as rare in homoploid systems. Here, we provide several lines of evidence supporting the hypothesis that the endangered Hawaiian duck (Anas wyvilliana) is descended from ancient hybridization between the mallard (A. platyrhynchos) and Laysan duck (A. laysanensis). Specifically, using coalescent methods, we reveal that gene flow from either of the putative parental species is necessary to explain the diversity and apparent genomic mosaic within the Hawaiian duck. We discuss how island systems might act as arenas for interspecific hybridization leading to speciation as a result of rapid isolation between hybrids and parental species. Hybrid speciation may be a more common mechanism than previously thought for generating biodiversity, especially during rapid radiations.

Rapid speciation along a genetic continuum in a neo-XY bark beetle

Ryan Bracewell, Barbara Bentz, Jeffrey Good

4C_302A-Speciation and Hybridization
Tuesday, June 24, 2014 2:15 PM-2:30 PM

The evolution of reproductive isolation represents a crucial link between evolution within populations (anagenesis) and the formation of new species (cladogenesis). Conceptually, understanding this fundamental problem requires linking population and quantitative genetics with the traditionally disparate fields of phylogenetics and systematics. Here, we describe research on the mountain pine beetle (Dendroctonus ponderosae) that is in the early stages of speciation and demonstrates characteristics of a ring species around the Great Basin Desert in western North America. Using a combination of crossing experiments, whole genome sequencing, Restriction Associated DNA sequencing (RAD-seq), and transcriptomics, we describe a series of male-specific hybrid incompatibilities that ratchet up in severity between increasingly genetically and geographically divergent populations. Crosses between populations close to a geographic boundary where incompatibilities first manifest show weak unidirectional hybrid male sterility, while the most genetically distant crosses exhibit strong bi-directional hybrid male sterility and weak unidirectional hybrid male inviability. Thus, this system presents a unique progression of hybrid incompatibilities usually observed over much deeper evolutionary time scales. To understand the evolution of reproductive isolation we analyzed whole genome sequences from 14 beetles (7 males and 7 females) sampled from across their range. Phylogenetic analysis of complete mtDNA genomes revealed no phylogeographic resolution among reproductively isolated populations. Consistent with this, we also found only partial correspondence between genetic structure across most of the nuclear genome and overall patterns of reproductive isolation. Rather, patterns of nuclear divergence more closely follow a pattern of simple isolation by distance. The mountain pine beetle possesses neo-XY chromosomes and to explore their potential role in the evolution of reproductive isolation, we computationally identified Y-linked, X-linked, and autosomal regions of the genome. We found extensive degeneration of Y-linked regions with multiple deletions spanning over a megabase of the neo-Y that are polymorphic across the mountain pine beetle's range. Strikingly, these deletions show a close correspondence with patterns of hybrid male sterility. Expanded population-level sampling using RAD-seq confirms that these deletions appear fixed between populations that generate sterile hybrid males. To determine the potential functional role of these Y-linked deletions, we generated genome-wide expression data (RNA-seq) from beetle heads, ovaries and testes. We identified multiple testis-specific transcripts within the deleted neo-Y regions, suggesting that these deletions may underlie reproductive problems in hybrid males. Our results reveal rapid speciation in its earliest stages by combining genetics, genomics and phylogeography to better understand the processes that generate biodiversity.

Barbara Bentz: Carried out the crosses involving the most genetically divergent cross pair.

Jeffrey Good: Served as mentor and helped conceive of the whole genome sequencing, RNAseq, and RADseq experiments and their analysis.

Polymorphic hybrid male sterility during the early stages of speciation

Erica Larson, Jeffrey Good

4C_302A-Speciation and Hybridization
Tuesday, June 24, 2014 2:30 PM-2:45 PM

There are often multiple intrinsic barriers that isolate closely related species, and during the early stages of speciation, these barriers may vary both within and among populations. Polymorphism for alleles contributing to reproductive isolation may be an inevitable stage in speciation, yet there are few cases of well-documented polymorphic incompatibilities. In the house mice alleles contributing to hybrid male sterility segregate within populations. Here use whole genome sequencing and quantitative genetic crosses within and between two subspecies of mice, M. m. musculus and M. m. domesticus, to dissect the basis of polymorphic incompatibilities within M. m. musculus. We identify three genomic regions that contribute to sterility phenotypes and two of these regions are independent of incompatibility loci identified in other crosses. These data underscore the surprisingly complex genetic basis of hybrid incompatibilities during the early stages of speciation in mice.

Sex-specific changes in the scaling relationships of sexually selected traits due to a novel host

Pablo Allen, Christine Miller

4C_302B-Sexual Selection
Tuesday, June 24, 2014 1:30 PM-1:45 PM

The emergence of novel insect-plant interactions is a common phenomenon in most current ecological landscapes. Despite the interest of evolutionary biologists and ecologists on these interactions, very few studies have evaluated the effects of novel host shifts on sexual selection dynamics of native insects. Male sexually selected weapons often exhibit heightened condition-dependence, which makes these structures particularly sensitive to environmental change. Here we examined the effects of a novel host on a native insect's phenotype, specifically the allometry of a sexually selected trait. The males of the sexually dimorphic heliconia bug (Leptoscelis tricolor) possess enlarge hind femurs used in male-male contests. These hind femurs also exhibit positive allometry - a disproportionate larger size on bigger individuals. In the wild the size and scaling relationship of these weapons is affected by native host plant species and their phenological state. In recent years the heliconia bug has begun using an exotic Heliconia species as host. Our results reveal that overall size and hind femur size were not affected by novel host use for either sex, but the allometric scaling of these two traits changed in distinct ways for each sex. In males, the allometric slope did do not change, but the Y-intercept was lowered by the novel host. In other words, for any given body size, males that developed on the novel host had smaller hind femurs than those males that developed on either native Heliconia species. In the case of females, the novel host caused the development of a negative allometric slope for hind femur size, instead of the expected isometric allometry obtained under natural conditions. This happened because smaller adult females exhibited disproportionately larger hind femurs than bigger females. Our study reveals that a novel host causes significant changes in the phenotypic expression of sexual traits. The novel host could be having major consequences on the sexual selection dynamics in this population, not only by producing males with relatively smaller weapons but by disrupting resource allocation in females. It is important to identify the effects of species introductions on the processes involved in sexual selection in wild populations. These recently altered settings not only provide great opportunities to study the evolutionary consequences of host shifts, but also carry vast conservation implications due to the prevalence of species introductions globally.

Factors promoting coexistence in a sexual/asexual minnow complex

James Barron, Troy Lawson, Brennan Zotovich, Philip Jensen

4C_302B-Sexual Selection
Tuesday, June 24, 2014 1:45 PM-2:00 PM

The Northern Redbelly Dace (Phoxinus eos) and the Finescale Dace (P. neogaeus) form an all-female, asexual hybrid (P. eos-neogaeus). The hybrid produces diploid ova that initiate development upon contact with sperm from males of one of the parental species (in this case, P. eos). The sperm genome is discarded, however, producing clones of the maternal hybrid (gynogenesis). Because all resulting hybrid offspring are females, the hybrid population can grow twice as quickly as the sexual population, potentially resulting in local extinction of the sexuals and therefore extinction in the hybrid population itself for lack of a sperm source. However, in this system, gynogenesis is not perfect; occasionally sperm fertilize the diploid, hybrid ova producing triploid females. These females contain two copies of the P. eos genome, and one copy of the P. neogaeus genome. Triploids reproduce by discarding the P. neogaeus genome and producing haploid ova containing only P. eos nuclear DNA that are then fertilized resulting in male and female nuclear P. eos. In other words, the asexual lineage continually produces occasional males that can serve as a sperm source. These apparently "pure" nuclear P. eos can be identified by molecular techniques because they carry mitochondrial DNA from P. neogaeus (the original hybridization event involved a female P. neogaeus). This research examines three hypotheses for the maintenance of the sexual/asexual complex including: male discrimination against hybrid females, fecundity differences between sexual and asexual females, and production of nuclear male sexuals from the asexual lineage.

Results suggest that male P. eos do not discriminate against asexual females, and both sexual and asexual females have similar fecundities. Computer simulations of population growth indicate that sexual populations of P. eos are quickly replaced by asexuals. Further, that the males necessary for maintenance of the asexual lineage are produced by the triploids, resulting in a population of apparent "pure" P. eos that all carry P. neogaeus mtDNA. Molecular work with fish collected in Montana support the modeling results: all male P. eos were found to have P. neogaeus mtDNA.

Do female dung flies minimize harm by preferring subordinate males?

Brian Gress, Victoria Finn, Scott Pitnick

4C_302B-Sexual Selection
Tuesday, June 24, 2014 2:00 PM-2:15 PM

Subordinate males are predicted to adopt alternative mating tactics (AMTs) that bypass male-male competition when doing so maximizes fitness. Many studies of these systems therefore investigate male-male interactions, the reproductive consequences for males adopting AMTs, and the maintenance of phenotypic variability; however, considerably less attention has been paid to understanding the impacts of AMTs on female fitness (e.g., via increased frequency of mating attempts and exposure to a greater diversity of male phenotypes) or whether female preferences are important in the evolution or suppression of male AMTs. To the extent that preferences in these systems are considered it is often with the assumption that females should prefer competitively dominant males to obtain direct and/or indirect benefits, but evidence for these hypotheses is equivocal. In the yellow dung fly, Scathophaga stercoraria, males adopt alternative competitor-patroller mating tactics in which large males primarily compete on dung pats (oviposition substrate) for gravid females, whereas small males avoid dung and instead search for females at feeding sites (e.g., rotting fruit) where agonistic encounters are absent. Larger (competitor) males are also present at feeding sites in roughly equal proportion to small (patroller) males and opportunistically attempt copula when foraging; nevertheless, small males monopolize most matings in this environment due in part to greater female resistance in response to mating attempts by large males. One possible explanation for this surprising pattern of discrimination is that large males inflict greater direct harm on females which outweighs the costs of resistance. Therefore, we investigate the effects of male size and mating rate on female lifespan, lifetime reproductive output and wing damage in S. stercoraria to gain insights into how mating patterns associated with AMTs influence female fitness, as well as the adaptive significance of the small male preference observed in this species.

Mating tactics and evolution of the female mimic morph of the ruff sandpiper, a bird with permanent genetic mating strategies

Susan McRae, *David B. Lank*

4C_302B-Sexual Selection
Tuesday, June 24, 2014 2:15 PM-2:30 PM

Female mimics (Faeders) represent a rare third permanent genetic male morph of the ruff sandpiper Philomachus pugnax alongside ornamented Independent and Satellite morphs. Displaying Independent males are territorial on the lek, and displaying Satellite males move among territories. However, Faeders have largely evaded detection on leks: none has been observed to mate in the wild. The introduction of wild-caught Faeders into a captive colony provided the opportunity to observe their unique mating tactics. Observations were restricted to a period each morning when displaying males were introduced into an aviary housing Faeders and females. Faeders are not chased by territorial males, and remain close to the most actively displaying male(s). Faeders sneaked copulations by quickly responding to crouching females. Faeders interrupted matings by attempting to insert themselves between males mounting receptive females. Their female-like plumage enabled them act as decoys luring males away from receptive females. Some females selected Faeders as mates, soliciting copulation in the absence of displaying males. Half of the sons of Faeders inherit the Faeder morph, and adult Faeder sons have been observed using some of the same tactics. Inheritance patterns indicate that the morph is specified by a single autosomal locus with a dominant Faeder allele, likely in an epistatic interaction with the Satellite locus. The Faeder locus has recently been mapped (Farrell et al. 2013. BMC Genomics). The Faeder allele produces a phenotype in males that is highly suited to female mimicry including development of small body size, female-like plumage and lack of display behavior. Female carriers of the Faeder allele are phenotypically small, and despite our attempts, we have been unable to breed 'female faeders' in captivity (Lank et al. 2013 Biology Letters). This raises the possibility of sexually antagonistic selection on the Faeder allele with reduced female fitness potentially being balanced by enhanced male fitness.

Why do female birds sing? Contrasting selection on males and females and the evolution of ornamentation in birds.

Catherine Sheard

4C_302B-Sexual Selection
Tuesday, June 24, 2014 2:30 PM-2:45 PM

Ornamentation, or the exaggeration of a trait unrelated or detrimental to survival, is often assumed to result from female-choice sexual selection and/or male-male competition. In birds, however, elaborate ornamentation, including plumage, song, and various courtship behaviors, is common in both sexes. To investigate the factors favoring the evolution of mutual ornamentation within a comparative framework, a trait is required that is geographically and taxonomically well studied, easy to quantify, relatively common, and as free of confounding pressures from natural selection as possible. The presence or absence of song in male and female birds fit these criteria. With a global dataset containing broad ecological, social, and environmental information on 10,257 species of birds along with a phylogeny of 9,993 species, we quantitatively examined the pressures driving the evolution of male and female bird song, using phylogenetic methods to test the associations among these traits. We found that male song responds more strongly to ecological pressures, whereas female song evolves in conjunction with both social and ecological pressures, with other factors, including environmental drivers, playing a secondary role. These divergent correlations correspond to the asymmetric distribution of song across the world and within the avian phylogenetic tree and can be further used to predict patterns of avian speciation and extinction across time.

Linking phenotype to expression: A comparative approach to understanding the effects of mating system on immune system processes

Jeremy Chase Crawford, *Scott A. Fay, Michael B. Eisen, Matthew MacManes*

4C_302C-Host-Parasite Evolution
Tuesday, June 24, 2014 1:30 PM-1:45 PM

A species' mating system has tremendous impacts on many critical aspects of an animal's life. In particular, variations in the number and extent of reproductive interactions are thought to correspond to variations in exposure to communicable diseases. To further understand the potential effects of mating system on an animal's exposure and biological response to pathogens, we investigated gene expression in two species of Peromyscine mice, Peromyscus maniculatus (the deer mouse) and P. californicus (the California mouse). These closely related congeners are highly sympatric and ecologically similar, but differ radically in social mating system: whereas P. maniculatus is highly promiscuous, the genetically monogamous P. californicus is characterized by exclusive, lifelong pair bonds. Previous comparative work on these species has demonstrated that, relative to the monogamous P. californicus, the promiscuous P. maniculatus has experienced enhanced selection on at least one immune gene and also maintains a greater bacterial diversity in the reproductive system. In accordance with the hypothesis that sexually promiscuous species are at a higher risk of contracting communicable diseases than their monogamous counterparts, we predicted that promiscuity would also correspond to greater expression of immune genes. To test this, we performed an RNA-Seq experiment using spleen tissue obtained from 10 adult P. maniculatus and 11 adult P. californicus specimens that were live-caught on a single trapline over a three day period. Illumina reads from individually indexed spleenic cDNA libraries were mapped to species-specific transcriptomes assembled from liver and spleen mRNA, and annotated transcripts shared between both species were tested for evidence of differential expression using eXpress. Contrary to our predictions, gene ontology enrichment analysis revealed that P. maniculatus expressed genes associated with many immunological processes at much lower levels than did P. californicus. However, this decrease in immune gene expression was generally limited to processes associated with adaptive immunity; in contrast, gene ontologies associated with the innate immune system were overrepresented among genes that were expressed in relatively higher levels in P. maniculatus samples. The differences in expression of genes associated with innate and adaptive immune processes observed between these two species may be driven by distinct pathogen pressures, as each species also demonstrated differential expression of genes related to tumor defense, bacterial proliferation, and viral replication. These findings highlight the importance of considering both adaptive and innate immune genes, as well as contemporaneous pathogen pressures, when using comparative frameworks to investigate the effects of mating system on immune processes.

Differential Coevolutionary Dynamics of E. coli and Lambda Phage in Two Resource Environments

Jeremie Brusini, Michael Sieber, Ivana Gudelj, Samantha Forde

4C_302C-Host-Parasite Evolution
Tuesday, June 24, 2014 1:45 PM-2:00 PM

The coevolutionary process between phage and bacterial populations is considered a driver of ecological in microbial communities. A major challenge remains whether the understanding of phage-bacteria interactions from laboratory studies can be translated into the wild. We investigated the role of the environment in the coevolutionary process between the bacterium Escherichia coli and the bacteriophage Lambda during a 20 day long coevolutionary experiment. Using a metagenomic approach, we found different levels of genetic polymorphism underlying host resistance evolution according to the nature of the carbon source available in the environment. More strikingly, those differences were found while the same resistance mechanism (i.e. the loss of the phage receptor) evolved in the two environments. An analytical model showed that a difference in the cost of resistance can be responsible for these results: a high cost of resistance in one environment triggers frequency dependent selection between resistant and sensitive genotypes allowing the maintenance of a high allelic polymorphism in the host population. This study underlines that environment is an important force for coevolutionary dynamics in phage-bacteria systems. It also highlights the complexity of the mechanisms responsible for the evolution and the ecology of microbial communities in the wild.

Patterns of single-cell phylogenies under different evolutionary models of cancer

Yuantong Ding, Andreas Aristotelous, Edward Patz, Rick Durrett, Allen Rodrigo

4C_302C-Host-Parasite Evolution
Tuesday, June 24, 2014 2:00 PM-2:15 PM

The current staging system of tumors based on radiology and pathology is inadequate to predict tumor progression and patient survival time. However, if we consider a tumor as a population of single cells, evolutionary analysis may give insight into the underlying process of tumor progression. In this project, the goal is to determine whether the phylogenetic structure of a sample of cells may help classify the tumor stage more accurately. We built an agent-base tumor growth model, which allows lineage tracking of single cells, and simulated whole genome sequences based on cell lineages with an infinite-site model of substitution. We preformed phylogenetic and population genetic analyses of samples of cells to evaluate whether there was any association between phylogenetic patterns and the metastatic potential of the tumor. Our approach may have potential applications in cancer prognosis and may also provide guidelines for appropriate experimental designs of single cell studies of cancer

---

Immunogenomics of non-model species: what can Ig-seq tell us about the evolution of the adaptive immune system?

Peter Larsen, C. Ryan Campbell, Anne Yoder

4C_302C-Host-Parasite Evolution
Tuesday, June 24, 2014 2:15 PM-2:30 PM

High-throughput sequencing applications have created new opportunities for eco-immunological studies and are allowing researchers to study the molecular interplay between the immune systems of non-model organisms and their pathogens. In particular, the high-throughput sequencing of expressed antibodies (Ig-seq) is a novel transcriptomic approach that holds great promise for eco-immunology research. To date, Ig-seq has been used for only a few organisms (e.g., humans, cattle, zebrafish) and data generated from humans have provided new insights into a variety of important areas including personalized medicine, cancer and HIV research, and vaccine development. We posit that the characterization of antibody repertoires in wild populations will provide a fundamental contribution to our understanding of the evolution of the adaptive immune system and will help to advance the field of eco-immunology. To this end, we used two advanced sequencing platforms (Pacific Biosciences RS and Ion Torrent PGM) to sequence the antibody repertoire of an endangered primate, Coquerel’s sifaka (Propithecus coquereli). We generated sequence data from over 150,000 expressed antibodies and these data allowed us to describe the amino acid variation within the heavy-chain antigen-binding region. Our analyses suggest that similar VDJ expression patterns exist across all primates, with sequences closely related to the human VH3 immunoglobulin family being heavily represented in sifaka antibodies. Moreover, the antigen-binding region of sifaka antibodies exhibited similar amino acid variation (length and composition) with respect to haplorrhine primates. Our study represents the first attempt to characterize sequence diversity of the expressed antibody repertoire in a species of lemur. We anticipate that methods similar to ours will provide the framework for investigating the adaptive immune response in wild populations of other non-model organisms and can be used to advance the burgeoning field of eco-immunology.

Bacteria-phage coevolution within plant hosts

Britt Koskella

4C_302C-Host-Parasite Evolution
Tuesday, June 24, 2014 2:30 PM-2:45 PM

The formation, stability and function of bacterial populations and communities are central to many ecological processes and are of key importance to the health of eukaryotic organisms. It is increasingly clear that these populations are highly dynamic over time, in part due to interactions with bacteriophage viruses. In this talk I examine the potential role that phages might play in shaping these populations and communities over both ecological and evolutionary timescales. I present data from a series of experiments in which the role of the plant host genotype in shaping bacteria-phage coevolution is explored, and discuss when and how phage-mediated selection might alter the interaction between plants and their bacterial pathogens.

Experimental Evolution of Increased Size and Complexity of Anabaena variabilis

Kristin Jacobsen, Michael Travisano, Ford Denison

4C_303-Experimental Evolution
Tuesday, June 24, 2014 1:30 PM-1:45 PM

The evolution of multicellularity has occurred more than 25 times in the history of life, facilitating transformative changes in biological diversity. Previously, we have shown that the evolution of multicellular traits can readily be observed in laboratory populations across a broad diversity of model unicellular organisms such as yeast, chlamydomonas, and E. coli. Cyanobacteria are the oldest multicellular organisms, dating back 3.5 billion years, and many species appear morphologically unchanged, suggesting they have remained primitively multicellular. Is this because they are incapable of evolving increased complexity? The model prokaryote, Anabaena, is a filamentous cyanobacteria, predating fossil records. It is of order nostacales, existing as single strands or loosely associated mats, and has three distinct cells types. A selection regime for rapid settling was used to select for increased size advantage. The initial response to selection resulted in dramatic size increase, from microscopic strands to inseparable macroscopic aggregates. With selection, the Anabaena also became more complex; growth rate increased, two distinguishable and heritable morphologies developed, and growth and reproduction patterns changed. This shows that Anabaena, although remaining primitively multicellular for billions of years, rapidly respond to selection, evolving increased size and complexity.

Structured Populations with Limited Resources Exhibit Higher Rates of Complex Function Evolution

Art Covert

4C_303-Experimental Evolution
Tuesday, June 24, 2014 1:45 PM-2:00 PM

The impact of population structure on evolving populations is difficult to study. Populations broken up into groups of organisms and connected by low levels of migration will experience different types of geneflow than normal unstructured populations. Various studies, spanning decades of research, have lead to seemingly contradictory conclusions. Some point to population structure as a means to improve adaptation, others argue that population structure hinders evolution. We investigate how population structure impacts the evolution of complex functions in environments with limited resources. We find that structured populations with limited resources tend to evolve complex functions at a higher rate than unstructured populations, across a broad range of migration rates. This suggests that population structure may have an important impact on evolution, in both sexual and asexual populations, at least at certain migration rates.

Keywords: Experimenatl Evolution, Structured Populations, Diversity, Limited Resources

---

Evolution of elemental composition in E. coli under carbon and nitrogen limitation

Caroline Turner, Richard Lenski

4C_303-Experimental Evolution
Tuesday, June 24, 2014 2:00 PM-2:15 PM

At the broadest level, organisms can be viewed as a collection of chemical elements in various ratios. These ratios vary between organisms. While this variation in elemental composition is known to have important ecological consequences, little is known about how it changes over evolutionary time. In previous work, we demonstrated that E. coli evolved higher nitrogen and phosphorus content and increased carbon use efficiency after 50,000 generations of evolution under carbon limited, high nitrogen and phosphorus conditions. However, this experiment did not differentiate between adaptation to carbon limitation and adaptation to other experimental conditions such as growth in batch culture and in a well-mixed environment. To isolate the effect of nutrient limitation, we further evolved clones from the original 50,000 generation experiment under either carbon limited or nitrogen limited conditions for 1,000 generations. We will present results on the changes in fitness, carbon consumption, and carbon, nitrogen and phosphorus content of the bacteria over the course of this experiment and discuss implications for understanding evolutionary changes in elemental ratios.

Positive natural selection on mitochondrial OXPHOS genes in fishes with different swimming performance

Feifei Zhang, Richard Broughton

4C_303-Experimental Evolution
Tuesday, June 24, 2014 2:15 PM-2:30 PM

Fishes exhibit the most extreme locomotive diversity in all vertebrates. High-performance fishes must have higher energy demands than their low-performance relatives. We examined how natural selection worked on the oxidative phosphorylation (OXPHOS) pathway, the major energy producing unit in eukaryotes under aerobic condition on 13 mitochondrial OXPHOS genes on high-performance fishes and their relatives by estimating both the ratio (ω) of nonsynonymous to synonymous substitution rates and the physiochemical change of amino acids. Several lineages excluding those leading to high-performance fishes were shown to be subject to positive selection. This pattern, however, was not observed on 5 randomly chosen nuclear genes that are not involved in OXPHOS. The identified positively selected amino acids in OXPHOS complex I, III and IV mitochondrial encoded subunits are not involved directly in proton or electron transport pathways but may be important in OXHOS assembly and the maintenance of structural stability. The results suggest a complex pattern of adaptation of OXPHOS genes in relation to energetic demands and shed new light on the evolution of fish swimming.

Biased gene conversion skews allele frequencies in human populations, increasing the disease burden of recessive alleles

Joseph Lachance, Sarah Tishkoff

4C_303-Experimental Evolution
Tuesday, June 24, 2014 2:30 PM-2:45 PM

Gene conversion results in the non-reciprocal transfer of genetic information between two recombining sequences, and there is evidence that this process is biased towards G and C alleles. However, the strength of GC-biased gene conversion (gBGC) in human populations and its effects on hereditary disease have yet to be assessed on a genomic scale. Using high-coverage whole genome sequences of African hunter-gatherers, other human populations, and primate outgroups we quantified the effects of gBGC) on population genomic datasets. We find that genetic distances (FST and population branch statistics) are modified by gBGC. In addition, the site frequency spectrum is left-shifted when ancestral alleles are favored by gBGC and right-shifted when derived alleles are favored by gBGC. Allele frequency shifts due to gBGC mimic the effects of natural selection, and these effects are strongest in high recombination regions of the human genome. By comparing the site frequency spectra of unbiased and biased sites the strength of gene conversion was estimated to be on the order of Neb » 0.009. We also find that derived alleles favored by gBGC are much more likely to be homozygous than derived alleles at unbiased SNPs (+42.2% to 62.8%). This results in a curse of the converted, whereby recessive alleles have an increased disease burden. Taken together, our findings reveal that GC-biased gene conversion has important population genetic and public health implications.

New insights on sheet web spiders phylogeny (Araneae: Linyphiidae)

Thiago da Silva Moreira, Gustavo Hormiga

4C_305A-Phylogenetics and Diversification
Tuesday, June 24, 2014 1:30 PM-1:45 PM

Linyphiidae is one of the most speciose lineages of spiders and the largest family within Orbiculariae, a large lineage that includes, among others, the ecribellate orb-weavers. Despite a large history of work in this group, the higher level phylogenetic relationships of linyphiids have not been satisfactorily resolved and only two of its seven proposed subfamilies have been empirically demonstrated to be monophyletic. We added to the most comprehensive phylogeny of the group (Arnedo et al. 2009) 10 more taxa (mainly focusing on groups with low support or uncertain placement), 25 new morphological characters and 3 more genes (18S, 28S and H3) and analyzed the expanded matrix under both parsimony and Bayesian frameworks. We report here the results of these preliminary analyses.

A molecular phylogeny of black fungus gnats (Diptera: Sciaridae) and the evolution of larval habitats

Seungqwan Shin, Sunghoon Jung, Frank Menzel, Kai Heller, Heungsik Lee, Seunghwan Lee

4C_305A-Phylogenetics and Diversification
Tuesday, June 24, 2014 1:45 PM-2:00 PM

The phylogeny of Sciaridae is reconstructed based on maximum likelihood, maximum parsimony, and bayesian analyses. Molecular results are largely congruent with one of the former hypotheses based on morphological data with respect to the monophyly of genera and subfamilies (Sciarinae, and Megalosphyinae); however, the subfamily Cratyninae is shown to be polyphyletic, and the genera Bradysia, Corynoptera, Leptosciarella, Lycoriella, and Phytosciara are also recognized as non-monophyletic groups. While the ancestral larval habitat state of the family Sciaridae, based on bayesian inference, is dead plant material, the common ancestors of Phytosciara and Bradysia are inferred to living plants habitat. Therefore, shifts in larval habitats from dead plant material to living plants may have occurred within the Sciaridae at least once.

The use of ultra-conserved elements in resolving nightbird (caprimulgiformes) phylogeny

Noor White, Brant Faircloth, Michael Braun

4C_305A-Phylogenetics and Diversification
Tuesday, June 24, 2014 2:00 PM-2:15 PM

A surprising finding of recent avian phylogenetics is the statistically unambiguous grouping of the diurnal order Apodiformes (swifts and hummingbirds) within the nocturnal order Caprimulgiformes (i.e. nighthawks and nightjars; hereafter called "Caprimulgiformes"). The pairing of the two orders in monophyly raises questions about the evolution of nocturnality in birds, especially how many times it occurred, what adaptations made it possible, and what genetic and molecular variation underlies those adaptations.

Previously mentioned phylogenies reconstructed this clade with modest datasets. I have used a novel massively parallel sequencing approach to resolve the "Caprimulgiformes" phylogeny using a dataset based on the informative flanking regions of ~5,000 ultra-conserved element (UCE) loci. I will present analyses that seek to extract the most phylogenetic information from this dataset using currently available techniques, including efforts to assign UCE loci to functional categories.

Danio Genus Phylogeny Resolved with RAD Phylogenomics

Braedan McCluskey, *John Postlethwait*

4C_305A-Phylogenetics and Diversification
Tuesday, June 24, 2014 2:15 PM-2:30 PM

Recent phylogenetic studies of the Danio genus (Cypriniformes: Cyprinidae) have inferred conflicting phylogenies with low support for several important relationships including the closest extant relative(s) of the zebrafish Danio rerio. To bring consensus to the relationships within Danio, we performed phylogenomic analyses using Restriction site Associated DNA Sequencing (RAD-Seq). Our 2.7 megabase dataset incorporates sequences from twelve Danio species at more than 30,000 orthologous RAD-Seq loci mapped to the zebrafish genome. Our analysis of the concatenated nucleotide sequences from these loci recovers a topology with all internal nodes unambiguously supported and provides strong evidence for Danio aesculapii as the closest extant relative of Danio rerio. This topology is consistent across analytical methods of genome-assisted and genome-independent datasets. Summary statistics of character state patterns and phylogenies inferred for individual RAD-Seq loci, however, are inconsistent with a single underlying topology and reveal that the diversification of the Danio genus involved appreciable levels of gene flow during speciation and/or introgression between species. In addition to inferring a well-supported topology for Danio, we characterized the degree of RAD-Seq locus conservation according to their mapping locations in the zebrafish genome. Results demonstrated that these loci are concentrated near exons and can be retained across several million years of evolution, suggesting that this phylogenomic approach is scalable to investigation of broad taxonomic groups even in the absence of a reference genome. Our genome-informed analysis of RAD-Seq loci also showed that the highly repetitive nature of the zebrafish genome is partially due to a recent expansion of some families of transposable elements during the diversification of Danio. To verify the results of this RAD-Seq approach and begin comparative protein analyses across the genus, we are analyzing sequences from protein-coding regions of zebrafish and some of its closest relatives. Together, our results provide a high-resolution profile of the genome-wide diversification of the Danio genus and provide further tools for the understanding of zebrafish in an evolutionary context.

Tracing the diversification of prorhynchid flatworms with cDNA-enriched genome libraries

Christopher Laumer, *Gonzalo Giribet*

4C_305A-Phylogenetics and Diversification
Tuesday, June 24, 2014 2:30 PM-2:45 PM

Methods to efficiently exploit high-throughput sequencing to generate taxon-rich phylogenetic datasets at intermediate scales of divergence (i.e., those between closely related species and genera) remain somewhat limited and resource-intensive. Ironically, this is also the scale at which most systematic research is conducted, and at which complexities such as introgression and incomplete lineage sorting – which strictly require data from many unlinked loci to detect and model – are expected to be most relevant.

We discuss ongoing experiments to generate such data for a "typical" species-level phylogenetic study. Our system of interest is Prorhynchida, a clade of mostly inconspicuous (~1-2 mm) non-model flatworms (Platyhelminthes) with unique reproductive biology, known from freshwater and terrestrial habitats worldwide. Twenty-nine valid prorhynchid species have been named, but undescribed species greatly outnumber these, and no well-justified phylogeny of Prorhynchida has been put forward. We have achieved a thorough taxon sampling of approximately 50 prorhynchid species in all known genera, and generated a preliminary estimate of their phylogeny using a Sanger dataset amplified from genomic DNA; however, many key relationships remain recalcitrant in our analyses of these data, justifying further study.

To this end, we present a novel approach designed to efficiently sequence orthologous exons across many taxa, leveraging DNA hybridization capture. In contrast to similar cross-species enrichment studies that use biotinylated RNA probes transcribed from a commercially-synthesized oligonucleotide panel targeting conserved sequences, we explore a method to agnostically capture exonic sequence using amplified, biotinylated cDNA libraries. Using such probe sets derived from two common species for which RNA is readily available, we enrich genomic DNA libraries from across the greater diversity of Prorhynchida and sequence in multiplex. We evaluate the success of these experiments using sets of orthologs mined from de novo transcriptome assemblies in select taxa, comparing the proportion of on-target reads for cross-species enrichments at varying genetic distance from the probe-seed species, and also considering the effects of diverse enrichment conditions (e.g. varying probe:library ratios, and the impact of touchdown-style hybridization programs). We also investigate the influence of gene expression level on the efficacy of enrichment using such cDNA probes. We conclude with a meditation on the general utility of this approach – which obviates the substantial up-front bioinformatic and financial investment required for enrichment using commercially-synthesized probes – for species-level phylogenetics in non-model systems.

Contrasting patterns of morphological diversity and climatic preferences in the genus Anthurium (Araceae)

Monica Carlsen, *Thomas Croat*

4C_305B-Diversification and Phylogeography
Tuesday, June 24, 2014 1:30 PM-1:45 PM

The genus Anthurium (Araceae) comprises more than 1,000 Neotropical species, distributed from southern Mexico to northern Argentina. The most recent molecular phylogeny of the genus recovered 18 strongly supported clades that vary in terms of their geographic range size, morphological diversity, and climatic niche preferences. This study makes use of distribution models, molecular phylogenetics, morphological analysis, and analogy with community ecology indices to understand what are the morphological patterns and climatic preferences of clades with either restricted or widespread geographical distributions. It was found that clade geographic extent is correlated with climatic niche width, but not with amount of morphological differentiation or number of species. Climatic niche diversity and morphological diversification seem to be decoupled within Anthurium. So that, species that belong to clades that have restricted distributions have more similar climatic niche preferences but are more dissimilar morphologically. On the contrary, widely distributed clades containing species with similar climatic niches show very uniform overall morphology. Interestingly, phylogenetic structure at the subgeneric level (i.e. among major clades) does not seem to play an important role in determining species richness, or influencing climatic niche width and morphological diversity within Anthurium.

Phylogeography and systematics of the southern redback salamander Plethodon serratus in the southeastern US

Catherine Newman, *Christopher Austin*

4C_305B-Diversification and Phylogeography
Tuesday, June 24, 2014 1:45 PM-2:00 PM

Studies have shown that historical barriers to gene flow, climate, and habitat play a critical role in maintaining observed patterns of genetic variation in the southeastern United States. The southern redback salamander, Plethodon serratus, is distributed in four disjunct regions in the Southeast: the Ozark, Ouachita, and Appalachian Mountains, and two parishes in Louisiana. We use genetic data and ecological niche modeling to describe the genetic structure within P. serratus and examine shifts in its geographic distribution through time in association with climate, with the ultimate goal of increasing our understanding of the evolutionary processes underlying amphibian geographic distributions in the Southeast. Mitochondrial and nuclear genetic data indicate that while the Appalachian and Ozark regions are each monophyletic, the Ouachita and Louisiana regions are not. Population structure analyses show a pattern consistent with recent gene flow among populations, further supporting the hypothesis that the four regions were recently more contiguous. In contrast to the numerous studies across many taxa supporting expansion of a species from glacial refugia, ecological niche and paleodistribution modeling for P. serratus suggest that its geographic range was likely much broader and more contiguous during the last glacial maximum (21,000 YBP) and has been restricted to its current distribution by a changing climate. Future work on this project will incorporate a large multilocus data set to generate a more robust phylogeny and estimate historical demographic parameters to further shed light on the evolutionary history of this species.

Effects of Ecological Interactions on Diversfication and Trait Evolution: Tests with Macroevolutionary Models

Matthew Dufort

4C_305B-Diversification and Phylogeography
Tuesday, June 24, 2014 2:00 PM-2:15 PM

Ecological theories yield sometimes contradictory predictions about the effects of interspecific interactions on macroevolutionary patterns. For example, adaptive radiation predicts that diversification and morphological evolution will both decrease in the presence of competitors, while ecological character displacement generally predicts that morphological evolution will increase with competition.

I tested for relationships between coexistence, ecological similarity, diversification, and ecomorphological evolution, in woodpeckers and related birds (Aves: Picidae). These birds have demonstrated relationships between skeletal morphology and ecological characteristics. I used a well-resolved phylogeny, skeletal measurements, and distribution data to test for a number of predicted relationships; the complete data set included approximately half of all described species. I found no correlation between coexistence with similar species and rates of morphological evolution. Surprisingly, diversification rate was positively correlated with overlap with similar species, a relationship not predicted by any of the models. This pattern may be driven by variation among clades in habitat partitioning, such that more diverse clades partition space more finely than the spatial resolution of this study, or by some as yet undetermined process.

Asynchrony of seasons: genetic differentiation associated with geographic variation in climatic seasonality and reproductive phenology

Daniel Cadena, *Ignacio Quintero, Paul-Camilo Zalamea, Sebastian Gonzalez-Caro*

4C_305B-Diversification and Phylogeography
Tuesday, June 24, 2014 2:15 PM-2:30 PM

Many organisms exhibit distinct breeding seasons tracking food availability. If conspecific populations inhabit areas that experience different temporal cycles in food availability spurred by variation in precipitation regimes, then they should display asynchronous breeding seasons. Thus, such populations might exhibit a temporal barrier to gene flow, which may potentially promote genetic differentiation. We test a central prediction of this hypothesis, namely that individuals living in areas with more asynchronous precipitation regimes should be more genetically differentiated that individuals living in areas with more similar precipitation regimes. Using mitochondrial DNA sequences, precipitation data, and geographical/ecological distances between individuals of 57 New World bird species mostly from the tropics, we examined the effect of asynchronous precipitation (a proxy for asynchronous resource availability) on genetic differentiation. We found evidence for a positive and significant cross-species effect of precipitation asynchrony on genetic distance after accounting for geographical/ecological distances, suggesting that current climatic conditions may play a role in population differentiation. Standing spatial asynchrony in climate may thus drive evolutionary divergence in the absence of overt geographic barriers to gene flow; this mechanism contrasts with those invoked by most models of biotic diversification emphasizing physical or ecological changes to the landscape as drivers of divergence.

Host Association Drives Deep Divergence in the Common Bed Bug, Cimex lectularius

Warren Booth, Ondrej Balvin, Edward Vargo, Coby Schal, Jitka Vilímová

4C_305B-Diversification and Phylogeography
Tuesday, June 24, 2014 2:30 PM-2:45 PM

The life histories of parasites are inextricably shaped by their hosts, creating a multitude of potential diversification mechanisms. One important mechanism is host-associated differentiation, which depends on the level of host specificity and local adaptation, and may ultimately lead to host switching and speciation. Yet, there is a paucity of empirical studies on the speciation process of parasites. The bed bug, Cimex lectularius, represents a potential model organism for elucidating the processes involved in host-mediated speciation of parasites. Bed bugs extended their host range from bats to humans when these two hosts shared cave domiciles in ancient times. Bed bugs that associate with humans have a cosmopolitan distribution, whereas those associated with bats appear common across much of Europe. We assessed genetic structure and gene flow within and among populations collected on each host using three classes of markers: mtDNA, nuclear microsatellite loci, and single nucleotide polymorphisms in knock-down-resistance genes. Both nuclear and mitochondrial data support a lack of significant contemporary gene flow amongst host-specific populations. Limited diversity and elevated levels of inbreeding within locations suggest that human-associated C. lectularius exist in a metapopulation framework, likely due to human-mediated movement and frequent pest control. In contrast, populations within bat roosts exhibit higher diversity and lower levels of relatedness, suggesting populations are stable with temporal fluctuations due to host dispersal and bug mortality. Combined with previously reported behavioral data, these results suggest C. lectularius may be undergoing divergence through host-association.

Sex determination and the young Asparagus Y chromosome

Alex Harkess, Jim Leebens-Mack

4C_306A-Sex and Evolution
Tuesday, June 24, 2014 1:30 PM-1:45 PM

The evolutionary processes driving the origin of sex chromosomes in association with shifts from hermaphroditism to dioecy is of fundamental interest. Garden asparagus (Asparagus officinalis) is a dioecious vegetable crop species with a recently evolved, homomorphic sex chromosome pair. Sex determination has been genetically mapped to a small (

Y fuse? Sex chromosome fusions in theory and in practice

Mark Kirkpatrick, Jun Kitano, Sarah Otto, Matthew Pennell

4C_306A-Sex and Evolution
Tuesday, June 24, 2014 1:45 PM-2:00 PM

Sex chromosomes are the most rapidly evolving part of the genome in many animals and plants. Fusions between sex chromosomes and autosomes are common. Sex-antagonistic selection is a leading hypothesis to explain that observation, but there are other ideas that invoke the unique combinations of selection, mutation, and drift that sex chromosomes experience. We present a metaanalysis of vertebrate karyotypes, focussing on the relative frequencies of fusions involving X, Y, Z, and W chromosomes. We then show how the patterns that emerge can be explained by quantitative models of the competing hypotheses.

Phylogenetics of polyploid African clawed frogs using RNAseq; inferences for sex chromosome evolution

Benjamin Furman, Ben Evans

4C_306A-Sex and Evolution
Tuesday, June 24, 2014 2:00 PM-2:15 PM

Classical theory dictates that, after establishment, sex chromosomes will begin to diverge from one another. However, it has become evident in recent years that non-diverged, “homomorphic”, sex chromosomes are quite common in nature, perhaps more so than heteromorphic sex chromosomes. Amphibians represent an interesting model for studying sex chromosome evolution because, unlike mammals, the sex determining regions or genetic triggers have changed dozens of times, and sex chromosomes tend to be minimally diverged with genetic recombination occurring over most of their length. This turnover of sex chromosomes allows for the study of evolutionary forces acting on sex chromosomes after their establishment, and can illuminate why some sex chromosomes diverged quickly while other appear not to diverge much at all. Within the African clawed frog lineage (Xenopus and Silurana), there has been at least one turnover of the sex chromosomes, as most species in the Xenopus genus have one sex determining system (based on DM-W) and species in the Silurana genus have another, non-homologous system. In addition to that, the species X. borealis appears to have another system, not homologous to either. In an effort to explore and characterize this third system, unique to X. borealis, we first reconstructed the phylogeny of Xenopus as, to date, many nodes are unresolved. Using whole transcriptome sequencing for 5 individuals, representing the major Xenopus clades, we designed an analysis pipeline to ensure that only orthologous comparisons are made following de novo transcriptome assembly, as these species are all tetraploid and lack a high quality genome to map to, and have conducted Bayesian phylogenetic analysis. One possibility is that X. borealis has retained the ancestral sex determining chromosomes, sharing homology with the Silurana sex determining system. Using an F1 cross, we assess inheritance of parental polymorphisms of genomic regions that are sex-linked in S. tropicalis. All analysis so far indicates that X. borealis has a novel, evolutionarily young, sex determining system, implying that there has been a third turnover of sex chromosomes within this group. Future work will aim to directly characterize the sex chromosomes in this species. Broader implications include furthering our understanding of the evolutionary history of the only known master sex-determining gene in Amphibians (DM-W) and contribute to the understanding of how divergent evolution occurs in tightly regulated genetic systems.

Testing the Meiotic Requirement for Recombination

Beth Dumont

4C_306A-Sex and Evolution
Tuesday, June 24, 2014 2:15 PM-2:30 PM

The rate of meiotic recombination is one of the most important quantities in genetics and evolution. Recent studies have shed light on the mechanisms and patterning of recombination across genomes, including the identification of genes that control the rate and distribution of crossing over. Despite these notable advances, one very basic question remains unanswered: What is the fundamental meiotic requirement for recombination? Some scientists have argued that a minimum of one crossover per chromosome is needed to ensure that homologous chromosomes correctly segregate at meiosis. A second camp has suggested that the physical constraint on crossing-over lies at the level of the chromosome arm. Genetic linkage maps and cytogenetic recombination maps that catalog the distribution and frequency of recombination have been developed for hundreds of diverse species' genomes. Surprisingly, these resources have never been systematically mined to resolve this open debate. Here, I combine meta-analysis of over 100 published recombination maps from diverse eukaryotic taxa with cutting-edge cytogenetic methods for in situ imaging of crossover events to comprehensively test the meiotic requirement for recombination at meiosis. My preliminary findings suggest that the physical scale of crossover constraint may vary across the eukaryotic phylogeny, with some species requiring just one crossover per chromosome and others with a more stringent criterion of at least one crossover per chromosome arm. These tentative results, if robust to further analyses, will carry important consequences for understanding global crossover rate variation, including it's coevolutionary response to chromosome rearrangements and species differences in the frequency of chromosome nondisjunction.

Sperm do not evolve to collaborate in female meiotic drive

Yaniv Brandvain, Graham Coop

4C_306A-Sex and Evolution
Tuesday, June 24, 2014 2:30 PM-2:45 PM

The harmony of the organism is upset during meiosis, a time when alternative alleles compete for representation in successful gametes. During female meiosis this competition is particularly stark as only one of the four products of meiosis are included in the egg. Numerous features of oogenesis appear to have evolved to minimize the potential for conflict. It is therefore surprising that by requiring fertilization before female meiosis is complete, females allow a complete stranger - a haploid sperm genome, to influence the outcome of female meiosis. While in principle this could be disastrous, we evaluate numerous population genetic models in which sperm could influence the outcome of female meiotic drive, and show that sperm evolve to increase fairness of female meiosis and the fitness of resultant progeny.

Interactions between behavioral thermoregulation and color change in pipevine swallowtail caterpillars (Battus philenor)

Matthew Nielsen, Daniel Papaj

4C_306B-Phenotypic Plasticity
Tuesday, June 24, 2014 1:30 PM-1:45 PM

Organisms can respond to environmental changes with plasticity in a wide variety of traits, from morphology to physiology to behavior. However, rather than being entirely independent, these different plastic phenotypic changes should influence each other's effectiveness and expression. We studied these interactions in the thermoregulation of Battus philenor (pipevine swallowtail) caterpillars, which can use behavior to avoid high temperatures, often leaving their host plant, but can also cool themselves via a slower, morphological change between black and red coloration. Using physical caterpillar models, we have shown that thermoregulatory behavior reduces the utility of color change, with the red color cooling models on a host plant, yet having no effect when the model is on a thermal refuge. Nevertheless, using field enclosures of live caterpillars, we have shown that being red does reduce how often caterpillars must leave their host to stay cool. These results suggest that the main benefit of color change is not increasing the caterpillar's overall ability to survive high temperatures, but instead allowing it to minimize how often it must leave its host during behavioral thermoregulation. Overall, we have demonstrated that plasticity in different traits cannot be considered purely independently, and instead we must consider how these traits can affect each other.

Playing smart and playing safe: the joint expression of phenotypic plasticity and diversification bet hedging

Andrew Simons

4C_306B-Phenotypic Plasticity
Tuesday, June 24, 2014 1:45 PM-2:00 PM

Adaptive phenotypic plasticity evolves when cues reliably predict fitness consequences of life-history decisions, whereas bet hedging evolves when environments are unpredictable. These modes of response should be jointly expressed, because environmental variance is composed of both predictable and unpredictable components, but little attention has been paid to their joint expression. Here, I examine the simultaneous expression of plasticity in germination rate and two potential bet hedging traits—germination fraction and within-season diversification in timing of germination—in seeds from multiple seed families of five geographically distant populations of Lobelia inflata (L.) subjected to a thermal gradient. Populations differ in germination plasticity to temperature, in total germination fraction, and in the expression of potential diversification in the timing of germination. The observation of a negative partial correlation between the expression of plasticity and germination variance (potential diversification), and a positive correlation between plasticity and germination fraction are suggestive of a tradeoff between modes of response to environmental variance. If the observed correlations are indicative of those between adaptive plasticity and bet hedging, we expect an optimal balance to exist and differ among populations. However, the assessment of local adaptation to a particular level of environmental variation remains a challenge, and I propose the potential utility of

dendrochronological methods.

Developmental plasticity and reproductive fitness in the house mouse

Wendy Hood, Aubrey Sirman, Zachary Donoviel, Mark Sadler

4C_306B-Phenotypic Plasticity
Tuesday, June 24, 2014 2:00 PM-2:15 PM

It has been argued that developmental plasticity allows young to match their phenotype to the environmental conditions experienced by their mothers. In particular, maternal diet is believed to 'adaptively program' young for performing well when they consume a diet that is comparable to what their mother consumed during gestation and lactation (i.e. the environmental matching hypothesis). Despite the ubiquity of this hypothesis, there is little empirical evidence addressing the impact of maternal diet on offspring fitness. The goals of our study were to 1) confirm that an individual's physiological phenotype is altered by maternal diet under natural conditions, and 2) determine if mice that consume a diet comparable to the diet of their parents have greater fitness than those that consume a mismatched diet. This work was conducted in wild-derived populations of house mice (Mus musculus) maintained in arenas that mimic natural home range and population size and density. The parental generation was maintained on 10% or 20% protein diet. After weaning, F1 offspring were kept on the same diet as their parents or switched to the alternate diet. Treatment impacted male and female mice differently and we found mixed support for environmental matching based on the physiological variables that were measured (including metabolic rate, maturation of the reproductive axis, body fat, and organ mass). We found no support for environmental matching based on reproductive performance. Females in the low to high protein group displayed the earliest age at first reproduction. Following their first reproductive bout, those females consuming a high protein diet displayed higher reproductive performance than the low protein females, regardless of the diet that their parents consumed. The implications of the results will be discussed within the context of the evolution of developmental plasticity.

Ecological genomics and plasticity of genetic regulation for saltwater tolerance

Hilary Smith, Nora Besansky, Changde Cheng

4C_306B-Phenotypic Plasticity
Tuesday, June 24, 2014 2:15 PM-2:30 PM

Evolution of osmoregulatory systems is a key factor in the transition of species between fresh- and saltwater habitats, including species such as anopheline mosquitoes that serve as vectors of disease. Here we use RNA-Seq to investigate gene expression differences between an obligate freshwater (Anopheles coluzzii) and euryhaline malaria vector (An. merus). After rearing in freshwater (FW), both young and old larval instars of each species were briefly (6 h) exposed to either saltwater (SW) or FW conditions to test the impact of water salinity on mRNA levels. We aimed to address three questions: (1) What is the transcriptomic response of anophelines (represented by An. coluzzii and An. merus) to water salinity? (2) How do transcriptomic responses to water salinity differ between species? (3) How does the transcriptomic response to water salinity differ with age, particularly for the tolerant species An. merus? Our results are congruent with the ability of gene induction to mediate SW tolerance, with the intolerant An. coluzzii exhibiting little difference in gene expression (An. merus. In the latter, >16% of the 11,025 genes assayed responded to saltwater exposure, with similar levels of up- and down-regulation. The impact of age at exposure was less dramatic than species identity, with 567 genes significantly differentially expressed in response to water type between young and old An. merus. Besides effector genes with putative roles in ion transport (e.g., Na+/K+-ATPase), we also report differential expression in response to water salinity by genes involved in general stress responses such as heat shock proteins, and potential cross-talk between the immune response and osmoregulation. Finally, we take a systems-biology approach by investigating gene co-expression networks, and present evidence for a potential role of a mosquito-specific mitogen-activated protein kinase (MAPK) in saltwater adaptation.

Using comparative transcriptomics and a whole genome to study the evolution of cold tolerance in stick insects

Thomas Buckley, Alice Dennis, Luke Dunning, Chen Wu, Richard Newcomb, Howard Ross

4C_306B-Phenotypic Plasticity
Tuesday, June 24, 2014 2:30 PM-2:45 PM

We have used comparative transcriptomics to investigate the genetic basis of cold tolerance across a phylogeny of stick insects from New Zealand. These species are found from subtropical northern forests to alpine areas, where they overwinter above the snow line. We investigate the prediction that related stick insect species use similar strategies to survive cold. We have built a phylogeny based on 274 conserved orthologous genes and used this as a phylogenetic framework. Using RNA sequencing (RNA-seq) we then compared differentially expressed genes following cold shock recovery in different species. A large number of differentially expressed genes were not shared among species. We did however observe shared patterns of expression in structural cuticular genes across five species. Maximum likelihood selection texts inferred a number of genes under positive selection in alpine and lowland species. We also present a preliminary genome assembly of the New Zealand stick insect Clitarchus hookeri whose genome was estimated by flow cytometry to be approximately 4.5 Giga base pairs (Gb) in size. The current assembly was constructed using ~4.7 and ~2.6 billion Illumina paired end and mate pair short sequence reads, respectively, from libraries of various insert size, resulting in a genome assembly size of 4.3 Gb. Multiple programs including SOAPdenovo, GapCloser, SSPACE and AllpathLG were used in the whole assembly pipeline, which we are currently optimising based on a number of evaluation criteria. This genome will be used for further studies on adaptive evolution in New Zealand stick insects.

Synthesis Centers as Research Incubators

Allen Rodrigo

4C_BalC-SSE Symposium: Seeing the forest for the trees: the contributions of synthesis to evolutionary science
Tuesday, June 24, 2014 1:15 PM-1:45 PM

Quite apart from promoting a synthetic approach to science, synthesis centers also function as incubators for promising -- but as yet unexplored -- research. In much the same way that business incubators provide administrative, legal and operational support to fledgling startups, synthesis centers provide research groups with the opportunity to engage in high-risk research without the distractions of day-to-day administration, and with the assistance of a skilled informatics team. In this talk, I will review this role of a synthesis center.

Extinctions with and without us: Paleontological baselines for evaluating contemporary extinction risk in coastal oceans

Paul Harnik

4C_BalC-SSE Symposium: Seeing the forest for the trees: the contributions of synthesis to evolutionary science
Tuesday, June 24, 2014 1:45 PM-2:05 PM

Human activities are altering marine ecosystems globally. How marine organisms will respond to the direct and indirect impacts of these activities is largely unknown. Until recently, most marine species were thought to be less vulnerable to extinction than terrestrial species. Consequently, few formal assessments of marine extinction risk exist and the data needed for such assessments are often lacking. The fossil record provides a rich source of information on past extinctions that can be used to identify taxa and regions of particular concern. The Determinants of Extinction in Ancient and Modern Seas working group developed a model of marine extinction risk based on analyses of the Neogene fossil record. We show that a relatively small suite of predictors related to geographic range and phylogeny explain a large proportion of extinction risk among marine animal genera over the last 23 million years. We used this framework to estimate the intrinsic extinction risk of marine genera alive today and to project these predictions onto global coastal biogeographic provinces. These estimates reveal a complex mosaic of extinction vulnerabilities that provide a baseline for the expected distribution of intrinsic risk in a world absent human stressors. We compared these estimates of extinction risk to recent spatial assessments of anthropogenic and climatic impacts to identify areas in which high intrinsic risk may coincide with elevated contemporary stress. Many of these hotspots are located in the tropics, suggesting that these diverse ecosystems may be particularly vulnerable to future extinctions. Synthetic approaches that integrate data for extant and extinct lineages can offer new perspectives on the vulnerability of contemporary faunas to environmental change in addition to the critical role they play in reconstructing the macroevolutionary history of diversification.

Climate change, fluctuating selection and eco-evolutionary dynamics

Carlos Andrés Botero

4C_BalC-SSE Symposium: Seeing the forest for the trees: the contributions of synthesis to evolutionary science
Tuesday, June 24, 2014 2:05 PM-2:25 PM

Evolutionary biology has played a relatively minor role in our current efforts to evaluate and address the potential consequences of climate change. This is somewhat surprising given our field's longstanding interest in understanding how organisms have coped with historic changes in their environment. A possible reason for this discrepancy is that evolutionary theory has been traditionally strong at explaining the past but weak at predicting the future. In this talk, I will discuss my efforts to develop and test a conceptual framework that uses evolutionary principles to predict organismal capacity to adapt to future environmental change. Using theoretical insights, large-scale comparative studies and empirical findings from my own work, I will describe some general principles of evolutionary adaptation to environmental change and suggest ways in which we can explore how ecology and evolution interact to determine the ultimate fate of biological systems as key environmental parameters are altered by anthropogenic activity and local weather patterns become more variable and unpredictable.

Seed dormancy: its effects on plant life cycles and diversification rates

Kathleen Donohue, Liana Burghardt, Charles Willis

4C_BalC-SSE Symposium: Seeing the forest for the trees: the contributions of synthesis to evolutionary science
Tuesday, June 24, 2014 2:25 PM-2:45 PM

Seed dormancy is a fundamental determinant of germination phenology and habitat selection in plants, and it can influence later life stages, life-cycle expression, and adaptive dynamics. First, the timing of germination can have ramifying effects across the life cycle. This is because, in seasonally variable environments, the timing of prior developmental transitions determines the environment experienced subsequently, which in turn affects subsequent development. We have developed a framework for modeling phenology that includes these interactions between seasonally variable environments and development across the life cycle. We show that variation in seed dormancy can influence the expression of plant life cycles and generation time, and that geographic variation in seed dormancy levels can canalize generation time across a species range. Second, seed dormancy can influence macro-evolutionary patterns of diversification. In an analysis of seed dormancy categories across the Angiosperms, we found that a certain dormancy type--physiological dormancy--appears to be an evolutionary "hub", such that other dormancy states evolve to physiological dormancy before evolving to other dormancy states. Physiological dormancy moreover was associated with higher diversification rates, attributable to increased speciation rates. Thus seed dormancy not only is a critical factor that determines the phenology, life histories and demographically important factors such as generation time in individual species; it also appears to influence basic dynamics of adaptation, ecological range expansion, and evolutionary diversification.

Genomic patterns of selection on genes of aerobic respiratory pathways in vertebrates

Richard Broughton, *Feifei Zhang*

4D_301A-Genome Evolution
Tuesday, June 24, 2014 3:15 PM-3:30 PM

Linking genomes to phenomes is one of the grand challenges of 21st century biology. Because the availability of ATP limits most cellular and physiological processes, organismal adaptations with even modest energetic demands should be influenced by the functional efficiency of cellular respiration. Signatures of natural selection on respiration genes may therefore reflect a significant role in the evolution of life history traits, organismal fitness and biodiversity. We investigated patterns of natural selection on component genes of the Krebs cycle and oxidative phosphorylation pathways in the genomes of mammals and fishes. Ratios of nonsynonymous to synonymous substitutions in coding regions of genes of respiratory pathways were compared to a set of non-respiratory housekeeping genes. Results suggest that specific targets of selection are variable but many organismal adaptations are associated with inferred positive selection on genes of the respiratory pathways.

The organization and evolution of the Responder satellite in the Drosophila melanogaster group: dynamic evolution of a target of meiotic drive

Amanda Larracuente

4D_301A-Genome Evolution
Tuesday, June 24, 2014 3:30 PM-3:45 PM

Satellite DNA can make up a substantial fraction of eukaryotic genomes and has roles in genome structure and chromosome segregation. The rapid evolution of satellite DNA can contribute to genomic instability and genetic incompatibilities between species. Despite its ubiquity and its contribution to genome evolution, we currently know little about the dynamics of satellite DNA evolution. The Responder (Rsp) satellite DNA family is found in the pericentric heterochromatin of chromosome 2 of Drosophila melanogaster. Rsp is well-known for being the target of Segregation Distorter (SD)– an autosomal meiotic drive system in D. melanogaster. I present an evolutionary genetic analysis of the Rsp family of repeats in species of the melanogaster subgroup using a combination of available BAC sequences, whole genome shotgun Sanger reads, Illumina short read deep sequencing, and fluorescence in situ hybridization. I show that Rsp repeats have euchromatic locations throughout the genome, that Rsp arrays show evidence for concerted evolution, and that Rsp repeats exist outside of D. melanogaster, in species of the simulans clade. The repeats in these species are considerably diverged at the sequence level compared to D. melanogaster, and have a strikingly different genomic distribution. Thus, the evolution of the Rsp family is highly dynamic over a short evolutionary time scale (

Whole genome sequence analysis of the allotetraploid Mimulus sookensis reveals a nuanced history of genome evolution

Jennifer Modliszewski, *John Willis*

4D_301A-Genome Evolution
Tuesday, June 24, 2014 3:45 PM-4:00 PM

Phenotypic evolution is dependent upon genetic variation, which arises in populations as a result of the introduction of migrant individuals, recombination, and spontaneous mutation. Polyploidization, or whole genome duplication, can both complicate the manner in which recombination is able to create new combinations of genotypes and intensify the occurrence of spontaneous mutation. Recombination between homeologous chromosomes (ie, homologous chromosomes from different species contained within a single genome) is one mechanism which may allow new allopolyploid species to capitalize on the wealth of genetic variation within their genome. Spontaneous mutation is also an abundant source of genetic variation in neopolyploids. To investigate the role of homeologous recombination and spontaneous mutation in genomic and phenotypic evolution post-polyploidization, we utilize Mimulus sookensis, a hybrid polyploid of Mimulus guttatus and Mimulus nasutus which has recurrently formed throughout its range in the valleys of western Oregon (USA) and on the southern tip of Vancouver Island (Canada). Mimulus sookensis has small flowers, like its highly selfing diploid progenitor, M. nasutus. In contrast, diploid F1 hybrids and synthetic neoallotetraploid Mimulus are large-flowered, like the predominately-outcrossing M. guttatus. This reduction in flower size between neoallotetraploids and naturally-occuring M. sookensis implies that phenotypic evolution has occurred in M. sookensis. Here, we present an analysis of whole-genome resequencing data from M. sookensis, and its diploid progenitors M. guttatus and M. nasutus, to address three questions: 1) is M. sookensis a fixed heterozygote throughout its genome, or is there evidence for homeologous recombination, which may have augmented the rate of phenotypic evolution?, 2) does one subgenome correspond closely to M. nasutus?, and 3) has there been differential evolution of the two subgenomes of M. sookensis, which may have facilitated phenotypic evolution? By examining whole genome sequence data from naturally-occuring allotetraploid Mimulus, and comparing it to M. guttatus and M. nasutus, we gain insight into genomic and phenotypic evolution post-polyploidization.

Exploring genome-wide signals of selection against gene flow

Simon Aeschbacher, *Graham Coop*

4D_301A-Genome Evolution
Tuesday, June 24, 2014 4:00 PM-4:15 PM

Selection against alleles which are maladaptive in a particular environment or genomic background can maintain local adaptations and species in the face of even high levels of gene flow. Such selection implies an effective reduction in rates of gene flow at and close to loci under selection. This may lead to heterogeneity in divergence along the genome and allow further differentiation due to selection and genetic drift at linked and unlinked sites. The idea of expressing the impact of selection on linked neutral diversity in terms of an effective migration rate goes back to Petry (1983) and has been subsequently developed by others. Here, we extend these ideas to a genome-wide context, and explore the extent to which selection against gene flow leaves a distinct and detectable signal in the patterns of neutral diversity. We test this approach against simulations and genome-wide sequencing data.

Understanding the evolution and genetic basis of variation in vernalization in Mimulus guttatus

Jannice Friedman, Jill Preston

4D_301B-Trait Evolution
Tuesday, June 24, 2014 3:15 PM-3:30 PM

The timing of flowering is one of the most important traits in the plant life cycle. Many plants synchronize their flowering to seasonal changes, so that vegetative and reproductive phases are tailored to local climate and edaphic conditions. One such cue is winter; certain plants do not initiate flowering unless they have experienced prolonged cold. The promotion of flowering by prolonged exposure to cold is known as vernalization. Mimulus guttatus (the yellow monkeyflower) is polymorphic for vernalization requirement, with most perennial populations requiring vernalization, and most annual populations not needing it. Thus, this is an excellent system for understanding both the genetic basis and the adaptive significance of this key flowering time difference. Here, we use growth chamber experiments that combine different photoperiods and temperature treatments to pinpoint the exact nature of responses. Quantitative Trait Loci mapping experiments have demonstrated that only a few major QTL underlie this trait. Focusing on 6 flowering-time genes in these regions, we use candidate gene expression analyses in different treatments and at various time points to determine each gene’s role in the evolution of flowering time responses. Characterizing the genetic architecture of natural variation in vernalization is a key step towards understanding the process of local adaptation in M. guttatus, and flowering time evolution more generally.

Genome-wide relationships among color-pattern forms in a polymorphic bumble bee

Jeffrey Lozier, Jason Jackson

4D_301B-Trait Evolution
Tuesday, June 24, 2014 3:30 PM-3:45 PM

Bombus bifarius exhibits dramatic divergence in pile coloration throughout its geographic range in the western United States. Populations in the easternmost parts of the species range (Colorado and southern Wyoming) exhibit a striking red hair color on the second and third abdominal segments (red-banded), while those in the westernmost parts have black colored pile (black-banded). Geographically intermediate populations (e.g., Wyoming and Utah) are more variable, sometimes appearing similar to one of the two extremes, but usually with some degree of mixed orange and black coloration. Previous analyses of population structure in B. bifarius using microsatellites have suggested some patterns of genetic structure consistent with both phenotypic and regional geographic differentiation, but the high variability and large population sizes in bumble bees has made distinguishing isolation from ongoing gene flow challenging. Here we apply two methods, total RNA sequencing and double-digest RAD tag sequencing, to analyze genome-wide nucleotide variation across a geographic and color-pattern transect in B. bifarius from Colorado to Oregon. We apply several approaches to test the strength of evolutionary isolation and relationships among these populations, and also to examine individual SNPs for unique patterns of shared similarity between red-banded and mixed populations in an intial effort to identify genome regions that may play a role in coloration.

Physical and chemical interactions mediate sex change in a protandrous gastropod

Abigail Cahill

4D_301B-Trait Evolution
Tuesday, June 24, 2014 3:45 PM-4:00 PM

Sequential hermaphroditism is a widespread phenomenon among animals. Theory suggests that sequential hermaphrodites maximize their lifetime reproductive output by changing sex in response to cues, including those from social environments. Crepidula fornicata (Gastropoda: Calyptraeidae) is a protandrous snail that lives in semi-permanent stacks of both males and females. Previous lab and field studies have shown that males change sex faster and at a smaller size when in isolation than when the males are associated with females. Additionally, the size-advantage model is more accurate within stacks than within a whole population, and males change sex at a larger size than predicted by theory. These results indicate that sex change in males is affected by conspecific interactions. However, the mechanism connecting conspecifics and sex change is unknown. I present results of an experiment that investigated the rate of sex change in C. fornicata when males were isolated, in physical and chemical contact with females, and in chemical contact only. Males only in chemical contact with females change sex at a similar rate to isolated males, suggesting that sex change is mediated by contact cues in this species. Results indicate that the relevant cue in C. fornicata is an inhibitor of sex change and that it requires physical contact with a live animal. This work provides a mechanism to explain the phenomenon of larger males than predicted by theory. It also allows for both further chemical characterization of the sex-change cue and further investigation of the assumptions and parameters of the size-advantage model in C. fornicata.

The Genetic Basis of Natural Aridity Tolerance in Anopheles gambiae

Simo Zhang, Matthew Hahn

4D_301B-Trait Evolution
Tuesday, June 24, 2014 4:00 PM-4:15 PM

A large inversion on chromosome 2L of the malaria vector, Anopheles gambiae, is associated with a latitudinal cline in aridity in Cameroon. High frequencies of the inverted karyotype are present in northern, arid regions and almost absent in southern, humid regions. In populations at middle latitudes the inversion is at intermediate frequencies. Some nucleotide polymorphisms within the inversion that are fixed for alternative alleles at either end of the cline show patterns suggesting substantial amounts of gene flux between the alternative arrangements in the central region. Populations from the central region may therefore represent a unique opportunity to apply association mapping to an inversion. Here, we use a pooled genome-wide association study (Pool-

GWAS) approach to fine-scale map the genomic loci contributing to natural variation in aridity tolerance. We examine aridity tolerance phenotypes in thousands of individuals of A. gambiae from the center of the cline. We pool individuals by phenotype—high aridity tolerance and low aridity tolerance—and divided each phenotype pool by inversion arrangement. For each combination of karyotype and phenotype, two replicates are used. We sequenced each replicate at approximate 20X coverage, and tested polymorphic variants for associations with aridity tolerance. We identify 95 SNPs showing significant associations with aridity tolerance variation in all four pools. 31 of these SNPs are mapped within 24 protein coding genes, some of which are promising candidates for proteins contributing to aridity tolerance.

Genetic pedigree analysis to evaluate supplementation and natural reproductive success of spring Chinook salmon in Newsome Creek, ID.

Thomas Backman, Andrew Matala, Shawn Narum

4D_301B-Trait Evolution
Tuesday, June 24, 2014 4:15 PM-4:30 PM

The Clearwater River in the Snake River Basin historically supported large spawning populations of Chinook salmon (Oncorhynchus tshawytscha); however, extirpation occurred throughout the basin following construction of the Lewiston Dam in 1927. Hatchery reared spring Chinook salmon have been released in many Clearwater tributaries since 1971. These populations are not considered wild because they were derived from reintroduction efforts, but progeny of fish spawning in the natural environment (instream) are designated as natural-origin. The Nez Perce Tribe is conducting an extensive monitoring and evaluation effort throughout the Clearwater River Sub-basin, with specific long term goals that include estimating the genetic effects of interactions between natural- and hatchery-origin populations, and evaluating demographic effects such as naturalization resulting from supplementation. The NPT Hatchery employs a Natural Rearing System technique designed to produce fish behaviorally, physiologically and genetically similar to natural populations. Newsome Creek, a tributary to the South Fork Clearwater River, receives hatchery outplanted fish (directed supplementation). A proportion of both marked and unmarked fish returning to Newsome Creek are collected for broodstock with the remainder passed upstream of an exclusionary weir. Relative reproductive success has varied (study period 2002-2012) we observed not only similar productivity between hatchery-origin and natural-origin or naturalized fish, but evidence that hatchery-origin Chinook salmon spawning naturally in Newsome Creek may be more successful than their naturalized counterpart. Based on assignment of 2011 juvenile progeny, we observed reproduce prior years, with a weighted geometric mean of 79% RRS. Whether or not reproductive success at observed rates will be comparable between the juvenile outmigration stage and subsequent returning adult progeny stage is a question that continued monitoring in Newsome Creek will strive to answer but one that remains unclear at this time.

In search of nuclear correlates of massive boreal mitochondrial DNA introgression in hares

Jose Melo-Ferreira, Liliana Farelo, Pierre Boursot, Paulo C. Alves

4D_302A-Reproductive Isolation and Hybridization
Tuesday, June 24, 2014 3:15 PM-3:30 PM

Mitochondrial DNA introgression is the most frequently described case of secondary interspecific gene exchange in nature. Whether this phenomenon is relevant to the evolutionary trajectory of the species or if it is most often a neutral marker of interspecific interactions remains a matter of debate. Given that mtDNA encodes for proteins involved in important metabolic processes, which closely interact with nuclear encoded proteins, we here use a situation of massive ancient mtDNA introgression from the boreal, cold-adapted, species Lepus timidus into the temperate Lepus granatensis to test for mt-nuclear co-introgression or co-evolution. This massive introgression is geographically structured, being absent in the southern range of the temperate species but predominant in the north. Using transcriptome sequencing data and SNP genotyping we identified nuclear genes that showed apparent high levels of differentiation between northern and southern regions, mimicking mtDNA but contrasting with the low differentiation inferred for most of the other nuclear genes, which may thus reflect mito-nuclear coevolution.

Hybridization increases fecundity and size in invasive taxa: meta-analytic support for the hybridization-invasion hypothesis

Stephen Hovick, Kenneth Whitney

4D_302A-Reproductive Isolation and Hybridization
Tuesday, June 24, 2014 3:30 PM-3:45 PM

The hypothesis that interspecific hybridization promotes invasiveness has received much recent attention, but tests of the hypothesis can suffer from important limitations. Here, we provide the first synthesis of studies experimentally testing the hybridization-invasion hypothesis in plants, animals and fungi. We identified 72 systems for which hybridization has been putatively associated with invasiveness, weediness or range expansion. Within this group, 15 systems (comprising 32 studies) experimentally tested performance (fecundity, survival, and/or size) of hybrids vs. their parental species and met our other criteria; a surprisingly large number of studies were uninformative because they neglected to compare hybrid performance to the most invasive parent. Both phylogenetic and non-phylogenetic meta-analyses showed that wild hybrids were significantly more fecund and larger than their parental taxa, but did not differ in survival. Resynthesized hybrids (which typically represent earlier hybrid generations than do wild hybrids) did not consistently differ from parental species in fecundity, survival or size. However, using meta-regression, we found that fecundity increased (but survival decreased) with hybrid generation in resynthesized hybrids, suggesting that natural selection can play an important role in shaping hybrid performance – and thus invasiveness – over time. We conclude that the available evidence supports the hybridization-invasion hypothesis, with the caveats that our results are clearly driven by tests in plants (which are more numerous than tests in animals and fungi) and that a minority of systems clearly have no link between hybridization and invasion.

One species or three? Resolving lineage boundaries in dusky salamanders through sexual isolation trials and next-generation sequencing

Justin Kratovil, David Weisrock

4D_302A-Reproductive Isolation and Hybridization
Tuesday, June 24, 2014 3:45 PM-4:00 PM
Study systems with low ecomorphological disparity and those lacking adequate genetic resources present a major challenge for systematics. The resolution of taxonomic ambiguities is further confounded in systems with a history of rapid evolutionary divergence and reticulate evolution. Disentangling these evolutionary relationships is an important goal and provides phylogenetic clarity useful for delimiting species and testing mechanisms responsible for generating and maintaining genetic diversity. In concert with the analysis of genetic markers collected from sequencing mitochondrial and nuclear loci, experimental measures of sexual isolation are useful for identifying lineages and species boundaries indicative of pre-zygotic isolation and the cessation of gene flow. Recent genetic surveys of dusky salamanders within the Southern Appalachians reveal extensive mitochondrial diversity within Desmognathus fuscus; a broadly distributed semi-aquatic plethodontid salamander. Controlled reproductive isolation trials involving crosses within and between haplotype assemblages from western North Carolina reveal patterns of asymmetric sexual bias that may limit gene flow and contribute to the observed patterns of genetic diversification across sharp biogeographic clines. Forthcoming parallel-tagged amplicon sequencing of multiple nuclear loci will leverage the power of next-generation sequencing at the population level to resolve long standing questions of lineage boundaries and models of diversification in D. fuscus and other closely related lineages.

Variation in Interploid Reproductive Isolation within the Campanula rotundifolia Polyploid Complex

Brittany Sutherland, Laura Galloway

4D_302A-Reproductive Isolation and Hybridization
Tuesday, June 24, 2014 4:00 PM-4:15 PM
Whole genome duplication events are often assumed to confer reproductive isolation (RI) between polyploids and their diploid progenitors and as such are often thought to be “instant speciation.” Although this pattern is demonstrated in many diploid-tetraploid systems, the evidence for such strong RI in polyploid complexes is sparser, and doesn’t always support a high RI assumption. This study seeks to investigate the effects of parental cytotype on RI in the circumboreal wildflower, Campanula rotundifolia, a polyploid complex comprising diploid, tetraploid, and hexaploid cytotypes. Thirteen populations of the dominant tetraploid cytotype spanning a range of genetic distances were reciprocally crossed with diploid and hexaploid test populations, and the resulting fruit set, seed number, and F1 germination rate were measured. 2X/4X crosses set slightly more fruit (3%) than 4X/6X crosses. However, germination rate was substantially higher (92%) in 4X/6X crosses than in 2X/4X crosses, and was commensurate with parental intraploid crosses. A cytotypic parent of origin effect was also found; when the paternal ploidy was greater fruit set was 24% higher, but when the maternal ploidy was greater germination rate was 97% higher. The substantial increase in germination rate in 4X/6X crosses suggests that RI in higher-order polyploid crosses may be lower than in those between diploids and tetraploids, calling into question the assumption of “instant speciation” as it pertains to polyploid complexes.

Hybrid taxa can mislead phylogeographic analyses in Tolpis (Asteraceae)

Michael Gruenstaeudl, Bryan Carstens, Robert Jansen, Arnoldo Santos-Guerra

4D_302A-Reproductive Isolation and Hybridization
Tuesday, June 24, 2014 4:15 PM-4:30 PM
Hybridization is a critical evolutionary process. It can significantly affect phylogenetic tree inference as well as downstream analyses, such as character state or phylogeographic reconstructions. The present investigation demonstrates the level of impact that hybrid taxa can have on (a) species tree inference under the multi-species coalescent model, and (b) subsequent phylogeographic reconstructions. Available metrics to measure departure from the multi-species coalescent model and, by extension, to identify instances of hybrid speciation are discussed. We illustrate the issue by conducting species tree inference and ancestral area reconstruction in the island plant lineage Tolpis (Asteraceae). Tolpis comprises several species of potential hybrid origin and displays a complex biogeographic history, including dispersals among and between island and continental habitats. Our results demonstrate that failing to recognize hybrid taxa can mislead phylogeographic inference of the genus and, more broadly, increase the uncertainty in evolutionary analyses.

Natural selection helps explain the unexpectedly small range of neutral diversity among species.

Tim Sackton, Russ Corbett-Detig, Dan Hartl

4D_302B-Recombination
Tuesday, June 24, 2014 3:15 PM-3:30 PM
The observation that levels of neutral diversity do not vary nearly as much among species as expected due to the vast range of census population sizes is perhaps the most puzzling and enduring paradox of molecular population genetics. Under a simple neutral Wright-Fisher model, levels of polymorphism within a species are expected to be directly proportional to the population size times the mutation rate. However, even allowing for demographic effects that can reduce the effective population size below the census population size, observed neutral diversity within species falls in an extremely compact range compared to the range of population sizes. One plausible contributor to this difference is the operation of natural selection in the genome. Both background selection and positive selection purge genetic variation from populations, and because natural selection is more effective in larger populations, we may expect larger populations to purge disproportionately more variation. Because selection at one site will also affect linked sites, genomic regions that recombine infrequently tend to harbor little polymorphism. The resulting correlation between

recombination and polymorphism has been reported in a number of species, offers an appealing means of quantifying the effect of selection on polymorphism throughout the genome, and makes testable predictions towards that goal. Specifically, species with larger census population sizes will experience stronger effects of selection on linked sites and will tend to demonstrate stronger correlations between levels of polymorphism and local rates of recombination.

To explore this hypothesis, we identified 40 species (including plants, insects, nematodes, and vertebrates) that have sufficiently high quality reference genomes, polymorphism data, and genetic maps to enable genome-wide comparisons between polymorphism and recombination rates. In total we aligned more than 30 billion short reads and across all linkage maps we analyzed recombination between more than 30 thousand markers. After developing a robust alignment and genotyping pipeline, and curating genetic maps, we computed the correlation between levels of synonymous site polymorphism and the local recombination rate for each species. Overall, the data are consistent with the hypothesis that natural selection truncates the distribution of neutral diversity at silent sites. As an example, one primary result is that invertebrates, which tend to have large census population sizes, have significantly stronger correlations between recombination and nucleotide diversity than vertebrates. This and other results therefore provide empirical support for the hypothesis that the action of natural selection plays an important role in limiting the range of neutral diversity observed among species, helping to finally resolve this longstanding paradox.

The evolution of functional trait syndromes: the ecological genetics of drought resistance in annual monkeyflowers.

Nicholas Kooyers, Anna Greenlee, Jack Colicchio, Benjamin Blackman

4D_302B-Recombination
Tuesday, June 24, 2014 3:30 PM-3:45 PM
Complex, multi-trait adaptations that repeatedly evolve through convergent responses to a single agent of selection are functional trait syndromes. The optimized evolution of these syndromes may be limited by evolutionary, genetic or biophysical tradeoffs that impede the evolution of certain character state combinations. We have investigated whether genetic correlations constrain the evolution of functional trait syndromes in response to drought stress. Plants adapt to drought stress through multiple physiological mechanisms including rapid reproduction (drought escape) and/or resisting drought conditions (drought avoidance). In theory, plants that flower early but can also maintain reproductive output as long as possible after the onset of drought will have the highest fitness. However, drought escape and drought avoidance are considered mutually exclusive because of the accompanying resource allocation tradeoffs. Through common garden and photoperiod response experiments, we assessed drought escape and drought avoidance traits in annual populations of the common monkeyflower, Mimulus guttatus, sampled across ten altitudinal transects in the Sierra Nevada and Cascade Mt. ranges. Our findings indicate that M. guttatus has repeatedly evolved both drought escape and drought avoidance strategies in populations with drought-abbreviated growing seasons. These strategies evolve primarily as independent syndromes, with negative genetic covariance between traits associated with each syndrome. However, in some populations with the short growing seasons, drought escape and drought avoidance traits coincide, suggesting a unified syndrome can evolve in the correct environmental conditions. Our findings highlight the diverse functional responses populations take to adapt to similar conditions and demonstrate evolutionary flexibility in the formation of functional trait syndromes.

The effects of inhibited recombination on the social chromosome of Solenopsis invicta

Rodrigo Pracana, Nichols Richard, Yannick Wurm

4D_302B-Recombination
Tuesday, June 24, 2014 3:45 PM-4:00 PM
Genomic rearrangements can locally inhibit recombination, and therefore are thought to be required for the formation of genomic structures like sex chromosomes and supergenes, which act to maintain divergent phenotypes in a population. However, little is know about the early evolution of sex chromosomes and supergenes, and how it is affected by genomic rearrangements and local inhibition of recombination. The fire ant Solenopsis invicta, in which a pair of young social chromosomes controls two divergent forms of colony organization, offers a unique opportunity to understand the evolution of genomic rearrangements. The two social chromosome variants, SB and Sb, have structural differences leading to lack of recombination spanning approximately 55% of the chromosome. To test how inhibition of recombination affects sequence divergence between the two chromosome variants, we have identified SNPs in the genomes of haploid SB males and of haploid Sb males. We show that the two chromosome variants are highly divergent within the non-recombining region. Within this region, the Sb variant has almost no diversity, while the SB variant has a level of diversity similar to the rest of the genome. This pattern is consistent with both neutral divergence (increased drift) and adaptive divergence between the two variants (selective sweeps). We use a population genetic approach to explicitly identify the balance between the two evolutionary forces. Furthermore, we report on heterogeneity of divergence along the non-recombining region, identifying the sequence of rearrangement events that led to the current genomics structure.

Evolution of Recombination Rate in Angiosperms

George Tiley, Gordon Burleigh

4D_302B-Recombination
Tuesday, June 24, 2014 4:00 PM-4:15 PM
The molecular mechanism of homologous recombination can affect genomic architecture as well as the efficacy of selection. Yet the evolution of recombination rate is not well understood on a macroevolutionary scale, and little is known about the patterns of variation in recombination rate among plant lineages. We investigated the evolution of global meiotic recombination rate in angiosperms using data from 30 species. We examined how recombination rate varies with genome size, LTR-retrotransposon content, composition biases, gene family size, and patterns of

molecular evolution using phylogenetic comparative methods. Our results are consistent with previous hypotheses that recombination rate is negatively correlated with genome size, which is likely caused, at least in part, by the removal of LTR-retrotransposon content. Our results also suggest a role for recombination in the preservation of duplicate genes, which can be explained by an increase in the efficacy of purifying selection. Thus, our analyses indicate the importance of population genetic processes on the evolution of species and demonstrate that genetic maps can be a valuable source of data for comparative genomics and inform evolutionary processes on a macroevolutionary scale.

Determining the relationship between changes in interspecies recombination rates and nucleotide divergence

Laurie Stevison, Jeff Wall

4D_302B-Recombination
Tuesday, June 24, 2014 4:15 PM-4:30 PM

Identifying and understanding the genetic basis of speciation is a central question in evolutionary biology. Work on chromosomal inversions has shown that the reduced recombination in hybrids leads to higher levels of nucleotide divergence in these regions. Additionally, work on 'islands of speciation' has found an accumulation of these 'islands' in regions of low recombination. Despite the accepted importance of reduced recombination in contributing to persistence of hybridizing species, no major genetic variants, other than inversions, have been identified which act as interspecific recombination suppressors. Here, we present a statistic, which quantifies differences in hybrid recombination relative to intraspecific recombination in closely related species pairs. Using sister species, we test the relationship between this statistic and nucleotide divergence across various model systems, including Drosophila and yeast. For Drosophila pseudoobscura and D. persimilis we show a siginificant negative relationship (rho=-0.5; p=0.02; N=32), owing to the presence of multiple chromosomal inversions. For the more divergent, S. cerevisiae and S. paradoxus we show no significant relationship (rho=-0.11; p=0.13;N=181). More recent results are from more closely related taxa with no major chromosomal differences. By quantifying differences in divergence based on our statistic, our aim is to identify novel recombination suppressors and perhaps enhancers of hybrid recombination. Once genetic variants contributing to differences in both recombination and divergence in closely related species are identified using our approach, future research can study these genetic variants in non-model systems to assess their broader importance in speciation.

Understanding variation in susceptibility and host response to the amphibian-killing chytrid fungus: a case study in two bufonid species

Thomas Poorten, Erica Rosenblum

4D_302C-Host-Parasite Evolution
Tuesday, June 24, 2014 3:15 PM-3:30 PM

In the wake of Bd epidemic waves, researchers have observed that some host species suffer massive die-offs and others persist. The mechanism(s) that underlie the difference between winners and losers remains a mystery. Although environmental and ecological factors can affect susceptibility, previous work suggests that intrinsic differences in host response exist. The purpose of this study is to compare infection dynamics and host response in two related frog species under controlled laboratory conditions. We performed a Bd infection experiment in two toad species that were believed to differ in susceptibility: Bufo marinus (resistant) and Bufo boreas (susceptible). After experimental inoculation with Bd, we observed higher disease incidence and higher pathogen loads in B. boreas compared to B. marinus. Histological examination of epidermal sections from ventral integument revealed higher infection intensities as well as structural disruption in B. boreas. In addition, B. boreas experienced a loss in body weight as compared to control individuals. We analyzed transcriptomic changes in Bd-exposed individuals compared to control individuals for both species. Overall B. boreas had a higher transcriptional response to infection than B. marinus, which may result from numerous and severe physiological disruptions associated with high pathogen load. In B. marinus, transcriptional patterns related to skin structure and water balance are host response pathways that may be critical for disease resistance. Together our results confirm that intrinsic host response differences are important for determining susceptibility.

Evolution of defenses against parasitoid wasps in the Drosophila melanogaster subgroup

Zachary Lynch, Jacobus de Roode, Todd Schlenke

4D_302C-Host-Parasite Evolution
Tuesday, June 24, 2014 3:30 PM-3:45 PM

Macroevolutionary tradeoffs occur when species have different fixed strategies for resource allocation across a set of traits. In some host-parasite systems, hosts can use multiple types of immune responses to alleviate the fitness consequences of parasitism. However, hosts must expend resources to deploy these defenses and maintaining strong defenses can be costly to host fitness. Therefore, ecological immunology theory predicts that tradeoffs will occur among immune responses, but direct evidence for macroevolutionary immune tradeoffs is lacking. Fruit flies in the Drosophila melanogaster subgroup, which coevolved with endoparasitoid wasps in the genus Leptopilina across their ancestral African ranges, are an excellent model system for investigating this prediction. Female flies can practice behavioral avoidance strategies to reduce the risk that their offspring will be parasitized, and fly larvae can mount melanotic encapsulation responses to kill developing wasps. We have found that the strengths of behavioral avoidance and melanotic encapsulation are highly variable across eight fly species. Several fly species are able to use melanotic encapsulation to survive parasitism by L. boulardi, but only one fly species shows significant survival against L. heterotoma, demonstrating that L. heterotoma is much more virulent across this host range. However, each fly species shows similar avoidance of both wasp species, suggesting that flies do not modulate avoidance behavior based on wasp virulence. There is no evidence for a macroevolutionary tradeoff between defenses against L. boulardi or L. heterotoma, as evidenced by the lack of significant negative correlations between behavioral avoidance and melanotic encapsulation across fly species. Future comparative studies of defenses against common parasites have the potential to reveal macroevolutionary immune tradeoffs and greatly improve our understanding of host-parasite coevolutionary trajectories.

Horizontal gene transfer between schistosomes and their hosts?

Bhagya Wijayawardena, Dennis Minchella, J. Andrew DeWoody

4D_302C-Host-Parasite Evolution
Tuesday, June 24, 2014 3:45 PM-4:00 PM

Horizontal gene transfer (HGT), the movement of genetic material between distinct evolutionary lineages, has long been known as a principal force of diversification and adaptation of prokaryotes. More recently, molecular data have increasingly contributed to the identification of possible gene transfers among various metazoan phyla (e.g., Porifera, Cnidaria, Nematoda, Arthropoda, Rotifera, and Craniata). Although the exact mechanism of eukaryotic HGT is often unknown, host-parasite interactions provide ample opportunities for HGT. Schistosomes, trematode parasites with complex life cycles, have been repeatedly implicated in HGT. We employed molecular and bioinformatic approaches to critically analyze published reports of HGT between schistosomes and their hosts to better understand the evolution of eukaryotic genomes. Our research suggests that reported cases of schistosome-associated HGT may be due to technical artifacts (e.g., contamination) as opposed to biological reality. Thus, we emphasize the importance of multiple lines of evidence to conclusively document HGT.

A global analysis of water and nitrogen relationship between mistletoes and their hosts: broad-scale tests of old and enduring hypotheses

Marina Scalon, Ian Wright

4D_302C-Host-Parasite Evolution
Tuesday, June 24, 2014 4:00 PM-4:15 PM

The association between mistletoes and their hosts is a fascinating co-evolutionary system. Mistletoes are parasitic angiosperms that connect to the host branch by a modified root called a haustorium, and acquire water and nutrients exclusively via the host xylem. Notably, mistletoes are known to use a vast amount of water for a given amount of carbon fixed during photosynthesis (low ‘water use efficiency’, WUE). The “nitrogen-parasitism hypothesis” posits that N would be the most limiting resource for mistletoes, so that they need to use more water (i.e., faster transpiration rates) in order to acquire enough N from the hosts. In a rather different context, the "Mimicry hypothesis" arose in the literature suggesting that some mistletoes mimic their host’s leaves morphology in order to avoid herbivory, and this allows them to accumulate larger amounts of leaf nitrogen. These two non-exclusive hypotheses share this element of trying to explain patterns of mistletoe leaf N concentration. We set out to test the generality of both hypotheses at unprecedented scale (168 mistletoes-host pairs, from 39 sites, and from all continents except Antarctica), drawing together literature data and our own field data for two key plant functional traits that represent N (leaf N concentration), long-term WUE and degree of stomatal control (leaf carbon isotopic composition, δ13C). Key findings included (1) little support for the N-parasitism hypothesis: higher nitrogen was not related to more similar δ13C between hosts and mistletoes, and nitrogen alone does not explain the lower δ13C exhibited by mistletoes; (2) little support for the mimicry hypothesis: mimic mistletoes generally did not have greater N concentration, except when associated with N-fixing hosts. More broadly, mistletoes showed the same shifts in leaf traits in relation to site climate as did their hosts, suggesting that mistletoes are similarly constrained by environmental drivers.

Accelerated molecular evolution in brood parasitic finches: demography or selection?

Allison Lansverk, Christopher Balakrishnan, Daniel Newhouse, Michael Sorenson, Michael Brewer

4D_302C-Host-Parasite Evolution
Tuesday, June 24, 2014 4:15 PM-4:30 PM

Indigobirds (Vidua sp.) are host-specific brood parasites that have become an important model for the study of speciation. Speciation in indigobirds has been driven by the colonization of new hosts; this process likely has resulted in repeated bottlenecks over the history of host-shifts in this group. Furthermore, brood parasitic species are generally less abundant than their hosts. These aspects of indigobird natural history should lead to a decreased effective population size (Ne) and therefore, a higher rate of fixation of nonsynymous substitutions (ω) in indigobirds relative to non-parasitic species. Indeed, Sorenson and Payne (2005) found support for this using 505 codons of the mitochondrial ND2 and ND6 genes, and this effect is also seen across the entire mitochondrial genome. Here we test whether this pattern of rate acceleration also spans the nuclear encoded portion of the genome. To do so, we sequenced and assembled the transcriptome of a male indigobird Vidua chalybeata. The transcriptome was sequenced from multiple tissues (brain, testes, liver) and the Illumina platform. Transcripts were assembled in Trinity and yielded a putative ortholog set of over 10,540 genes. We used Phylogenetic Analysis using Maximum Likelihood (PAML) to compare rates of evolution in the indiogbird lineage relative to transcriptomes of three non-parasitic species: zebra finch Taeniopygia guttata, song sparrow Melospiza melodia and white-crowned sparrow Zonotrichia leucophrys. The finding of an accelerated rate of evolution throughout the indigobird genome would support the hypothesis that small effective population sizes have caused the accelerated molecular evolutionary rates in these parasitic species. Alternatively, if the rate acceleration is restricted to the mtDNA, that could suggest selection acting specifically on female lineages, perhaps in the context of selection on genes associated with the evolution of host mimicry by parasites.

The rate of adaptation in a changing environment

Leonard Nunney

4D_303-Evolution on Environmental Gradients
Tuesday, June 24, 2014 3:15 PM-3:30 PM

Global warming is a major threat to biodiversity that goes beyond precedent. Historically, many species survived by shifting their range, but now human-induced habitat loss and fragmentation commonly restricts range shifts, forcing species to adapt in situ or face extinction. Simulations, using a model integrating population dynamics, mutation, environmental variance, and genetic change, examine the relationship between maximum phenotypic and genetic rates of change. Not surprisingly, small populations of range-bound species (103 or less) will be severely limited in their long-term response to very rapid climate change; however, linked populations can adapt effectively if gene flow between neighboring reserves is adequate.

Identifying a potential for early assortative mating between the morphs of Giant Kelp down its environmental gradient along Central California's coast

Heidi Hargarten, Mattias Johansson, Nelson Coelho, Sarah Jeffries, Michael Graham, Filipe Alberto

4D_303-Evolution on Environmental Gradients
Tuesday, June 24, 2014 3:30 PM-3:45 PM

Organisms living along environmental gradients often utilize phenotypic plasticity to maximize their survival across a range of conditions. Wherever gradients occur, there is potential for divergence through isolation-by-adaptation (IBA) to build-up between genotypes experiencing different selective pressures. Plasticity in traits pertaining to mating systems in particular are likely to constitute an interesting and revealing model for the study of the underlying mechanisms behind parapatric speciation. Giant kelp, Macrocystis spp., shows striking plasticity in holdfast morphology and reproductive strategy when colonizing intertidal (M. integrifolia morph) versus subtidal (M. pyrifera morph) areas along temperate rocky coastlines of the eastern Pacific Ocean. In the intertidal, high photosynthetically-active radiation (PAR) and UV radiation limit development of spores, recruitment of microscopic gametophytes, and growth and survival of embryonic sporophytes of M. pyrifera. Although depth of parent sporophytes influences spore survival in irradiance-stressed environments, few studies have examined the effects of irradiance stress on M. integrifolia's developmental stages. This study focuses on understanding the roles of IBA and plasticity in maintaining Macrocystis morphs along the California coastline. To test for genetic isolation caused by ecological divergence in the intertidal, we performed fine scale spatial sampling and molecular analysis of parapatric intertidal and subtidal populations off of the Central Californian coast. Using seven microsatellite markers, we compared genetic differentiation between morphs within sites and among morphs across different sites. Furthermore, we identified the presence of clonal replicates in intertidal populations. Results show higher differentiation between adjacent subtidal and intertidal morphs than between the same morph at larger spatial scales, suggesting isolation-by-adaptation. Several potential mechanisms could explain this result: assortative or other non-random mating, longer generation times promoted by asexual growth (intertidal morph), and differential mortality due to early adaptive divergence. Spatial analyses of clonal structure do not indicate asexual reproduction as the dominant strategy in the intertidal. To explore the hypothesis of differential mortality due to adaptive divergence, we will experimentally test assortative mating at different early development stages using controlled crosses of the two morphs under different treatments of irradiance (PAR and UV) stress. Surviving embryonic sporophytes will be genotyped and a paternity analysis will be conducted. Specifically, we hypothesize offspring from M. pyrifera parents will experience higher than expected mortality under irradiance stress, such that paternity analyses will reveal lower than expected numbers of M. pyrifera offspring among surviving embryonic sporophytes.

Divergence along an elevational gradient in Borneo

Daniela Sorger, Jan Zima jr., Ian Butler, Daniel Kronauer, Rob Dunn, Milan Janda

4D_303-Evolution on Environmental Gradients
Tuesday, June 24, 2014 3:45 PM-4:00 PM

Elevational gradients and the divergence along them have taken an increasingly prominent role in biogeography because it is along these gradients that the effects of climate change are most readily observed. Typically species along elevational gradients are treated as though they are discrete entities with low and high elevation limits. Yet, a key feature of how species respond to elevational changes in climate and to our understanding how they diverged historically is population genetic structure of species and the gene flow among populations.

Here we use chemical, morphological and genetic tools to investigate trap-jaw ant populations (genus Odontomachus) along an elevational gradient in Sarawak, Borneo. We use nDNA and mtDNA markers to discern the evolutionary history of low and high elevation populations of what is currently a single named species. Our results indicate that while models suggest many species need to move uphill to track climate change that, at least in our focal species, historic gene flow up and downhill has been relatively reduced.

Why tropical species have narrow ranges and niches: a theoretical exploration of Janzen's hypothesis

Xia Hua

4D_303-Evolution on Environmental Gradients
Tuesday, June 24, 2014 4:00 PM-4:15 PM

Janzen's hypothesis of "why mountain passes are higher in the tropics" has led to the idea that tropical species may be evolutionarily adapted to a narrower range of temperatures due to the limited seasonal temperature variation in the tropics and may then inhabit narrower elevational ranges. These conditions are hypothesized to promote parapatric speciation along elevational gradients as well as faster rates of climatic niche evolution. Numerous empirical studies have documented latitudinal patterns in species elevational ranges, temperature tolerances, and species richness that are consistent with Janzen's hypothesis, but conflicting patterns have also been found. This study presents the first mathematical model to examine the population-level processes that lead to Janzen's hypothesis on the physiological responses of individual thermal tolerance to seasonal temperature variation, and how these responses lead to narrower species elevational ranges and higher speciation rate.

Germination time, asymmetric competition, frequency-dependent selection and the emergence of the "irrelevant fraction"

Arthur Weis, Kyle Turner, Emily Austen, Susana Wadgymar

4D_303-Evolution on Environmental Gradients
Tuesday, June 24, 2014 4:15 PM-4:30 PM

Phenological traits act much like habitat choice. A plant that emerges early in the season will experience a different environment than one emerging later. For example, early and late plants will be exposed to a different slice of the seasonally shifting climate, and to pollinator and herbivore communities differing in diversity and abundance. Beyond these differences in the general environment, early and late germinants will also experience different social environments. During growth and development, the early germinants can have a size advantage by virtue of their head-start. Later, they will exchange pollen with different sets of mates. Thus, a small difference in start date can have cascading effects throughout the growing season.

We used a phenotypic manipulation experiment with Brassica rapa to explore the cascading fitness effects a gene that accelerates germination. The 'gene' was simulated simply by planting vernalized seeds in two cohorts, one week apart. We planted at two densities, and three 'gene frequencies'— 0.0, 0.5 and 1.0. Growth, flowering time and seed production were recorded. Differences between the two pure treatments (i.e., frequencies 0.0 and 1.0) revealed effects of the general environment on fitness, while the contrast of the mixed treatment to the combined pure treatments reflected effects of a heterogeneous social environment.

General environment lent a small advantage to early germination. The social environment, in contrast, conferred a ~100-fold fitness benefit to the early germinants through their success in asymmetric competition. Competition also led to a 50% increase in the time for late germinants to reach flowering.

In heterogeneous social environments selection clearly favored the evolution of early germination. However, the potential for natural selection on later expressed traits was diminished. The increased variance in fecundity in the high-density, mixed treatment reduced effective populations size (Ne/N = 0.32), making loci contributing to later expressed traits prone to drift. This effect was also manifest in selection on flowering time. The environmental variance caused by competitive suppression increased the intensity of phenotypic selection, but it also acts to reduce heritability. Calculations show that in this environment the potential response to selection by flowering time could be adequately described by considering the early germinants only. In other words, the contribution of the late germinants was irrelevant to potential selection response.

Analysis of a multi-gene phylogeny: Discriminating between alternative hypotheses and phylogenetic noise

Lauren Eserman, Richard Miller

4D_305A-Phylogenetic Methods
Tuesday, June 24, 2014 3:15 PM-3:30 PM

An important goal in evolution is to construct phylogenies to represent the relationships among species. DNA sequence data provides an important source of information for phylogenetic reconstruction. There is substantial interest in estimating species relationships using results from many gene regions. However, in some cases there can be a high degree of discordance between gene trees. We are left with the important question of whether differences among gene trees represent true alternative hypotheses of species relationships or are simply phylogenetic noise. We propose a heuristic method to evaluate gene regions for their reliability as phylogenetic data using benchmarks for particular clades representing established relationships. This method was motivated in part by the fact that datasets of DNA sequences for most groups of organisms do not contain all loci for all species. However, each gene tree contains some level of phylogenetic information. Therefore, by using well-established clades as benchmarks, we can use results from each gene tree to develop a meta-tree to represent our best estimate of species relationships. We apply this method to a systematic study of morning glories (members of the tribe Ipomoeeae) based on the results from 29 gene regions. Furthermore, we present alternative hypotheses for species relationships, highlighting areas within the phylogeny that will require additional information to further examine these alternatives topologies.

Towards inferring the history of life in the presence of lateral gene transfers

Bastien Boussau, Gergely Szöllősi, Eric Tannier, Vincent Daubin

4D_305A-Phylogenetic Methods
Tuesday, June 24, 2014 3:30 PM-3:45 PM

Lateral gene transfers have been found to affect all gene families, especially in unicellular organisms. Together with population-level processes and events of gene duplications and losses they introduce conflict between gene phylogenies and species phylogeny. In addition, scarcity of information in gene sequences, along with model inadequacy, make confidently reconstructing accurate gene trees impossible. As a result, the species phylogeny becomes extremely difficult to identify with current reconstruction methods that assume that all sequences have evolved along the same tree. In this talk, I will present a new method developed in Lyon that relaxes the assumption that all sequences have evolved along a single tree. Instead, this method explicitly models events of gene transfer, duplication, and loss, and allows each gene family to follow its own unique evolutionary trajectory. Importantly, it does not assume that gene trees are known without error, but considers an entire tree distribution per gene family to account for all the phylogenetic uncertainty present in gene alignments. Computation of the likelihood is costly but can be achieved in parallel on clusters of computers, enabling us to conduct statistical inference for dozens of species at a time. We develop a new MCMC algorithm combining tempering and biased moves to infer a species phylogeny in which nodes are ordered, together with rates of gene transfer, duplication and loss. In addition we use gene family-specific rates to identify gene families frequently or rarely transferred, much like the Gamma distribution is used to identify slow or fast-evolving sites of a gene. We demonstrate our method on simulations as well as on the billion year-old Cyanobacteria clade, and present our ongoing work addressing the history of life from whole genome data.

Nextgen data and phylogenetics-- can we ignore incomplete lineage sorting and gene tree/species tree conflict in phylogenetics?

David Althoff, David Rivers, Clive Darwell

4D_305A-Phylogenetic Methods
Tuesday, June 24, 2014 3:45 PM-4:00 PM

One of the major areas of research in phylogenetics is whether and how to combine data from multiple markers when estimating phylogenies. Using multiple markers introduces the possibility of conflict among markers due to incomplete lineage sorting and gene trees that do not reflect the 'true' species tree. These issues are extremely relevant given the large number of markers generated by NextGen sequencing technologies. Using over 6000 genes from closely related Drosophila species, we simulated NextGen datasets based on 100 bp and 500 bp reads from these genes. We demonstrate that concatenation of sequences from all loci produces a highly supported species tree even though roughly 40% of the genes produce alternate topologies when analyzed singly. Furthermore, the results are robust to changes in sequence length, demonstrating that improved sequencing technologies yielding more data will not change the outcome. We suggest that the sheer volume of data from markers scattered across the genome will produce highly supported species tree even when the phylogenetic histories of some of those markers are inconsistent with the species trees.

Approaches to reducing spurious signal in phylogenomic datasets

Randee Young, Vinson Doyle, Gavin Naylor, Jeremy Brown

4D_305A-Phylogenetic Methods
Tuesday, June 24, 2014 4:00 PM-4:15 PM

Topological heterogeneity among gene trees is widely observed in phylogenomic analyses and some of this variation is likely caused by systematic error in gene tree estimation. Systematic error can be mediated by improving models of sequence evolution to account for the complex evolutionary processes that shape genes across genomes and lineages. Alternatively, we can identify those genes whose evolution conforms to existing models and are thus most likely to produce reliable phylogenetic estimates. However, the best method for identifying such genes is not well established. Here, we ask if we can identify reliable gene tree estimates by filtering genes according to their clock-likeness or posterior predictive effect size (an inference-based measure of model violation). We compare these results to the commonly used approach of filtering based on overall rate. We assess the utility of these filtering approaches using two different metrics. First, we looked for greater than expected topological similarity among gene trees in filtered sets. Second, we compared gene-tree topologies to accepted reference topologies. Our results suggest that filtering genes based on their clock-likeness and posterior predictive effect size can yield a collection of genes with more reliable phylogenetic signal.

Phylogeographic model selection using approximated likelihoods

Nathan Jackson, Ariadna García, Bryan Carstens, Brian O'Meara

4D_305A-Phylogenetic Methods
Tuesday, June 24, 2014 4:15 PM-4:30 PM

Phylogeography aims to elucidate the evolutionary processes that underlie the spatial distribution of genetic variation in closely related groups. One way to achieve this is by estimating the values of parameters thought to have contributed to observed phylogeographic patterns by fitting genetic data to a specific coalescent model in either a likelihood or Bayesian framework. If the appropriate model is uncertain, another option is to compare the relative probability of two or more such models, and estimate parameters from the most probable model (for example, using ABC). However, a remaining question is how can we evaluate the quality of our set of considered models relative to the set of possible models that are not under consideration? Phrapl is a novel method for phylogeographic model selection that evaluates the fit of sampled gene trees to all possible models using approximated likelihoods. These models consist of the different combinations of parameters that define one or more coalescent events, migration rates, and effective population sizes. Here, we evaluate the performance of phrapl using both simulated and empirical datasets. Results from these analyses suggest that phrapl can be a powerful tool for phylogeographic model selection, helping to ensure that we estimate parameters of interest while fitting the data to the most probable model.

Genomic signatures of life history divergence during speciation: diapause as a complex target of selection in Rhagoletis fruit flies.

Gregory Ragland, Thomas Powell, Glen Hood, Peter Meyers, Meredith Doellman, Daniel Hahn

4D_305B-Divergence
Tuesday, June 24, 2014 3:15 PM-3:30 PM

Ecological speciation in phytophygous insects often involves shifts to new hosts with different seasonal availability. These shifts cause strong divergent selection on life history traits involved in seasonal synchrony that may ecologically isolate races that infest different hosts. We have identified genomic variation associated with a recent shift of Rhagoletis pomonella (Diptera: Tephritidae) from native haw to introduced apple that is consistent with strong selection on life history variation. Here, using genome-wide snp genotyping and resprirometric analysis of metabolic depression, we identify specific targets of selection on diapause, the central life history trait that mediates seasonal synchrony. We discuss how patterns of linkage disequilibrium and correlations among diapause life history traits influence the patterns of divergence at the genomic level.

Dissecting the physiological basis of allochronic isolation in Rhagoletis

Thomas Powell, Qinwen Xia, Jeffrey Feder, Greg Ragland, Daniel Hahn

4D_305B-Divergence
Tuesday, June 24, 2014 3:30 PM-3:45 PM

Much of the research on ecological speciation has focused on identifying traits underlying reproductive isolation and examining the resulting patterns of differentiation in the genome. However, drawing concrete connections between ecologically divergent phenotypes and genomic variation has proven difficult, particularly in the case of complex, polygenic traits. Closing the gap between ecological and genomic data may be accomplished through a physiologically-informed framework to identify the intermediate phenotypes involved in the manifestation of the trait under selection. Here we report results from a study aimed at examining the physiological basis for divergent life history timing in Rhagoletis flies. The two host races in the classic Rhagoletis pomonella system show strong differences in their adult eclosion phenology corresponding to phenological differences of their two host plants, downy hawthorn and domestic apple. This is thought to be be a particularly important component of reproductive isolation in Rhagoletis; association studies and within-generation selection experiments have strongly implicated life history timing in the genome-wide patterns of divergence observed in this system. We compared the post-winter metabolic trajectories of hawthorn and apple pupae to determine whether the allochronic isolation between the races is driven by the regulation of diapause termination or post-diapause development rates. We found that apple flies typically terminate diapause within the first few weeks of warm temperatures, while hawthorn flies stay in a state of metabolic suppression long into spring. Our results show that the precise stage of developmental divergence between the two races occurs shortly after the cessation of winter, allowing for finely focused studies comparing the endocrine, transcriptomic, proteomic, and metabolomics profiles of the two races during this critical phase.

Genomic atolls of divergence in Hypoplectrus coral reef fishes

Oscar Puebla, Owen McMillan, Eldredge Bermingham

4D_305B-Divergence
Tuesday, June 24, 2014 3:45 PM-4:00 PM

Because the vast majority of species are well diverged across most of their genome, relatively little is known about the genomic bases of speciation during the early stages of divergence. ‘Recent’ or ‘rapid’ evolutionary radiations provide rare opportunities to address this fundamental question, because species within such radiations may be ecomorphologically distinct and reproductively isolated yet minimally diverged from a genomic perspective. Here, we take advantage of such a situation in the hamlets (Hypoplectrus spp, Serranidae), brightly colored reef fishes from the Tropical Western Atlantic. Transect surveys and spawning observations in Belize, Honduras and Panama confirm that sympatric barred (H. puella), black (H. nigricans) and butter (H. unicolor) hamlets are phenotypically distinct and reproductively isolated from a behavioral perspective. Yet close to 100,000 restriction-site associated SNPs genotyped in 126 samples from the same populations indicate that these species are extremely similar across most of their genome, with i. a genome-wide Fst estimate between species of 0.0038, ii. per-locus Fst estimates of 0 at 57% of the SNPs, and iii. a consistent genetic structure between sympatric species in only ~20% of the SNPs. A very small proportion of SNPs (0.04% on average) are identified as outliers between sympatric species, and remarkably a single one as a repeated outlier in different populations.

Divergent phenotypes despite (mostly) homogeneous genomes: insights from a recent avian radiation

Leonardo Campagna, Luís Fábio Silveira, Irby Lovette

4D_305B-Divergence
Tuesday, June 24, 2014 4:00 PM-4:15 PM

In diverging species, reproductive isolation may initially be achieved at key loci involved in generating speciation phenotypes, with differentiation extending throughout the genome only with substantial time. Recent radiations, such as that of seedeaters in the avian genus Sporophila, provide an opportunity to explore the genetics of the early stages of speciation. These eight species have extremely low neutral genetic differentiation and lack of species level monophyly, which we interpret as the consequence of recent common ancestry and ongoing hybridization and introgression. These species are predominantly sympatric and differ mainly in adult male vocalizations and coloration patterns, suggesting an important role for sexual selection in driving their differentiation. We used a reduced representation genomic approach (restriction site-associated DNA tag sequencing) to sample and compare single nucleotide polymorphisms (SNPs) from their genomes. We assess levels of divergence across ≈75k unlinked markers using tree based methods, summary statistics and Bayesian assignment tests. Consistent with previous findings, the species show low overall genetic divergence, with FST generally ST outliers and showed signals of divergent selection. Some such SNPs were outliers consistently across independent contrasts involving different species pairs. Highly diverged loci were mapped onto the Zebra Finch genome to obtain a putative chromosomal location and function. Our findings suggest that the genomes of these phenotypically diverse incipient species are mosaics of evolutionary histories, with different loci exhibiting varying degrees of divergence.

Repeatability of genomic divergence during non-ecological speciation

Ricardo Pereira, Felipe Barreto, Miguel Carneiro, Tessa Pierce, Ron Burton

4D_305B-Divergence
Tuesday, June 24, 2014 4:15 PM-4:30 PM

The repeated evolution of traits in organisms facing similar selective constraints is considered to be fundamental evidence for the role of natural selection on the formation of new species. Repeated patterns of genomic divergence have been well described in taxa undergoing ecological divergence, where extrinsic or “environmentally-dependent” selection often targets the same genomic regions. Theoretically, the same pattern can arise by means of intrinsic selection favoring intragenomic co-evolution during non-ecological divergence, but empirical demonstrations of this process are scarce. We test this hypothesis by examining allopatric population of the marine copepod Tigriopus californicus, between which hybrid breakdown has evolved repeatedly, likely as a result of co-evolving gene complexes. Analyses of transcriptome-wide patterns of divergence and polymorphism show that low effective population sizes cause an exponential sorting of genetic variability during allopatric divergence, leading to a genome-wide fixation of alternative alleles in independent populations. Five inter-population comparisons at three different stages of divergence show that non-synonymous mutations tend to accumulate in hotspot genes, suggesting that these could cause constant selection over functional interacting proteins during species formation. Likewise, there is a significant overlap in the proteins with stronger signatures of positive selection, suggesting that intrinsic selection often targets continuously the same loci. Together, our results suggest that, in the absence of extrinsic selection, intragenomic co-evolution can result in repeatable and predictable patterns of genomic divergence.

Sexual reproduction: (epi)mutagenesis and selective bottlenecks engender pre-selected variation

Kurt Heininger

4D_306A-Reproductive Strategies
Tuesday, June 24, 2014 3:15 PM-3:30 PM

The question as to why sexual reproduction is so ubiquitous is still unanswered in evolutionary biology. In a systems biology approach, my recent comprehensive work with 8,700 references (Heininger K. 2013. The mutagenesis-selection-cascade theory of sexual reproduction. WebmedCentral REPRODUCTION 4: WMC004367) elaborated the ecological and molecular biological processes that render sexual reproduction the predominant mode of reproduction in multicellular organisms. Environments never remain static. They continuously undergo changes that alter the fitness landscapes, displacing populations towards suboptimal fitness regions. Stressed microorganisms resort to a bet-hedging strategy, the evolutionary risk-spreading response to uncertainty, gambling with their genome. However, since mutations are rather deleterious than beneficial, mutagenesis only pays when the mutators have large population sizes.

What evolved as reactive process to environmental challenge, was accommodated as the proactive evolutionary tool of sexual reproduction. A multitude of both direct and indirect evidences reveal the metabolic/oxidative stress, particularly in males (explaining e.g. male-biased mutation rates, lower-temperature comfort zone of male fishes or mammalian testicular extra-abdominal descent), under which higher taxa generate the genetic and epigenetic variation of gametes. The vast excess of mutant gametes is subjected to a cascade with various selective bottlenecks generating pre-selected (epi)genetic variation. Metabolic/oxidative stress is also the effector of germ cell/gamete quality control through cell competition. These selection principles are increasing mutational and environmental robustness and adaptation to life in general, rather than to any particular environment. Traditional concepts imply the action of stochastic bottlenecks during sexual reproduction. Mutagenic gamete overproduction (e.g. during human lifetime ca. 7 million female germ cells and 2 trillion mature sperm) and stochastic gamete bottlenecks, however, should have put sexually reproducing organisms at a substantial disadvantage, inevitably resulting in mutational meltdown and extinction. Along the phylogenetic axis, the oxidative stress during gametogenesis and the population size of gametes that is subjected to sexual selection cascades were increased and the population size of offspring that is exposed to natural selection was reduced.

In resource-limited habitats (the vast majority of habitats), offspring quantity-quality trade-offs are observed in sexually reproducing plants and animals and the theoretical twofold cost of sexual reproduction has no evolutionary meaning. In addition, the non-linear, inverted “U”-shaped sex-stress relationship and the superior colonizing ability of asexuals explain the ecological distribution of sex/asex. Since sexual reproduction is so pervasive in nature, deciphering its underlying mechanisms provides, as a corollary, insights into a variety of evolutionary conundrums and controversies.

The Effect of Parasites on the Ability of Self-Fertilization to Invade Outcrossing Host Populations

Samuel Slowinski, Levi Morran, Raymond Parrish, Eric Cui, Curt Lively, Patrick Phillips

4D_306A-Reproductive Strategies
Tuesday, June 24, 2014 3:30 PM-3:45 PM

The ubiquity of biparental reproduction in nature poses an important problem in evolutionary biology. A two-fold cost of biparental reproduction, in species that maintain separate sexes, results from the inability of males to directly produce their own offspring. Given this fitness cost, populations that reproduce biparentally should be susceptible to invasion by mutants that reproduce uniparentally. However, because biparental reproduction is so often maintained in natural populations, it must be associated with substantial fitness benefits that offset the costs. The Red Queen hypothesis (RQH) predicts that coevolutionary interactions between hosts and parasites can generate persistent selection favoring recombination and biparental reproduction in host populations, thus preventing invasion of uniparental reproduction. We tested the prediction that coevolutionary interactions with parasites can prevent self-fertilization (uniparental reproduction) from invading obligately outcrossing (biparentally reproducing) host populations. We introduced Caenorhabditis elegans hermaphrodites, carrying a dominant wild-type allele permitting both outcrossing and self-fertilization, into C. elegans populations harboring a recessive mutant allele, fog-2(q71), conferring obligate outcrossing. Hermaphrodites carrying the wild-type allele were derived from the obligately outcrossing populations, simulating de novo mutation within the population. Replicate C. elegans host populations were allowed to evolve under three parasite-treatment regimes. In the control treatment (1) hosts were exposed to avirulent heat-killed Serratia marcescens bacteria. In the fixed-parasite genotype treatment (2) hosts were exposed to the same isogenic stock population of the highly virulent S. marcescens parasite every generation. In the co-passaged parasite treatment (3) C. elegans hosts were exposed every generation to potentially coevolving S. marcescens from the same population. Male frequency was measured over 33 host generations, and used to estimate the frequency of self-fertilization in host populations. We found that self-fertilization rapidly invaded host populations evolving in the control environment. Self-fertilization remained rare initially, and then rapidly invaded host populations evolving in the fixed-parasite treatment. However, self-fertilization rates remained low throughout the entire experiment in the co-passaged parasite treatment host populations. Hence, our results support the Red Queen hypothesis, and suggest that coevolutionary interactions with virulent parasites can prevent self-fertilization from invading obligately outcrossing host populations.

Empirical evidence for a continuum between semelparity and iteroparity

P. William Hughes, Andrew Simons

4D_306A-Reproductive Strategies
Tuesday, June 24, 2014 3:45 PM-4:00 PM

Semelparity and iteroparity are considered to be distinct life-history strategies, but life-history theorists (e.g. Harper 1977, Roff 1992) have suggested that “pure” semelparity and iteroparity are endpoints of a continuum of modes of parity. This hypothesis predicts predictable variation in reproductive phenotypes within the “big bang” of semelparous reproduction, just as there exists variation between clutches of offspring in iteroparous organisms.

Empirical support for the continuity hypothesis is sparse, particularly in semelparous organisms. Here, we report the results of three tests of the continuity hypothesis in the classically semelparous herb Lobelia inflata (Campanulaceae). First, we test the ability of L. inflata to exhibit variation in reproductive phenology and offspring traits in response to a manipulation of the timing of the initiation of reproduction. Second, we report observed differences in fruit development timing and offspring size among fruits produced at different times within the semelparous episode. Finally, we report the results of a lab study that explores the conditions under which L. inflata is capable of eliciting a second bout of reproduction.

Life cycle evolution and wnt signaling in the Hydractiniidae (Cnidaria: Hydrozoa)

Steven Sanders, Paulyn Cartwright

4D_306A-Reproductive Strategies
Tuesday, June 24, 2014 4:00 PM-4:15 PM

Many members of the cnidarian group Hydrozoa display a complex life cycle, alternating between a benthic asexual hydroid stage and a sexual pelagic medusa stage. However, most hydrozoans lack a free-swimming medusa and instead reach sexual maturity with a gonophore that remains attached to the polyp. These sexually mature, yet under-developed gonophores have been traditionally split into two morphologically distinct categories that mirror different stages of arrested medusae development: (1) sporosacs are sexually mature gonophores that lack any trace of medusae characters, and (2) medusoids are gonophores that possess some medusae-like characters, but unlike medusae, medusoids cannot feed and often remain attached to the polyp. Previous phylogenetic studies have recovered the free-living medusa as ancestral for Hydrozoa, with medusae reduction to medusoids and sporosacs occurring multiple times in hydrozoan evolution. Wnt pathway genes appear to play an important role in axial patterning in hydrozoans and we hypothesize that these genes may be involved in the evolution of medusae reduction. Here we report the comparative gene expression of Wnt pathway components in hydractiniid medusae and sporosac bearing representatives (Podocoryna carnea and Hydractinia symbiolongicarpus, respectively). These data suggest that simple changes in the regulation of the Wnt pathway may be involved in the loss of a free-swimming medusa in hydrozoan life cycle evolution.

The evolution of semelparity and egg size

Holly Kindsvater

4D_306A-Reproductive Strategies
Tuesday, June 24, 2014 4:15 PM-4:30 PM

Salmonids have evolved two contrasting life-cycles, semelparity (reproducing once) and iteroparity (reproducting multiple times). Egg size diverges dramatically among salmon species, but there are few comprehensive explanations for why. To address this question, I use a comparative dataset on variation in egg size within and across salmonid species to show that egg size varies with latitude and with parity. I then use a matrix model to show how costs of reproductive investment to maternal survival could explain both the evolution of delayed semelparity and larger eggs. T his result suggests that female investment tactics could explain the striking diversity in life-histories across salmonids.

Non-equilibrium dynamics lead to long-term persistence of ancestral floral forms in modern angiosperms

Brian O'Meara, Stacey Smith, W Scott Armbruster, Lawrence Harder, Christopher Hardy, Lena Hileman, Larry Hufford, Amy Litt, Susana Magallon, Stephen Smith, Peter Stevens, Charlie Fenster, Pamela Diggle

4D_306B-Evolutionary Innovations
Tuesday, June 24, 2014 3:15 PM-3:30 PM

Why are some traits exceptionally common across the tree of life, whereas others are vanishingly rare? The distribution of trait diversity is shaped by microevolutionary processes that govern the origin and fixation of new phenotypes within species, macroevolutionary processes of speciation and extinction, as well as stochastic forces and non-equilibrium dynamics. Here we develop a novel approach to address the concerted effects of microevolutionary innovation and differential diversification on the evolutionary history of angiosperms, a clade known for its marked disparity in numbers of taxa per clade and representation of trait combinations across clades. Our analysis reveals that a synergy of three floral character states (corolla present, bilateral symmetry, reduced stamen number) acts as a key innovation in angiosperms, leading to a doubling of diversification rates for lineages in which this combination evolves. The overall low rates at which these characters arise, however, has kept even lineages with the key three-character combination in the minority — for now. Stochastic simulations of angiosperm evolution suggest that angiosperms will remain far from the predicted equilibrium distribution of character states well into the future, as well. Such non-equilibrium dynamics may be common in clades where major innovations evolve relatively rarely, thus allowing lineages with ancestral forms to persist and even outnumber those with diversity-enhancing states for tens of millions of years.

Is the ectomycorrhizal lifestyle an evolutionary key innovation? Trophic evolution in the Tricholomatoid clade (Agaricales)

Marisol Sanchez-Garcia, Brandon Matheny

4D_306B-Evolutionary Innovations
Tuesday, June 24, 2014 3:30 PM-3:45 PM

The Tricholomatoid clade is one of several major clades of Agaricales, the largest order of mushroom-forming fungi. Members of this clade exhibit variation in nutritional modes, including mycoparasites, saprotrophs, termite-associates, and ectomycorrhizal (ECM) symbionts. The Tricholomatoid clade represents an ideal group for the study of evolution of the ECM habit because it contains a variation of trophic modes and several independent origins of the ECM association. Here, we evaluate whether the ECM mode is a key innovation that promoted diversification within the Tricholomatoid clade. Nutritional modes are inferred from carbon and nitrogen stable isotope signatures. We will reconstruct a time-calibrated phylogenetic tree and identify any diversification rate shifts. In order to detect the effect of switches from saprotrophic to ECM mode on diversification rates and to evaluate whether these switches represent an evolutionary key innovation, we will implement the binary state speciation and extinction model (BiSSE). We will present evidence to accept or reject the hypothesis that ECM mode represents a key innovation that promoted diversification in the Tricholomatoid clade.

The evolutionary genetics of shape variation in penis bones

Nick Schultz, Matt Dean, Jesse Ingels, Rob Williams, Lu Lu

4D_306B-Evolutionary Innovations
Tuesday, June 24, 2014 3:45 PM-4:00 PM
The evolutionary genetics of shape variation in penis bones

Nicholas Schultz, Jesse Ingels, Lu Lu, Rob Williams, and Matthew D. Dean

The baculum, a bone that occurs in the penis of many mammals, is one of the fastest evolving morphological features known. Aside from its utility as a taxonomic marker, our understanding of its form and function has suffered from a lack of adequate methodology for studying landmark-free shapes in three dimensions. Here we develop novel morphometric methods to study baculum variation across the "BxD" recombinant inbred panel of mice. We find that baculum shape variation has a genetic basis, with heritability>0.4. A single quantitative trait locus was mapped to chromosome 16, and we discuss possible candidate genes in the region. This study is a significant step forwards towards understanding the evolution of male genitalia.

Phylogeny and evolution of pharmacophagy in tiger moths (Insecta: Lepidoptera: Erebidae)

Jennifer Zaspel, Susan Weller, Taylor Wardwell, Reza Zahiri, Niklas Wahlberg

4D_306B-Evolutionary Innovations
Tuesday, June 24, 2014 4:00 PM-4:15 PM

Tiger moths are comprised of at least 11,000 described species worldwide. They are well known for their bright coloration, mimicry and unique defensive strategies. Moths in this lineage are known to feed on toxic plants as larvae in order to gain chemical protection against vertebrate predators (a.k.a. pharmacophagy). Some species sequester these toxic plant compounds and use them to defend themselves during the adult stage and also attract and protect their mates. Other tiger moth species engage in sound production to deter predators and signal mates. Despite the important role of tiger moths in chemical ecology and behavioral studies, few molecular investigations of arctiine phylogeny exist. Previous molecular studies support the monophyly of Arctiini, Lithosiini, and Syntomini but do not support the limits of all subtribes within Arctiinae. To test the monophyly of tiger moth subtribes and address the evolution of tiger moth life history traits, a phylogenetic hypothesis of Arctiinae was generated based on DNA sequence data from 9 genes for 95 taxa; a total of 6984 bp was obtained for most species. We examined origins of pyrrolizidine alkaloid (PA) associations and the evolution of PA pharmacophagy in adults. This study also investigated whether specialized proboscis structures are associated with adult pharmacophagy. Our results corroborate earlier studies on the evolution of adult pharmacophagous behaviors, suggesting that this behavior arose multiple times and is concentrated in derived clades within the subfamily. Our results also suggest PA specialization arose early in the phylogeny of the subfamily and that that facultative larval PA acquisition is the derived condition.

An ecological diversification history of marine animals

Matthew Knope, Noel Heim, Jonathan Payne

4D_306B-Evolutionary Innovations
Tuesday, June 24, 2014 4:15 PM-4:30 PM

The ecological diversity of marine animals is widely assumed to be greater today than at any point in Earth's history. However, unlike taxonomic diversity, the ecological diversification history of marine animals has not previously been quantified in a single systematic framework across time. To address this knowledge gap, we present new ecological data on 22,000 extinct and extant genera of bilaterian marine animals, ~85% of such animals in the fossil record. We based ecological assignments on the first principles of functional morphology for three fundamental niche axes (habitat tiering in relation to the seafloor, feeding mode, and motility level) that combine to describe the "ecospace" utilization of each taxon. These assignments indicate at least a six-fold increase in ecospace utilization between the Cambrian (542 - 485 Ma) and the present day. Moreover, ecospace-genus diversity relationships were dissimilar during the Cambrian, the remainder of the Paleozoic (485 - 252 Ma), the Mesozoic (252 - 66 Ma), and the Cenozoic (66 Ma - Recent) with progressively increased ecospace utilization for any equivalent number of genera from one interval to the next. We also find that the oceans have not only become increasingly ecologically complex across time, but that high energy demanding modes of life (e.g., fully motile predators and grazers) have become increasingly common. Further, whereas mass extinctions permanently eliminated many taxa, they eliminated a very small proportion of ecospace. In contrast, many new ecospaces first appear during recovery intervals in the first ten million years following the Permo-Triassic and Cretacecous-Paleogene mass extinctions. Mass extinctions appear not only to have enabled adaptive radiation of existing types replacing previously dominant forms, but also to have opened fundamentally new opportunities in restructured ecosystems.

A critical synthesis of indirect genetic effects in adaptive evolution

Michael Wade

4D_BalC-SSE Symposium: Seeing the forest for the trees: the contributions of synthesis to evolutionary science
Tuesday, June 24, 2014 3:15 PM-3:35 PM

I review some of the key features of our understanding of adaptive evolution that change as a result of indirect genetic effects. These features include heritability and increased role of population genetic structure in evolution. I contrast adaptation to abiotic environments when there is genotype-by-environment interaction with adaptation to biotic environments. We find that there is an opportunity for run-away coevolution between genes for social environments and genes adapting to the social environment.

Evolution of a biome

Erika Edwards

4D_BalC-SSE Symposium: Seeing the forest for the trees: the contributions of synthesis to evolutionary science
Tuesday, June 24, 2014 3:35 PM-3:55 PM

Grasslands cover large regions of Earth, but are relatively young, with many grassy biomes becoming prominent only during the late Miocene, 8-3 million years ago. Grassland ecosystems are unusual in that they are mainly defined by the dominance of a single lineage- grasses- and the grassy biome may be the most salient illustration of the intimate connection between the history of a landscape and the history of the lineages that inhabit and shape it. The rapid rise and spread of C4 grasslands in particular has piqued the interest of workers in many disciplines- geologists, ecologists, evolutionary biologists, and physiologists- and each of these fields have developed important bodies of knowledge that, when integrated, have the potential to tell our most ‘complete’ evolutionary history of a biome. NESCent has supported this integration throughout the last five years, and I’ll report on what we have learned, particularly from our efforts to disentangle the evolutionary origins of C4 photosynthesis from the diversification of C4 lineages, and ultimately from the origins of a relatively select set of grass species that actually dominate the world’s grassy biomes.

Contemporary Human Evolution and Infusing Evolutionary Thinking into Medical Education

Stephen Stearns

4D_BalC-SSE Symposium: Seeing the forest for the trees: the contributions of synthesis to evolutionary science
Tuesday, June 24, 2014 3:55 PM-4:15 PM

A NESCent catalysis meeting on evolutionary medicine spawned two NESCent working groups and a 2009 Sackler Symposium at the National Academy, "Making Evolution a Basic Science for Medicine". The first working group focused on measuring evolutionary change in contemporary human populations using cohort data; the second focused on developing evolutionary materials for medical educators. Here I report briefly on the results and impact of both projects. Papers resulting from the project on contemporary human evolution focused on data collected for the Framingham Heart Study. They demonstrated that natural selection was operating on this population to decrease total cholesterol, decrease blood pressure, decrease height, increase weight, decrease age at first birth, and increase age at menopause in women. Selection on men was constraining responses in women, and selection in women was constraining responses in men. There were phenotypic survival costs of reproduction in women whose genetic component could be detected with both the animal model of quantitative genetics and through a GWAS that identified candidate genes. The project on infusing evolutionary thinking into medical education helped to spark the creation of a new open-access journal, Evolution, Medicine, and Public Health, on whose editorial board several of the participants now sit; two papers that lay out strategies for bringing evolutioinary thought into medical education; a new category of publication, Clinical Briefs, that provides medical students and physicians with capsule summaries of key evolutionary insights; and key input into a set of 45 lectures on evolutionary medicine now available for free online. NESCent has been making a substantial and continuing contribution to the growth of evolutionary thinking in the medical sciences.

Variation of the plant-mycorrhizal interaction in a gynodioecious plant species

Katharine Putney, Shu-Mei Chang

Saturday, June 21, 2014 -Poster #1

The symbiosis between plants and their root-associated arbuscular mycorrhizal fungi (AMF) can serve as a testable system to understand how biotic interactions can affect the evolution of plant populations. It has been shown that the plant benefit from this mutualism may be determined by the AMF community available in the soil, therefore the assembly of AMF communities on a plant's roots is likely to affect a plant's individual fitness and thus shape the pattern of selection in plant populations. For gynodioecious plant species (both female and hermaphroditic plants in some populations), the establishment and success of females in some populations hold the key to our understanding of the evolution of separate sexes, considering gynodioecy is the most likely intermediate step between hermaphroditism and dioecy (separate male and female individuals). One common pattern found in gynodioecious species is that females tend to become established in the "harsher" portion of their distribution. Sex Differential Plasticity hypothesis suggests that females are more likely to establish in stressful environments that would induce hermaphrodites to allocate more resources to their male function, allowing females to exceed the threshold relative seed fitness they require to invade a population. We are exploring the idea of treating the available AMF partners in a site as the environmental conditions in terms of plant benefit. If AMF communities are indeed important factors for female establishment, we would predict that females may establish in populations with lower quality AMF partners. Specifically, we asked (1) How do the root-associated AMF communities of Geranium maculatum vary across the range of this species? and (2) to what extent does AMF community composition and/or species richness predict the presence of females in a population? We conducted a survey of the root tissue from both sexually dimorphic and monomorphic populations across the range of G. maculatum. We used a terminal-restriction fragment polymorphism (T-RFLP) database approach to identify AMF species present on roots and compared species composition and richness between populations with or without females present. We found that females were found in populations that associated with communities of lower overall AMF species richness than those of all-hermaphrodite populations. In addition, within the dimorphic populations, females associated with a more rich AMF community. These findings show that biotic factors could play a role in sexual dimorphism within this species.

Experimental evolution of parasitoid performance on two aphid hosts

Emily Mohl, George Heimpel

Saturday, June 21, 2014 -Poster #2

Host-parasite interactions can generate strong reciprocal selection, and many insect parasitoids specialize on a small number of hosts. However, some parasitoids have relatively broad host ranges but appear to have variable performance across hosts. We used a quasi-natural selection experiment to investigate factors that may contribute to the evolution of host range in the generalist aphid parasitoid, Lysiphlebus testaceipes. We hypothesized that high gene flow and/or temporal variation in host availability could maintain a broad host range in this species. At the same time, we expected a tradeoff in performance across hosts to constrain the evolution of increased performance on each host. Our results demonstrate significant change in aspects of parasitoid performance over time; however, we do not find evidence consistent with local adaptation between selection lines. Instead, our results are most consistent with parasitoid evolution to rearing conditions.

The utility of target capture and high-throughput sequencing of ultraconserved elements across an avian hybrid zone

Nick Vinciguerra, Brant Faircloth, John McCormack

Saturday, June 21, 2014 -Poster #3

Significant advances in next-generation DNA sequencing technologies now make genome-scale data readily available for comparative studies of non-model taxa. Despite these advances, a bottleneck has been the identification of orthologous loci among distant related taxa spanning different evolutionary timescales. Recent empirical studies suggest ultraconserved DNA elements (UCEs) are informative high-throughput markers for addressing evolutionary questions at deep and shallow timescales. Here, we assess the efficacy of using ultraconserved elements at the population genomics level across an avian hybrid zone. Using target enrichment and high-throughput sequencing of UCEs, we recovered up to 4200 loci across a hybrid cline of Western Scrub-Jays (Aphelocoma californica) lineages that diverged approximately 2 million years ago. Analyses are underway to identify the number of single nucleotide polymorphisms and the extent to which these loci are informative for inferring patterns of divergence and gene flow at a shallow scale across a zone of secondary contact.

Keywords: Population Genomics, next-generation sequencing, hybrid zone, bioinformatics, UCEs

---

Sexual selection on damselfly wing pigmentation in Calopteryx maculata

Oumar Sacko, Idelle Cooper, Tom Getty

Saturday, June 21, 2014 -Poster #4

How selection drives phenotypic variation between sexes as well as between species has been the focus of long-standing debates in evolutionary biology. Wing pigmentation in Jewelwing damselflies (Calopteryx) differs between closely related, sympatric species, presumably to reduce hybridization, but the role of that trait in mate choice within species is unknown. To identify how wing pigmentation and size may be under mate choice within a single species, we compared wing pigmentation and size with mating success in Calopteryx maculata damselflies. While there was no difference in wing traits between mated or unmated females, mated males had significantly longer and more pigmented wings and held territories more successfully. These findings indicate that male wing traits are under sexual selection in this species, perhaps as a visual cue during courtship or beneficial during male territorial defense.

Lekking, intrasexual competition, and predator defense in the parasitoid wasp (Hymenoptera: Braconidae: Euphorinae)

Andy Kulikowski, Delina Dority, Will Robinson, Scott Shaw

Saturday, June 21, 2014 -Poster #5

Ritualized staging grounds called leks are used by sexually competing males of various species. Lekking behavior differs from other forms of aggregate sexual competition in that female choice is absolute and not dictated by resources conferred by males. Lekking has been studied extensively in vertebrates but is less understood in insects, particularly in the parasitoid wasp family Braconidae. Over the course of two field seasons in the cloud forest of Ecuador we observed facultative lekking in the recently described species of braconid wasp Napo townsendi. Both solitary and aggregated males employed a stereotypical display behavior coupled with the wafting of sex pheromone. While female wasps were attracted to and mated with displaying singletons, we also observed females making choices among lekking males. Males also used display behavior during agonistic encounters within leks and for predator defense. In over 600 person-hours of observation not a single successful predation was witnessed despite multiple predatory attempts. Details of displays, leks, female choice, mating and predator defense are described.

Ecological character displacement between the sexes?

Stephen De Lisle, Locke Rowe

Saturday, June 21, 2014 -Poster #6

Theory predicts the evolution of sexual dimorphism in ecologically relevant traits can evolve purely through competition for a shared resource. Although these models of ecological character displacement between the sexes are widely cited, more parsimonious hypotheses exist for the evolution of ecological dimorphisms, and no empirical test to date has excluded these likely alternatives. Using an ongoing series of experiments, we present evidence for competition as a contributing force to the evolution of sexual dimorphisms in a pond breeding salamander (Notophthalmus viridescens). Past work suggests that sexual size and gape dimorphism manifests sex-specific responses to community structure. A second experiment shows significant disruptive selection on size and that the sexes suffer a growth cost with an increase in frequency of the same sex, consistent with predictions of character displacement. Although the shape of selection on size changes with sex ratio in different ways for males and females, as expected, the shape of the female fitness function in male-biased environments is opposite of predictions. This suggests the possibility that responses to mating activity (e.g. a female habitat shift) may interact with the effects of resource competition during the evolution of ecological dimorphisms. An additional experiment and surveys are in progress to further explore this putative case of character displacement between the sexes.

Male mate choice and female receptivity lead to reproductive interference

Savannah Nease, Jennifer Hamel, Christine Miller

Saturday, June 21, 2014 -Poster #7

Mating between species is common, but seldom adaptive. Mate preferences and receptivity to mating attempts may both contribute to such matings, also called reproductive interference. Here, we tested the hypothesis that both male mate preference for female body size and female receptivity contribute to reproductive interference between two secondarily sympatric insect species. In north central Florida, the squash bug Anasa tristis co-occurs with a recently introduced, smaller congener, A. andresii. Smaller male A. andresii are frequently found copulating with larger female A. tristis in the field. We found that male A. andresii direct mating effort toward larger females in simultaneous choice tests including both con- and heterospecific females, that female A. tristis accept some mating attempts by heterospecific males, and that female A. tristis are more promiscuous with conspecifics than are female A. andresii. Our findings show that both male mate choice and female receptivity contribute to mating between these species, and that males prefer larger heterospecific females over conspecific females.

Genetic variation for age at sexual maturity in wild baboons

Emily McLean, Jeanne Altmann, Susan Alberts

Saturday, June 21, 2014 -Poster #8

The timing of sexual maturation can greatly influence variation in individual fitness. In order to understand the evolution of age at sexual maturity in response to ecological and environmental pressures, we must understand the genetic influences on this trait in natural populations. In this study, we combined behavioral ecology with quantitative genetic methods to analyze the genetic (co)variation underlying age at sexual maturity in wild baboons (Papio cynocephalus) in the Amboseli basin, Kenya.

Using statistical methods typically applied by animal breeders (i.e., ‘the animal model’) we measured male age at testicular enlargement and female age at onset of menarche; each of these are standard indicators of the onset of sexual maturity. We found segregating genetic variation for both traits in this population, despite the known fitness advantages of early maturation. We also found that the two traits are not genetically correlated, suggesting a different underlying genetic basis to the timing of male versus female maturation. We report on these analyses as well as our investigation of maternal genetic effects for this trait.

Using a New Zealand Freshwater Snail to Evaluate the Fate of Genes Under Relaxed Selective Constraints

Christopher Rice, Cynthia Toll, Jeffrey Boore, Maurine Neiman, John Logsdon

Saturday, June 21, 2014 -Poster #9

Evolutionary theory predicts that evolution in genes subject to relaxed selection can serve as an important source for new genetic variation and generate valuable insights into the rates and processes of molecular evolution. From these perspectives, characterization of patterns of molecular evolution in genes that have recently experienced a shift from purifying to relaxed selection provide valuable empirical tests of these theoretical expectations. Here, we compare and contrast patterns of molecular evolution in genes used only for sexual reproduction (i.e., meiosis-specific genes) in sexual vs. asexual Potamopyrgus antipodarum, specifically asking whether these genes are subject to relaxed selective constraint following transitions to asexuality. This New Zealand freshwater snail provides a powerful means of addressing hypotheses regarding the fates of meiotic genes in asexuals because closely related and phenotypically similar sexual and asexual P. antipodarum often coexist and compete, enabling direct comparisons between sexuals and asexuals without confounding effects of different evolutionary histories or source population. Asexual lineages of P. antipodarum have been derived on multiple occasions from sexual P. antipodarum, meaning that we can treat each of these lineages as an independent experiment into the evolutionary consequences of the absence of sex. While this project is still ongoing, to date we have generated sequence data from 2 candidate meiotic genes (Msh4 and Msh5) that are involved in Holliday Junction resolution and stabilization from multiple sexual and asexual P. antipodarum lineages. We are using these data to evaluate whether the evolutionary signatures of relaxed purifying selection (e.g., increased rate of accumulation of typically harmful mutational types) and/or neofunctionalization (e.g., molecular evidence for adaptive evolution) in genes used only for sexual reproduction are apparent in asexual P. antipodarum. An absence of evidence for either relaxed selection or neofunctionalization in asexuals points instead to the maintenance of at least some meiosis-specific genes in asexual lineages. We will address these possibilities by expanding the candidate gene inventory and by including asexual lineages that are thought to be of relatively ancient derivation from sexual P. antipodarum.

Crossing fitness-valleys without the help of Mendel

Matthew Osmond, Sarah Otto

Saturday, June 21, 2014 -Poster #10

Interactions between loci/traits lead to rugged fitness "landscapes", where adaptation eventually requires populations to cross "valleys" of low fitness. Previous theory of fitness-valley crossing has focused on symmetrical, Mendelian genetic models. Here we expand the theory of fitness-valley crossing by keeping the vertical transmission probabilities unspecified. This generalization allows insights into valley-crossing scenarios with more complex genetics, such as uniparental inheritance and meiotic drive, and allows us to consider cultural traits under cultural selection. The results clarify the role of transmission bias in adaptation on rugged fitness landscapes: transmission bias greatly alters the ability of populations to cross fitness-valleys.

Environmental constraints on nest-mate recognition molecules in Pogonomyrmex harvester ants

Michael Herrmann, Sara Helms Cahan

Saturday, June 21, 2014 -Poster #11

Cuticular hydrocarbons (CHCs) are important dual-purpose molecules found on insect exoskeletons that serve both desiccation resistance and social communication functions. To satisfy both of these functions, however, insects face a trade-off, as the more complex molecules that are the most informative communication cues decrease the density of the waxy hydrocarbon coating relative to simple straight-chain molecules, causing a reduction in desiccation resistance. This may be especially costly for desert-adapted organisms, leading to a compositional shift toward desiccation resistance at the expense of signaling effectiveness in xeric environments. CHCs are generally produced de novo in the insect, and have a strong genetic component to their production. We investigated the composition and inheritance of CHC profiles in a complex of seed harvester ants in the genus Pogonomyrmex whose range extends across the southwestern U.S., from P. barbatus in more mesic grassland habitats of coastal and central Texas, to P. rugosus, which occurs in more xeric desert environments in Arizona and California. The two species historically hybridized in an ecologically intermediate contact zone in southern New Mexico, resulting in two pairs of relic populations, or lineages, that obligately interbreed to produce F1 hybrid workers. Results show a trend toward a higher proportion of desiccation-resistance alkanes in P. rugosus than in P. barbatus, as predicted by their environment, but an even stronger effect of reproductive caste, with queen CHC profiles significantly more biased toward alkanes than workers. This may reflect the greater diversity of communication functions of CHCs in the worker caste, including nest identity and task role. In addition, discriminate analysis shows that F1 hybrid workers are intermediate between the profiles of interbreeding lineages, indicating a strong additive genetic component to CHC composition; however, workers show more similarities with their maternal lineage, suggesting that queens impart signaling CHCs to their workers in the colony through hydrocarbon exchange.

Sequence, cis-regulatory evolution and expression profile of HSPs in Ants

Andrew Nguyen, Sara Helms Cahan, Nicholas Gotelli

Saturday, June 21, 2014 -Poster #12

The heat shock response (HSR) is an evolutionarily conserved inducible mechanism for limiting damage to macromolecules from heat and other environmental stressors through the production of heat shock proteins (HSPs), molecular chaperones that bind to and refold denatured proteins. The eusocial Hymenoptera (ants, bees and wasps) occur in highly diverse terrestrial environments and engage in active thermoregulatory behavioral strategies, suggesting that temperature has played an important selective role in their evolution; however, little is known about the diversity, molecular evolution or inducibility of HSPs within the social Hymenoptera. We reconstructed the molecular evolutionary history of three classes of HSP (HSP90, HSP70, HSP40) across 12 hymenoptera as well as 5 species from 4 other insect orders to identify gene duplications, losses, and sequence changes resulting from selection. To determine the role of HSPs in the HSR, we bioinformatically analyzed the number and distribution of cis-regulatory heat shock elements (HSEs) in the upstream regulatory region, and characterized gene expression patterns across a range of temperatures in a warm-climate (Pogonomyrmex barbatus) and a cool-climate (Aphaenogaster picea) ant species to test whether variation in thermal niche is associated with shifts in basal and/or inducible HSP expression. We found evidence of multiple duplications, losses, and regulatory shifts in two of the three HSP gene families in the Hymenoptera in comparison with other insect orders. For HSP90, there was a single duplication in Hymenoptera, with a subsequent loss of one paralogue in ants; in HSP70, the typical inducible form characterized in D. melanogaster is absent in the Hymenoptera, which instead has undergone a gene duplication and a shift to inducibility of the cognate form (HSC70). Inducibility of HSPs under experimental heat stress was consistent with patterns of cis-regulatory HSEs. Comparisons between the two ant species suggest that changes in both basal expression and inducibility may contribute to variation in thermal tolerance. Pogonomyrmex barbatus, whose critical thermal maximum is ~5°C higher than A. picea, expressed HSC70-4 h1 at a significantly higher basal level and showed greater induction of this protein, as well as HSP90, under heat stress. In ants, shifts in basal and inducible expression of HSP90 and HSC70-4 h1 may have been important molecular targets in mediating greater thermal tolerance.

Phylogenetic signal in carnivore anatomy, life history, neurology, and ecology: how strong is it and does allometry make a difference?

Heitor Barcellos Ferreira Fernandes

Saturday, June 21, 2014 -Poster #13

Phylogenetic signal (PS; also phylogenetic inertia, phylogenetic constraints, or simply phylogenetic effects) is an important measure for comparative studies, influencing the choice of method for the study of evolutionary covariance among traits, and affecting the capacity to predict values of species with missing data and for reconstructing ancestral traits. PS indicates the extent to which close relative taxa are more similar than more distant ones, being commonly measured with Pagel's lambda (ranging from zero = no PS and thus evolutionary independence of phylogeny; to unity = conformity to the Brownian motion model) and Blomberg and colleagues' K (ranging from zero = no PS, to infinity; unity indicates conformity to Brownian motion, and K>1 suggests phylogenetic conservatism). I tested with a large array of variables (25) whether the pattern of variance in PS (within and among categories of variables) among Carnivores is similar to that recently found among Primates. Secondly, as there is still debate on whether and when allometry should be controlled in comparative studies, I examined the impact of allometric control on PS for variables where significant allometry is found, which has not yet been thoroughly explored in the literature. I collated data for 254 Carnivore species for variables of anatomical, neurological, life-history, ranging-patterns, environmental, dietary, and mechanical categories. I computed lambda and K for each raw variable (log-transformed), and for each variable residualized against log-transformed adult body mass, except for adult body mass itself, body length, and environmental variables (e.g., mean annual precipitation). Lambda was significantly higher than zero for 84% of raw variables and 65% of residuals of body size; and significantly smaller than unity for 80% of raw variables and 88% of residuals of body size. K was significantly higher than zero for 80% of raw variables and 71% of residuals of body size; and significantly smaller than unity for 60% of raw variables and 77% of residuals of body size. The decreasing order of PS strength for the categories of variables was anatomical, life-history, ranging-patterns, mechanical, neurological, dietary, and environmental variables. This order is considerably consistent with that found for Primates, however whereas in the latter only brain volume presented K>1, among Carnivores only neonatal body mass did. I discuss implications to various phylogenetic comparative methods with Carnivores and to the understanding of evolutionary patterns of the various categories of variables in Carnivores, and I discuss the role of allometric controls in estimates of PS.

Rapid evolution of mimicry following local model extinction

Chris Akcali, David Pfennig

Saturday, June 21, 2014 -Poster #14

Instances of Batesian mimicry—in which a harmless prey species (the 'mimic') evolves to resemble a conspicuous, noxious species that predators avoid (the 'model')—are some of nature's most exquisite adaptations. Here, we evaluated whether—and in which direction—Batesian mimicry has evolved in a natural population of mimics following extirpation of their model. We specifically asked if the precision of coral snake mimicry has evolved among kingsnakes from a region where coral snakes recently (around 1960) went locally extinct. We found that these kingsnakes have evolved more precise mimicry; in contrast, we observed no such change in a sympatric non-mimetic species or in conspecifics from a region where coral snakes remain abundant. Presumably, more precise mimicry has continued to evolve after model extirpation because relatively few predator generations have passed, and the fitness costs incurred by predators that mistook a deadly coral snake for a kingsnake were historically much greater than those incurred by predators that mistook a kingsnake for a coral snake. Indeed, these results are consistent with prior theoretical and empirical studies, which revealed that only the most precise mimics are favored as their model becomes increasingly rare. Thus, highly noxious models can generate an 'evolutionary momentum' that drives the further evolution of more precise mimicry—even after models go extinct.

The benefit of being a social butterfly: Communal roosting deters predation

Susan Finkbeiner, Adriana Briscoe, Robert Reed

Saturday, June 21, 2014 -Poster #15
Aposematic passion-vine butterflies from the genus Heliconius form communal roosts on a nightly bases. This behavior has been hypothesize to be beneficial in terms of information sharing and/or anti-predator defense. To better understand the adaptive value of communal roosting, we tested these two hypotheses in field studies. The information-sharing hypothesis was addressed by examining following behavior of butterflies departing from natural roosts. We found no evidence of roost mates following one another to resources, thus providing no support for this hypothesis. The anti-predator defense hypothesis was tested using avian-indiscriminable Heliconius erato models placed singly and in aggregations at field sites. A significantly higher number of predation attempts were observed on solitary models versus aggregations of models. This relationship between aggregation size and attack rate suggests that communally roosting butterflies enjoy the benefits of both overall decreased attack frequency as well as a prey dilution effect. Communal roosts probably deter predators through collective aposematism in which aggregations of conspicuous, unpalatable prey communicate a more efffective repel signal to predators. Based on our results, we propose that predation by birds is a key selective pressure maintaining Heliconius communal roosting behavior.

Patterns and genetic mechanisms of nonfunctional trait loss

Samuel Perez, Jeffrey Conner, Doug Schemske

Saturday, June 21, 2014 -Poster #16
Keywords: phenotypic traits, trait loss, Arabidopsis thaliana, altitudinal cline, genetic mechanisms

A common theme in phenotypic evolution is the reduction or loss of a structure. One of the major problems in studying mechanisms of trait loss is that it has occurred in the past and thus the traits currently lack phenotypic variation. Previous work has shown that natural populations of Arabidopsis thaliana lose their two short stamens, the severity of loss follows a latitudinal cline, and three quantitative trait loci are associated with the trait loss. To further investigate the genetic mechanisms of short stamen loss, we conducted a line-crossing design between two Italian and Swedish populations and scored stamen loss on approximately 1500 parental, F1, F2, backcrossed, and reciprocally crossed plants. In parallel to the latitudinal cline, we found an altitudinal cline in stamen loss across 16 populations ranging from 109 to 668 meters above sea level from Northeastern Spain, with little loss at high latitudes and substantial loss in lowland populations.

Investigating the genetic structure of a fragmented chorus frog species complex

Lisa Barrow, Alyssa Bigelow, Christopher Phillips, Emily Lemmon

Saturday, June 21, 2014 -Poster #17

Species complexes with disjunct distributions raise interesting questions in biogeography, but can also pose problems for resolving taxonomy and informing conservation decisions. The Illinois chorus frog (Pseudacris illinoensis) occurs in small and fragmented pockets in Arkansas, Illinois, and Missouri and its survival has been threatened by habitat loss from agricultural practices and unpredictable drought conditions. The species status of P. illinoensis is unclear, as there has been some debate about whether it is a subspecies of the more wide-ranging Strecker's chorus frog (Pseudacris streckeri) or an entirely different species. Mitchondrial DNA evidence has demonstrated a paraphyletic relationship between P. streckeri and P. illinoensis, and morphometric data has shown geographic variation inconsistent with current taxonomic boundaries. We further investigated the evolutionary history and genetic structure across the range of P. streckeri and P. illinoensis with a large multi-locus genetic dataset. We sequenced 27 loci (23 anonymous nuclear, 4 mitochondrial) from 34 individuals on an Illumina MiSeq, and genotyped 14 microsatellite loci from 294 individuals (103 P. streckeri, 191 P. illinoensis). Phylogenetic analysis of the sequence data support the paraphyletic relationship, demonstrating a highly divergent P. streckeri clade from Central Texas and suggesting that the disjunct range of this species complex occurred recently. Bayesian clustering analysis in Structure using microsatellites confirmed that there is evidence of genetic distinction between P. streckeri and P. illinoensis. We found significant isolation by distance across the range, suggesting that geography contributes to genetic differentiation. Given the disjunct range of P. illinoensis, the limited dispersal ability of individuals, and the genetic differences already observed, we conclude that it should be protected as an evolutionarily significant unit. Further study of behavioral traits, such as whether male acoustic signals or female preferences have diverged, and unique ecological characteristics (P. illinoensis has been associated with remnant patches of sand prairie habitat) may be needed before a final conclusion can be drawn about species status.

Comparison of Aggressive and Advertisement Call Types in the Upland Chorus Frog, Pseudacris feriarum

Hannah Ralicki, Emily Lemmon

Saturday, June 21, 2014 -Poster #18
Behavioral interactions among individuals can have complex effects on trait evolution. Aggressive vocal signals function in defense of calling sites and inter-male spacing in breeding choruses of frogs and males that successfully defend their calling site likely benefit from higher reproductive success. Selection on aggressive signals could therefore indirectly influence the evolution of other calls in the vocal repertoire, yet few studies have explored this hypothesis. The Upland Chorus frog (Pseudacris feriarum) produces aggressive vocalizations and has reproductive character displacement (RCD) in advertisement vocalizations. Given the similarities of aggressive and advertisement calls, I hypothesized that male-male aggressive encounters may have influenced RCD in advertisement signals. To investigate this hypothesis, I collected aggressive and

advertisement calls from approximately 15 individuals per population of Pseudacris feriarum from populations where RCD has been observed (FL, SC, GA) and where it has not (AL, NC, VA, SC). Pulse number and pulse rate, two temporal call characteristics that show high inter-population variation consistent with RCD, were measured from vocal recordings. I present how aggressive and advertisement vocalizations vary among individuals and across populations to understand the strength of correlation between call types. These results provide the first population level examination of the relationship between aggressive and advertisement calls in the chorus frog and have important implications for understanding mechanisms of character displacement and the evolution of vocal signals in anuran amphibians.

Natural replication for testing the influence of landscape processes on genetic structure across the disjunct range of the Pine Barrens treefrog

Alexa Warwick

Saturday, June 21, 2014 -Poster #19

Species populations are distributed in a landscape matrix, and connectivity (gene flow) among populations is therefore likely to be influenced not only by the Euclidean distance between pairs of population localities (isolation by distance), but also by how well the landscape matrix allows for movement and/or contains resources of interest for the species. In a conservation context, understanding which types of landscapes are conducive for movement between populations is key to managing a species of concern. Landscapes conducive to movement can help minimize inbreeding depression in smaller populations and allow the possibility of recolonization after local extinctions. The Pine Barrens treefrog (Hyla andersonii) is a state-threatened, seepage-bog specialist found in three widely disjunct regions in the eastern United States. This species lacks detailed landscape genetics information vital to management efforts and is ideal to test the response of genetic structure to landscape processes in different parts of its range with three naturally replicated regions. In this study I test models that predict genetic distances (microsatellite markers) between populations using a measure of the suitability of the intervening habitat along a straight-line distance. I also use a least cost path approach to describe the path of least resistance, given a cost surface, in order to identify locations of potential corridors for dispersal. The results will not only be influential for conservation management of H. andersonii at a local scale but will also advance the field of landscape genetics. This study will be one of the first to consider a species across multiple parts of its range, allowing for a comparison of model selection and specific landscape features that are important in each region.

Gene tree discordance and species delimitation in the widespread skink species Mabuya dorsivittata

Danielle Rivera, *Ana Carolina Carnaval*

Saturday, June 21, 2014 -Poster #20

The Neotropical genus Mabuya has a tenuous taxonomic history and many species therein are poorly studied. My aim is to provide much needed comparative data from southern, montane lineages of one species, M. dorsivittata, by comparing the genetic relatedness of individuals from multiple populations across its widespread distribution. M.dorsivittata occurs throughout the mountains of eastern Brazil, the neighboring Brazilian Cerrado, and the Chaco corridor of Argentina, Bolivia, and Uruguay. Localities for this study are restricted to previously unsampled areas of northern Argentina, coastal Brazil and the Brazilian Cerrado. DNA was extracted from tissue samples and fragments of 10 genes (12S, 16S, Bach1, Dnah3, Cmos, cytochrome b (cytb), Myh, Rag1, Rpl35, and Sincaip) were amplified. Heterozygous genotypes were resolved using PHASE, models of evolution were determined using Akaike information criterion in PartitionFinder, and genetically clustered populations were determined using Structurama. Gene trees were generated for each locus using MrBayes, and species delimitation was inferred using the program BEST, which allows for gene tree discordance due to incomplete lineage sorting. Results showed incongruence between mitochondrial and nuclear gene trees. Tests for ILS and mitochondrial introgressions are discussed as well as future inclusion of morphometric data to identify possible variations in morphology between populations.

Spider Phylogenomics Shifts the Paradigm for the History of Earth's Most Diverse Predator Lineage

Jason Bond, *Nicole Garrison*

Saturday, June 21, 2014 -Poster #21

Spiders represent an ancient predatory lineage known for their extraordinary biomaterials, including venoms and silks. These adaptations make spiders key arthropod predators in most terrestrial ecosystems. Despite ecological, biomedical, and biomaterial importance, relationships among major spider lineages remain unresolved or poorly supported. Current working hypotheses for a spider "backbone" phylogeny are largely based on morphological evidence, as most molecular markers currently employed are generally inadequate for resolving deeper level relationships. Our study represents the first phylogenomic analysis of spiders including taxa representing all major spider lineages. Our robust phylogenetic hypothesis based on >300 loci recovers some fundamental and uncontroversial spider clades, but decidedly rejects a number of generally accepted groupings. Consequently, the fundamental shift in our understanding of spider phylogeny, we propose here, has broad implications for interpreting the evolution of spiders, their remarkable biomaterials, and a key extended phenotype—the spider web.

Quantifying niche overlap in Neotropical Gladiator Frogs (Hylidae: Hypsiboas)

Brandon Baird

Saturday, June 21, 2014 -Poster #22

The breadth of ecological niches vary dramatically between species, and recently much work has been devoted to measuring interspecific niche overlap and niche conservatism. These studies are useful for predicting ranges of invasive species, projecting species distribution shifts due to climate change, and are important for conservation planning and management decisions. Here, we present a study measuring niche overlap within a broadly distributed genus of Neotropical frogs. The genus Hypsiboas contains over 70 species found throughout South America and parts of Central America; they also occupy a variety of biomes throughout this range, and are ideally suited to compare niche differentiation between sister taxa and among clades. Focal species have diversified throughout the Atlantic Forest, Amazon, Andean Montane Forest, Cerrado, Caatinga, and Guyana Lowlands, and exhibit varying degrees of niche differentiation between closely related taxa.

Interspecific niche overlap will be quantified using the method developed by Broenniman et al, which utilizes a kernel smoothing approach to compare overlap of species occurrence densities in environmental space. This method does not necessitate the construction of ecological niche models in order to measure overlap, and therefore is unaffected by statistical artifacts due to model fitting. Additionally, we propose a modification to this method in order to account for potentially available niche space, and based on this we only make niche comparisons within shared available climate space. In absence of this correction, all niche comparison metrics potentially overinflate niche dissimilarities (leading to type I errors). This is due to the fact that species' realized niches are limited to environmental space that is regionally available, and may or may not reflect each species' ecological tolerances. When comparisons are made in shared available climate space, higher confidence can be placed in measured differences and statistics associated with these differences.

Is deep ancestral mtDNA clade divergence associated with contemporary nuclear genomic variation in threespine stickleback?

Emily Lescak, Susan Bassham, Julian Catchen, Jeffrey Colgren, Mary Sherbick, Frank von Hippel

Saturday, June 21, 2014 -Poster #23

Does deep evolutionary divergence influence contemporary evolution? Two ancestral mitochondrial lineages of threespine stickleback (Gasterosteus aculeatus) co-occur in populations in the North Pacific Basin that range in age from tens to thousands of years old. These two clades are estimated to have diverged approximately 1 million years ago during a prolonged period of geographic isolation. Our aim was to determine whether this deep divergence in the cytoplasmic genome is influencing variation of the nuclear genome as well. When we associated clade frequencies of populations from Alaska with degree of geographic isolation and phenotypic variation, we found a mosaic pattern of mtDNA clade distributions, with more variation among coastal than inland populations. At a population scale, there is evidence for a relationship between phenotype and mtDNA lineage, but this relationship breaks down at the individual level. Using RAD-seq data, we compared the overall distribution of nuclear genetic variation with mtDNA haplotype. We examined genomically-localized patterns of variation in individuals from the two mitochondrial lineages using FST and linkage disequilibrium across the genome. Nuclear genetic variation is not structured by mtDNA lineage and tests of linkage disequilibrium do not reveal an association between mtDNA haplotype and nuclear loci. Overall, our findings suggest that the two mtDNA clades are not spatially segregated or reproductively isolated, and this deep divergence has little residual influence on contemporary genetic variation. The mosaic pattern of variation that we observe is likely due to stochastic population dynamics and genetic drift.

The effects of age and genetic variation on the metabolome of Drosophila melanogaster

Jessica Hoffman, Daniel Promislow

Saturday, June 21, 2014 -Poster #24

Aging is a complex and ubiquitous phenotype, and the longevity of an individual is a major determinant of its lifetime fitness. While large variation in longevity exists between species, we also find large differences within species, and many of the genetic and molecular mechanisms that influence natural variation in aging and longevity are unknown. To begin to dissect the molecular correlates of genetic variation on aging, we completed a high sensitivity metabolomics study on 15 genotypes of Drosophila melanogaster at six different ages. We were able to determine metabolites that not only changed with age or genotype, but also found substantial age-by-genotype interaction. These metabolites and metabolic pathways whose age trajectories vary among genotypes offer great potentially as potential causal pathways for the differences in longevity we see within species.

Evolution and development of tubers in sweet potato and other morning glories

Lauren Eserman, Jim Leebens-Mack

Saturday, June 21, 2014 -Poster #25

The repeated evolution of complex morphological traits has long been of interest to evolutionary biologists. In morning glories (ca. 700 species), species that produce starch-rich tuberous storage roots, such as sweet potato, are often more closely related to species that produce only fibrous roots than they are to other tuber-forming species. It appears that this trait has been independently derived multiple times; however, it is unclear whether having fibrous or tuberous roots is the ancestral condition in morning glories. Therefore, we are interested in understanding whether the molecular components of tuber formation are shared across all morning glories or whether tuber formation has evolved independently multiple times. This question is being addressed using two main approaches, transcriptome sequencing and evaluations of root anatomy. Pairs of closely related species were sampled broadly from across the morning glory phylogeny. Both early developing tuberous roots and fibrous roots were sampled from tuber-forming species and only fibrous roots were sampled from species that do not make tubers for transcriptome and anatomical analyses. Previous work so far implicates the involvement of two genes in sweet potato tuber formation. One of these genes (IbMADS1, a MADS-box transcription factor) is highly expressed in tubers compared to fibrous roots; in contrast, the other gene (IbEXP1, an α-expansin gene) is highly expressed in fibrous roots and other vegetative tissue compared to tubers. Therefore, if the molecular building blocks for tuber formation are present in all morning glories, we expect to see similar patterns of up- and down-regulation of these genes in species from across the morning glory phylogeny. In contrast, if this pattern of differential gene expression is not shared across all species, this would suggest that tubers have been independently derived multiple times in the evolutionary history of morning glories. These predictions will be discussed in light of gene expression data as well as comparisons of root anatomy.

A framework to study compensatory evolution

Gabriela Toledo

Saturday, June 21, 2014 -Poster #26

Most adaptive changes in one trait may result in detrimental pleiotropy in other traits, which places constraints on directional evolution. Molecular compensatory mechanisms are thought to decrease negative pleiotropic effects of new adaptive mutations by restoring secondarily affected phenotypes. Compensation may result from the combinatorial effect of multiple mutations that diminish correlations between traits effectively reducing the adaptive conflict that limits evolution of new characters. The evolution of novel adaptive functions in proteins offers an opportunity to study compensatory evolution in natural populations. This requires a system in which proteins are adapted to new functions while being conserved for ancestral functions. The evolution of tetrodotoxin [TTX] resistance in garter snakes allows studying the role of compensatory mechanisms during protein function evolution. These snakes evolved resistance through mutations in sodium channels that lower TTX binding, effectively reducing toxicity. TTX-resistant mutations in snake sodium channel proteins disrupt critical biophysical properties of the channel, providing the selective force for compensatory mutations to arise that restore conserved channel properties while allowing directional increases in resistance. Measuring the single and combinatorial effect of observed mutations on channel properties may reveal patterns of molecular compensation during the evolution of TTX-resistance in snakes. This has the potential to unravel important features of compensatory evolution and its role in the maintenance of new adaptive changes in naturally adapted species.

Strong seasonal selection results in rapid life history adaptation in Drosophila

Emily Behrman, *Paul Schmidt*

Saturday, June 21, 2014 -Poster #27

Variation in spatial and temporal selection pressures can maintain genetic diversity in natural populations. In temperate environments seasonal variation creates climatic gradients such that different generations of multivoltine organisms experience distinct environments within a calendar year. This predictable environmental variation over short time scales in many ways parallels the environmental change associated with latitudinal clines and may elicit a similar adaptive response. Alternatively, species that cannot respond to seasonal environmental changes may annually recolonize temperate environments. Here, we assess the seasonal response in two species of Drosophila across seasonal time by estimating demographic composition of wild populations and as well as partitioning patterns of life history variation into effects associated with seasonal change in environmental quality (e.g., phenotypic plasticity) and temporal change in genetic composition (e.g., response to environmentally mediated selection). We find that there are distinct trajectories by species; D. melanogaster is a resident population that responds rapidly to environmental selection pressures while the transient D. simulans cannot respond to changes. The observed variance in life histories across seasonal time reflects parallel gradients along latitudinal clines; thus, seasonal dynamics may be driving spatial variation patterns. The rapid changes in life histories over seasonal time predict that seasonality significantly impacts the evolutionary dynamics of natural populations.

The implications of life history on the molecular evolution of chemoreception in predatory paussine beetles

Tanya Renner, *Wendy Moore, Amanda Romaine*

Saturday, June 21, 2014 -Poster #28

Many paussine flanged bombardier beetles form complex relationships with their host ants, making them interesting from both an ecological and evolutionary standpoint. Because of their unique life histories, this makes them excellent model organisms to study diversity and selectivity of the insect sensory system. Using a transcriptomics approach, we studied the molecular evolution of odorant receptors in two members of Paussinae, Metrius contractus (a generalist arthropod predator) and Spinicoxipaussus spinicoxis (a host ant specialist). To analyze processes and patterns involved in diversification, we combined bioinformatics with phylogenetics.

Island invaders: how island conditions alter the reproductive dynamics of wild house mice

Megan Serr, *Caroline Leitschuh*

Saturday, June 21, 2014 -Poster #29

Invasive house mice (Mus musculus) have been introduced to islands worldwide by human travelers, who often did not stay permanently. In the absence of humans, house mice have adapted to island conditions, including extreme temperatures, various climates, lack of traditional food sources and fresh water, and little to no shelter. Additionally, the geographical constraints on some islands have led to social crowding during population irruptions, when the mice are forced to live in close contact with one another. Presumably, these unusual conditions have led to behavioral adaptations. Our aim is to characterize the social and reproductive behaviors of wild house mice on islands in order to help control their populations on islands where they threaten biodiversity. Invasive rodents are found on 80% of islands worldwide and are implicated in the majority of extinctions on islands. Traditional methods for rodent eradication, toxicants, are not very effective for mice, safe for the environment, or species-specific. We are exploring the possibility of using genetic engineering to design a mouse strain that could be used for wild mouse population control on islands. Understanding the reproductive strategies of wild island mice is important in order for this approach to be effective. We obtained wild mice from the Farallon Islands and are starting a breeding colony. We will test their behavioral interactions with our genetically engineered mouse strain in order to determine if genetic engineering is a viable potential solution for controlling wild mouse populations on islands.

Evolution of the leaf economic spectrum under habitat divergence across the genus Helianthus

Chase Mason, *Lisa Donovan*

Saturday, June 21, 2014 -Poster #30

The leaf economics spectrum (LES) is one of the central modern paradigms in plant ecology, describing covariation in key leaf traits that drive carbon and nutrient relations. While the majority of investigations of the LES have examined broad cross-species variation, typically within or among communities, recent work has emphasized the importance of understanding how such broad ecological patterns arise from smaller-scale evolutionary processes like divergences within closely-related groups of species and among populations within species. This study uses the extreme diversity of the genus Helianthus, the sunflowers, to investigate the evolution of the LES at both microevolutionary and macroevolutionary scales. The genus Helianthus occurs across North America and includes a variety of growth forms and life histories, with habitat usage as varied as wetlands, deserts, forests, grasslands, coastal dunes, and rock outcrops. Plants from multiple populations from across the ranges of 27 species of Helianthus were grown in a common garden greenhouse experiment and phenotyped for key LES traits. A phylogenetic comparative approach was used to test for shifts in LES strategy during speciation into divergent habitats. Additionally, within-species tests of differentiation in LES strategy among populations with environment were performed. Significant differences in LES traits were found both among growth forms and among habitats, and repeated shifts in LES strategy support the importance of the LES during speciation and with population differentiation across small evolutionary scales.

Odd for an ericad: nocturnal pollination of Lyonia lucida

John Benning

Saturday, June 21, 2014 -Poster #31

Background

It has been hypothesized that every species on the planet is involved in a mutualism to some degree (Bronstein et al. 2006). Animal-mediated pollination is one of the best known and important of these symbioses, with significant ecological, evolutionary and economic impacts. Here I explore pollination of Lyonia lucida, a widespread ericaceous shrub of the Southeastern coastal plain, at Archbold Biological Station (ABS). Despite large floral displays and urceolate, “bumblebee” flowers, L. lucida has been noted by previous observers to have a striking paucity of visitors, while two congeners at ABS attract a host of bees, wasps and other insects. Floral morphology (i.e., corolla length) differs markedly between these other Lyonias and L. lucida, which may be the result of selection against heterospecific pollen transfer. No studies to date have investigated the mating system or pollinator assemblage of this species. To obtain a better understanding of this ubiquitous but understudied shrub, a number of facets of its pollination ecology were explored. Mating system, pollen limitation and diurnal/nocturnal visitation were examined via hand-pollinations, floral observations and temporally-varied floral exclusion treatments. Pollen loads were examined on nocturnal visitors (moths) and the possibility of pollination by thrips was also tested for.

Results

Nocturnal visitation to L. lucida was five times more frequent than diurnal visitation. Diurnal visitors were dominated by one species, Bombus bimaculatus, while nocturnal visitors consisted of mostly Noctuid moths . Thrips were shown to not be effective pollinators. Moth proboscides were found to carry substantial pollen loads, averaging 1002 pollen grains. Temporally-varied pollinator exclusion experiments showed nocturnal visitors to be important pollinators of L. lucida, with nocturnally pollinated stems setting fruit at levels comparable to controls, and marginally higher than those stems only open during the day. Mating system experiments showed L. lucida to be pollen limited and highly self-incompatible. As far as the author knows, this is the first time nocturnal pollination has been shown to be a significant contributor to fruit set in this plant family (Ericaceae). Future work will further investigate the divergence in floral morphology exhibited by L. lucida and test hypotheses regarding heterospecific pollen transfer, floral visitor exclusion and morphological variation across the species' range.

Mechanisms of batrachotoxin resistance in toxic birds: sodium channel evolution in Pitohui

Megan Kobiela, *Jack Dumbacher, Butch Brodie*

Saturday, June 21, 2014 -Poster #32

Birds in the genus Pitohui were found to harbor one of the most potent classes of neurotoxins on the planet, batrachotoxins (BTX), over 20 years ago, but the mechanism behind the birds’ resistance to BTX is still a mystery. Since BTX attacks voltage-gated sodium channels, we have begun to sequence sodium channel genes in the two most toxic pitohuis and their relatives in Corvoidea. Preliminary work has revealed a unique amino acid substitution in corvid sodium channels that potentially confers resistance. This research will illuminate the putative mechanism for avian resistance to BTX and determine whether such genetic changes are pre-adaptations (as suggested by preliminary data) or arise in association with toxicity in this clade.

Variation in pair-bond and related behaviors of male prairie voles

Andrea Vogel, Caitlin Clement, Caroline Leitschuh, Megan Serr, Lisa McGraw

Saturday, June 21, 2014 -Poster #33
Prairie voles (Microtus ochrogaster) are one of the few socially monogamous mammalian species and have traditionally been used as a model for understanding the neuroendocrine basis of social affiliation, focusing on oxytocin and vasopressin hormones. Despite decades of ecological studies showing the contrary, most lab-based prairie vole research has been conducted under the assumption that all prairie voles mate for life and form strong pair-bonds, dismissing natural variation in affiliative behaviors. We are characterizing the extent of variation in a male's propensity to form a pair-bond with his mate in an outbred laboratory population of prairie voles. We observe considerable variation between males in the amount of time he spends with his partner as well as in related social behaviors including aggression, anxiety, and care for young. These are behaviors that can change after a male has sexual experience. Preliminary results show the duration and number of aggressive behaviors in the alloparental care and resident intruder behavioral tests are higher after mating in males. Characterizing variation seen in pair-bond strength and other behaviors measured set the stage for measuring heritability of this and related behaviors and provide a foundation to begin exploring the genetic basis of behavioral variation in social behaviors. Other factors that may also influence social behaviors, such as seminal fluid proteins and male or female mate choice, will also be investigated.

The deep roots of animal sociality: hints from Williams-Beuren Syndrome genes

Cassondra Vernier, Yehuda Ben-Shahar

Saturday, June 21, 2014 -Poster #34
Since E.O. Wilson proposed that social behavior is a result of evolutionary processes, many biologists have searched for genes that influence or control sociality. Williams-Beuren Syndrome (WBS) presents an interesting case in humans, in which the hemideletion of 28 genes on chromosome 7 results in a hyper-social phenotype. Surprisingly, 18 of these genes are conserved in the fruit fly, Drosophila melanogaster. Thus, we hypothesize that some WBS genes that affect sociality in humans have similar conserved roles in insects. To test this hypothesis we examined the role of WBS-related genes in fly sociality, measured as nearest neighbor distances. Preliminary screens using RNA-interference knockdown and disruption by transposable element indicate that at least four of the 18 WBS genes in the fly may play a role in the social phenotype of the fruit fly, indicating remarkable similarity across great evolutionary distances.

Expression Evolution of Dosage Balanced Ohnologs

ammon Thompson

Saturday, June 21, 2014 -Poster #35
For many genes, the relative abundance of their protein products with other proteins is phenotypically important and evolving under purifying seleciton. These stiochiometric constraints mean that over or under expression of these genes will be harmful to the organism and thus duplication of these genes is selected against. If these genes duplicate through polyploidization then selection maintains both copies in order to maintain correct stoichiometry with their duplicated interaction partners. This creates interesting implications for the functional evolution of dosage balanced duplicate genes since selection actually maintains these genes in a redundant state. We present an example of a duplicate pair of genes which exhibit comparative patterns consistent with an interesting mechanism of neofunctionalization long after genome duplication.

Resistance against Botrocetin induced platelet aggregation in Didelphid Marsupials: Evidence for a Coevolutionary Arms Race

Danielle Drabeck

Saturday, June 21, 2014 -Poster #36
Naturalists have long known that certain opossum species (members of the South American marsupial family Didelphidae), are not only resistant to snake venom but also attack and eat pit-vipers with impunity. Von-Willebrand Factor (vWF), a blood regulatory protein, has been identified as a site under positive selection in species of opossums that are known to be venom resistant, and has been proposed to be a mechanism by which these species mitigate vWF-binding venom components. Molecular models suggest that vWF can no longer bind the snake venom derived protein Botrocetin (Bothrops jararaca) in resistant opossums, but physiological evidence to support this claim was lacking. To determine if this modified vWF provides physiological resistance to Botrocetin, I developed a Botrocetin-induced platelet aggregation assay using platelets and plasma from Didelphis virginiana, and tested its reactivity in comparison with normal human samples. These assays show that human platelets aggregated as expected in the presence of Botrocetin, but opossum platelets failed to react with Botrocetin in both presence or absence of other plasma proteins. These data strongly suggest that the identified amino acid changes in opossum vWF do in fact have physiological importance: these mutations – in absentia of other adaptive plasma proteins – are likely responsible for opossum resistance to Botrocetin. These data are also suggestive of a potential coevolutionary arms race ongoing between South American vipers and Didelphid marsupials, of which, the relationship between vWF and Botrocetin-like C-type Lectin proteins that target vWF may be an important extractable component.

Geographical coincidence and mimicry between harmless snakes (Colubridae: Oxyrhopus) and harmful models (Elapidae: Micrurus)

Renan Bosque, Guarino Colli

Saturday, June 21, 2014 -Poster #37

Batesian mimicry has captivated researchers for years. However, aspects of mimicry dynamics, such as multiple model systems and the geographical overlap between mimics and models remain unclear. In the coral-snake complex, Micrurus species are presumably Batesian models for species from Colubridae, including Oxyrhopus. We used these two genera to test for the degree of distribution overlap between model and mimics, the association between species and pattern richness of model and mimic, and between the quality of mimic colour patterns and the number of model patterns. We classified the colour patterns and delineated the geographical distributions of each species. We identified 4 patterns exclusive to Oxyrhopus, 10 to Micrurus, and 6 shared by both genera. In general, pattern-specific cases of Micrurus presence and richness explained the presence and richness of Oxyrhopus colour patterns. However, when confronted with alternative patterns, specific colour mimics had little explanatory power, except in few cases. In general, the presence of each Oxyrhopus pattern was positively correlated with the richness of Micrurus patterns, regardless of mimetic quality of colour pattern. Our results indicate a possible relationship between the colour patterns of Micrurus and Oxyrhopus, but highlight the importance of including other species or colours when performing mimicry tests.

A preliminary analysis of ontogenetic integration in the gray short-tailed opossum, Monodelphis domestica

Arthur Porto, John VandeBerg, Gabriel Marroig, James Cheverud

Saturday, June 21, 2014 -Poster #38

Marsupials have recently been the focus of several studies of adult craniofacial variation. The interest in marsupials is justified by their overall level of integration among craniofacial elements, since they are much higher than in most eutherian mammals. Theoretically, this strong integration among traits in the adult morphology should emerge as a consequence of strong covariation among traits during cranial ontogeny. To test this hypothesis, this study presents a preliminary analysis of ontogenetic integration in a genetically homogeneous population of the gray short-tailed opossum, Monodelphis domestica. Since marsupials have a very short period of intra-uterine development and complete most of their cranial development after birth, our analysis is restricted to the post-natal stages of ontogenetic development. In particular, a total of 129 Monodelphis domestica specimens, equally distributed across 6 age classes, were obtained from the Texas Biomedical Research Institute (TBRI) and posteriorly measured for 35 different traits using a Microscribe MX digitizer. Pooled-within group variance/covariance and correlation matrices were computed for each age class, controlling whenever appropriate for sex differences. Matrices were then compared across age classes using several methods available in the literature. Similarly, the magnitude of morphological integration in each age class was computed using the average coefficient of determination of the correlation matrix. Our results suggest that the strong covariation among traits in marsupial adult morphology is indeed a reflection of strong covariation among traits across all age classes.

Was the radiation of the western chipmunks (genus Tamias, subgenus Neotamias) adaptive?

Ana Paula Aprígio Assis, Gabriel Marroig, James Patton

Saturday, June 21, 2014 -Poster #39

Although adaptive radiation is at the core of evolutionary theory, its actual contribution to the emergence of current biological diversity remains uncertain. Thus, recognizing an adaptive radiation event is an important component in our understanding of how biodiversity is generated. According to Schluter, the recognition of such an event requires four steps: 1) common ancestry; 2) rapid speciation; 3) natural selection acting in the diversification process; 4) correlation between phenotype and environment. Chipmunks (genus Tamias, subgenus Neotamias) comprise 23 species that occur throughout western North America. These species occur in many varied types of habitats, from sea level to 4000 meters, from dry to coastal humid areas. They form a monophyletic group and are part of a recent radiation, thus fulfilling the first two of the premises defining an adaptive radiation. Here we tested the other two of Schluter's premises: the phenotype/environment correlation and the action of natural selection on the diversification of this group. To do this, we combined cranial morphometric and climatic data from the distribution of these species. To test if natural selection played a role in the diversification process, we performed a genetic drift test based in a quantitative genetic framework using the cranial data. The test is based on the expectation under drift that divergence between groups will be proportional to the amount of within-group variation. This test was performed on each node in the phylogeny, and the basal nodes rejected the null hypothesis of evolution by genetic drift. In addition, the group that gave rise for the small-bodied chipmunks (T. alpinus, T. amoenus and T. minimus) also showed a signature of natural selection. This pattern of natural selection in the deep nodes is what one would expect in an adaptive radiation. To test the association of phenotype and environment, we calculated correlations between the principal components (PC) of the morphological covariance matrix and the climatic correlation matrix. There was a significant correlation between the first PC of the morphological data and the second PC of the climatic data. Also, the second PCs of climate and morphological data were highly correlated. This result indicates that there is a correlation between the environment (in this case climatic data) and the phenotype (skull's morphology). Our analysis gives support for the hypothesis that the radiation of these chipmunks has been adaptive.

Are mpi and pgi Under Balancing Selection in Heliconius Butterflies?

Ryan Jenks, Luana Maroja

Saturday, June 21, 2014 -Poster #40

Heterozygote advantage has been studied in many different organisms, and has been found to occur even in genes originally thought to be highly conserved, such as metabolic genes. Here we tested for heterozygote advantage in two metabolic genes, mpi and pgi, in the tropical butterflies Heliconius petiverana and Heliconius rosina. The two genes were chosen based on previous evidence pointing to balancing selection. For pgi, balancing selection has been described in two high latitude butterflies, Colias and Melitaea cinxia. For mpi, a previous study in Heliconius found very high nucleotide variability and incongruence between gene trees and species trees. Taken together, these results could be indicative of balancing selection. Using cDNA we ran statistical tests, including Fu and Li's, Tajima's D and HKA, of both genes and created gene trees for each. None of the tests were statistically significant, and our gene trees were identical to the species tree. Tajima's D value was negative for each individual gene, indicating change acting across the entire genome (possibly population expansion). There was no evidence for balancing selection acting on either gene for our species. The types of habitats Heliconius butterflies live in could explain the lack of balancing selection, as they do not occur in metapopulations like Melitaea cinxia. However, it could also be due to environmental factors. Butterfly species which exhibit balancing selection, live in moderate to cold temperatures, but homozygotes for pgi have an advantage in higher temperatures. As Heliconius butterflies are from tropical environments, the higher temperatures could account for the lack of balancing selection found.

Dengue virus type 3 evolution and epidemic activity in Indonesia: A historical study of outbreaks from 1976-1979

Sean Edgerton, Duane Gubler, Shannon Bennett

Saturday, June 21, 2014 -Poster #41

Dengue viruses are one of today's most significant vector-borne disease agents threatening human health throughout the tropics and subtropics, infecting hundreds of millions of people annually. Dengue is primarily transmitted by Aedes aegypti mosquitoes. There are four known serotypes circulating in humans (DENV-1 to -4) all of which can cause a febrile illness known as dengue fever that can progress to more severe and potentially fatal disease involving hemorrhage or shock (DHF/DSS). We report here follow up sequence data on DENV-3 strains isolated during epidemics that occurred in Indonesia between 1976 and 1979. The epidemics began with the detection of fatal DHF/DSS associated with DENV-3 in Jakarta in Jan-Mar, 1976. The virus spread to Bantul, Central Java in Oct, 1976, and to Surabaya, East Java and Pontianak, West Kalimantan in 1977. All of these were explosive epidemics with associated severe disease. A smaller outbreak with more sporadic transmission, milder illness and much lower viremia levels occurred in Sleman, Central Java in 1978. Viruses were isolated by one of us (DJG) from all of these epidemics and stored in infected mosquitoes at -70 C for nearly 40 years. The viruses had not been passaged in mice nor mammalian cell cultures. Full genomic sequence analysis suggests that a single strain of DENV-3 with greater epidemic potential and possibly virulence emerged in Jakarta and spread rapidly along the main transportation routes to Central and East Java, and to Kalimantan. Interestingly, the Sleman DENV-3 viruses were genetically distinct, belonging to a separate clade from the other strains. There were two unique Bantul isolates that also belonged to the Sleman clade, suggesting that the Sleman virus descended from these Bantul viruses. Our findings emphasize the importance of dengue evolution and genetic variation as a contributor to epidemic intensity and severe dengue disease.

Comparative Genomics of Desert Adaptation Among Mice in the Genus Peromyscus

Lauren Kordonowy, Matthew MacManes

Saturday, June 21, 2014 -Poster #42

Understanding the genetics of adaptive phenotypes represents an outstanding question facing modern evolutionary biology. One such suite of adaptions – those revolving around the ability to survive in deserts – is particularly relevant in the context of global climate change. Mice within the genus Peromyscus provide a unique opportunity for the study of this desert adapted phenotype, because there are over 50 species residing in a variety of ranges and habitats, including the desert specialists P. eremicus and P. crinitus. Closely related to these specialists are the habitat generalist P. maniculatus, and P. californicus which occupies coastal Californian grassland and forest habitats. The development of genomic resources by the MacManes lab and broader Peromyscus community make this group particularly well suited for a comparative genomics project that aims to understand the genetic underpinnings of desert adaptation. This poster presentation will (1) describe the bioinformatics pipeline used to analyze genomic differences between these four divergent Peromyscus species, and (2) present preliminary results aimed at understanding gene family expansions and contractions as well as genes undergoing positive selection, which may elucidate genes critical for desert survival.

To play, or not to play, that's a resource abundance question

Jeremy Auerbach, Gordon Burghardt

Saturday, June 21, 2014 -Poster #43

Although play is observed in many animals, how or why this behavior evolved is unclear. We propose a novel mathematical model to explore a possible mechanism for the evolution of play in a non-sexual animal. Here the organisms initially have two strategies at each time step: rest or forage. Foraging attempts, determined by an energy threshold, are costlier in terms of energy and mortality than resting. Play is introduced as an activity that uses energy, has an increased mortality over resting, but has no direct fitness benefit. Agent based simulations are run with cohorts of a fixed population size living in an environment of limited non-renewing resources. The surviving animals reproduce after a set time period and weak selection acts upon individual energy levels where those with more acquired energy have greater fitness. Play behavior evolves and maintains a low frequency in the population by reducing the energy of the players which results in more frequent foraging attempts. This change in time scale to forage reduces the abundance of resources in the environment, thus making it more costly just to rest when not hungry. The model is modified so that the play behavior leads to an increase in foraging ability, but now play does not persist in the population due to an increase in foraging and ultimately exhausting the finite resources in the environment. When there is an abundance of resources or play facilitates exploiting additional types of resources, play evolution would presumably be augmented. Nonetheless, the early origins of play may have evolved in the absence of direct fitness enhancing qualities.

Selection during domestication affects the circadian clock and the expression of ecophysiological traits.

Yulia Yarkhunova

Saturday, June 21, 2014 -Poster #44

Selection during domestication affects the circadian clock and the expression of ecophysiological traits.

Y. Yarkhunova1, C. Edwards2, B. Ewers1, C. Weinig1

1Department of Botany and Program in Ecology, University of Wyoming

2Center for Conservation and Sustainable Development, Missouri Botanical Garden

Selection during domestication can result in dramatic changes in morphology. Brassica rapa (Brassicaceae) shows morphological differentiation as a consequence of domestication, with the evolution of leafy vegetable crops (subspp. pekinensis and chinensis), root vegetable crops with enlarged below-ground storage structures (subspp. ssp. rapa or rapifera), and oilseed crops with high seed allocation (subspp. oleifera).Here, we examine developmental and physiological diversification associated with domestication.

For our study, we used multiple genotypes within each of three different croptypes (turnip, cabbage, and oilseed) to test for possible physiological differentiation.

There is significant divergence among crop types in circadian rhythms. We observe that oilseeds have circadian cycles approximately 1 hour shorter than those of vegetable crops, and closer to 24 hours on average than either cabbages or turnips. Oilseeds have higher CO2 assimilation rates, while cabbages are the lowest in this parameter. Stomatal conductance is the highest in the oilseed varieties, and these differences may be the result of increased stomatal density. There is also a robust association between gas-exchange parameters and circadian period, consistent with past observations in experimental segregating progenies of B. rapa. We consistently observed that maximum Rubisco carboxylation rates are higher in turnip type. Thus, oilseeds seem to attain high carbon fixation via increased stomatal conductance; although the vegetable crop, turnip, has more favorable photosynthetic biochemistry, stomatal conductance may be limited by midday water stress.

Is the susceptibility to chytridiomycosis related to niche conservatism?

Isis Arantes

Saturday, June 21, 2014 -Poster #45

Chytridiomycosis is a disease that infects amphibians throughout the world, causing wide spread mortality in populations. The biodiversity of Brazils' immense amphibian species richness is threatened by several factors. The main threats to amphibian conservation include: mortality caused by the fungus Batrachochytrium dendrobatidis (chytridiomycosis), climate change, over-exploitation and habitat loss, UV- B and introduction of new species. The Batrachochytrium dendrobatidis is an aquatic fungus and amphibians can be greatly affected by this because part of their life cycle is dependant on water. Increasing the knowledge base of the chytrid proliferation in Brazil is important for amphibians' conservation. In addition, greater understanding of its phenology is essential to understanding the ecological and evolutionary aspects of chytrids and amphibians. The aim of this study is to verify if there is a relationship between the presence of the chrytrid fungus, and the phylogeny and ecology of amphibians. The specimen data were compiled from the literature of occurrence of chytridiomycosis in Brazil. The data is based on the compilation by Schloegel et al (2012), and has been updated with additions from recent literature (post 2012) about Batrachochytrium dendrobatidis in Brazil. The dataset contains165 Batrachochytrium dendrobatidis records on 97 amphibian species in all Brazilian biomes. In addition, I included the preferred habitat for each amphibian species based on scientific literature. Then, I built a phylogenetic hypothesis for the species of frogs sampled based on the recent literature and the branch lengths were determined by the Grafen (1989) method, using the R program and the Picante package. Also, I verified the phylogenetic signal for the presence of chytridiomycosis and the community phylogenetic structure according to the microhabitats used by the species. The result indicated that there is a phylogenetic signal (K=0.0678, P=0.042), and the pattern observed could be a convergent trait and is a nonrandom pattern. Furthermore, the co-occurrence analysis indicated that there is correlation between co-occurrence and phylogenetic distance (C-scoreobs = 0.4483; P = 0). The species that have arboreal, rheoliphic and semi-aquatic habit have a high percentage of chytrid infection (70-100%). The main conclusion is that there is a phylogenetic relationship between the prevalence of chytridiomycosis and the niche used by the amphibian species.

A molecular phylogeny of microgastrine (Braconidae) wasps that attack Eois caterpillars (Lepidoptera: Geometridae)

Kyle Parks

Saturday, June 21, 2014 -Poster #46

Parapanteles Ashmead is a genus of wasp that represents one of three trophic levels in a tritrophic Neotropical system. This system is the subject of a collaborative study investigating cascading evolutionary patterns between a plant host genus (Piper), an herbivore (Eois), and a parasitoid (Parapanteles). Parapanteles was chosen as a focal genus because it was thought to be the most abundant, morphologically diverse, and ecologically diverse genus of microgastrine reared from Eois caterpillars. We built a molecular phylogeny built from 3 genes (Cytochrome oxidase I, wingless, & ribosomal subunit 28s) of Parapanteles wasps and have found that Eois-attacking Parapanteles form two non-sister clades. One clade is closely related to the microgastrine genera Cotesia and Glyptapanteles and the other is closely related to the microgastrine genus Dolichoenidea. Therefore, the current morphological definition of Parapanteles does not reflect a monophyletic group when applied to Neotropical species. Based on these findings, Neotropical wasps identified as Parapanteles are comprised of at least two clades that are more closely related to other microgastrine genera than they are to each other. This finding challenges our initial hypothesis that Parapanteles contains the most species of Eois-attackers, and that it is the most commonly reared microgstrine genus from Eois caterpillars. This suggests that small numbers of Eois-attacking microgastrine species are found in several genera, but there is no known genus that is especially rich with Eois-attacking species.

Comparative phylogeography of amphibians in the southeastern U.S. with Anchored Phylogenomics

Lisa Barrow

Saturday, June 21, 2014 -Poster #47

Spatial patterns of genetic variation provide important insights into evolutionary processes as genetic structure can facilitate local adaptation and ultimately promote lineage diversification. The Southeastern U.S. has been a classic system for studying spatial genetic variation across multiple species and has been the foundation for many ideas in phylogeography. Although the region remained unglaciated, changes in sea level and habitat shifts during Plio-Pleistocene glacial-interglacial cycles as well as numerous river drainages and physiographic differences have created a complex history that is often reflected in the distribution of genetic lineages. The majority of studies in this region thus far have focused on a single species at a time and one or few loci (often mitochondrial DNA) due to logistical limitations. Therefore, it is still unclear which major patterns are concordant across loci, species, and proposed biogeographic features. We employ targeted sequence capture combined with high-throughput sequencing (termed anchored phylogenomics) to produce a massive dataset with hundreds of the same loci sequenced across four co-distributed anuran amphibian species sampled from the same localities in the Southeastern Coastal Plain. We report on the utility of this approach for comparative phylogeography and provide initial insight regarding the level of concordance across loci, species, and previously described biogeographic features in this region.

The Significance of Integrating Genetic Patterns of Diversity with Geographic Patterns of Suitability

Sarah Duncan, Nichole Mattheus, Erica Crespi, Leslie Rissler

Saturday, June 21, 2014 -Poster #48

Low genetic variation can have many evolutionary implications including negative fitness effects, decreased adaptive potential and increased extinction risks for populations. In turn, the role of genetic diversity in natural populations has had a considerable impact on the management of populations experiencing habitat fragmentation, isolation, and high levels of inbreeding. The Core-Periphery (C-P) hypothesis predicts that populations located at the edge of a species range should have lower levels of genetic variation than those at the center of the range. However, most of the research on the C-P hypothesis focuses on geographic distance and not environmental distance. We assess whether genetic diversity varies across a species range in relation to distance from range center or environmental distance based on climatic suitability. We use natural populations of the wood frog (Rana sylvatica) and examine 30 populations spanning the entire eastern geographic range from Alabama to Nova Scotia. Twelve polymorphic microsatellites were used to estimate changes in heterozygosity, allelic richness, and population differentiation in populations located in the core (high environmental suitability, mid-range) and edge (low environmental suitability, range margin) of the wood frog's distribution. Core and edge populations showed no significant differences in heterozygosity, allelic richness or population differentiation across the range which might suggest that fluctuating selection pressures are high and genetic variability is being maintained at the periphery to allow for survival at the extremes where habitat suitability is low.

Environmental influences on germination and sex expression in Silene vulgaris

Malcolm Augat, Austin Yantes, Butch Brodie

Saturday, June 21, 2014 -Poster #49

Populations of gynodioecious species – those with separate hermaphrodite and female individuals – often vary greatly in sex ratio. One explanation for this sex ratio variance is that when resources are limited, hermaphrodite individuals will only invest in either male or female gametes, but not both. As such, populations in poor quality environments will behave as though dioecious – with hermaphrodites acting either as functional males or functional females. This predicted correlation between sex ratio and habitat quality has support in many gynodioecious species, but it is agnostic to mechanisms driving the sex ratio variance. The sex ratio of a population can evolve either by (1) frequency dependent selection on genotypes that produce hermaphrodites and females, or by (2) the evolution of plastic sex expression. This work tests mechanism (2) in the gynodioecious weed Silene vulgaris. Habitat soil quality was assessed for 5 populations by reciprocally transplanting seeds in wild-collected soil from each population. Further, the plasticity of sex determination and sex expression were evaluated by tracking plants to flowering, then scoring sex and measuring secondary sexual characters (floral morphology). Understanding the genetic and environmental basis of sex and sexually dimorphic characters is important for predicting how traits evolve within these species, and has consequences for the evolution of the mating system itself.

The Effects of Social Status on Immune Function in Male Vertebrates: A Meta-Analytic Review

Bobby Habig, Elizabeth Archie

Saturday, June 21, 2014 -Poster #50

In both humans and animals, immune function is often strongly linked to individual social status. These relationships are especially important in male vertebrates, where two disparate and somewhat contradictory paradigms have been suggested to explain status-related variation in male immune function. The first paradigm predicts that low-ranking males will have poorer immune function than high-ranking males because low social status is often associated with chronically elevated glucocorticoid hormones and immunosuppression. Conversely, the second paradigm predicts that high-ranking males will have worse immune function than low-ranking males because dominant males allocate more resources towards reproductive effort, generating energetic tradeoffs with immune function. Here we use a meta-analytic approach to test the explanatory power of these two paradigms. Based on an analysis of 113 papers across 30 tests of immune function, we found limited support for both models. Dominant males had relatively stronger immune responses across multiple tests of adaptive and induced immunity including antibody production, delayed-type hypersensitivity, and in vitro proliferation to phytohemagglutinin (PHA). Subordinate males exhibited relatively lower natural helminth burdens and significantly higher IL-6 responses to immune stimulants. However, most analyses yielded inconclusive results. We conclude by proposing a modified model that incorporates measures of allostatic load in predicting status-related differences in immune function.

Fine-tuned adaptive responses of larval anurans to a combination of natural enemies

John Marino

Saturday, June 21, 2014 -Poster #51

Most animals undergo threats from multiple natural enemies, often simultaneously. In many situations, the optimal response to one natural enemy may differ from the response to another enemy, resulting in a potential tradeoff. The nature of such a tradeoff likely depends strongly on individual traits involved in susceptibility to these enemies, which can differ between species or across ontogeny. In an aquarium study, I examined differences between larval anuran species (Rana sylvatica and R. clamitans) and size classes in responding to one such tradeoff. Behavioral responses of tadpoles to the presence of predators (larval dragonflies) can increase susceptibility to parasites (Digenea: Echinostomatide), and vice versa. I hypothesized that tadpoles would moderate their response to the combination of natural enemies in line with differences in the relative risk associated with each enemy, depending on individual size and species identity. My results reveal species and size-dependent differences in tadpole behavioral responses and infection establishment across a gradient of predation risk. My findings suggest that tadpoles have fine-tuned responses to a susceptibility tradeoff, with implications for how animals adapt in response to multiple enemies.

Genome-wide phylogeography using RAD-Seq: cryptic vicariance in the Albertine Rift and gene flow into the Kenyan Highlands in Afromontane mammals

Terrence Demos

Saturday, June 21, 2014 -Poster #52

The Eastern Afromontane biodiversity hotspot (EABH) has the highest concentration of biodiversity in tropical Africa yet has been little studied to date. To better determine how historical climatic processes could have driven these elevated biodiversity patterns, we use restriction-site associated DNA-sequencing (RAD-Seq) based population genomic analysis to study co-distributed mouse (Hylomyscus) and shrew (Sylvisorex) species complexes. To this end we dually investigate genetic variation that is partitioned within and among these two taxa to reconstruct their spatio-demographic history. We sampled populations from both focal genera across the Albertine Rift (AR) and Kenyan Highlands (KH) sub-regions of the EABH and then analyzed complete SNP matrices of 18,628–20,012 RAD loci to delineate populations, reconstruct the history of isolation and admixture, and uncover potentially evolutionarily independent regions with cryptic genetic diversity. Concordant results from these multiple analyses clearly demonstrate that persistently unsuitable habitat isolated the Itombwe Massif and AR populations to the north and Mt Elgon and KH populations to the east, with KH populations in both genera exhibiting reduced genetic diversity due smaller areas of suitable habitat that persisted through Pleistocene climate cycles. Graphs of population splits and admixture constructed with TreeMix support substantial gene flow from AR into KH shrew populations subsequent to isolation that occurred 2.5-3.5 million years earlier. Phylogenetic analyses support greater historical isolation among AR populations of both shrews and mice while genetically isolated populations from both of these focal genera are inferred for the Itombwe Massif and Mt Elgon. Sylvisorex populations exhibited greater population structure in accordance with their limited dispersal capabilities relative to Hylomyscus. These results demonstrate the power of genome-wide sequencing for identifying present population genetic structure, inferring historical demographic processes and helping identify putative regions of cryptic biodiversity and bioclimatic stability, in this case for montane rainforest associated mammals.

TESTING WHETHER ECOLOGICAL DIFFERENTIATION SUPPORTS THE TAXONOMY OF THREE HIBISCUS SPECIES IN NORTHEAST TEXAS

Melody Sain, John Placyk, Randall Small, Lance Williams, Marsha Williams, Joshua Banta

Saturday, June 21, 2014 -Poster #53

Ecological and evolutionary theory state that sympatric species should be differentiated from each other ecologically if in fact they are truly different species. We tested whether the nomenclature of three congeneric and co-occuring herbaceous perennial marsh plants (Hibiscus dasycalyx, Hibiscus moscheutos, Hibiscus laevis) is supported. Specifically, we used ecological niche modeling methods to test for ecological non-overlap among the species. One of these three species, the Neches River Rose Mallow (H. dasycalyx) has recently been listed as a threatened species under the Endangered Species Act by the US Fish & Wildlife Service, so determining whether it is, in fact, a unique entity is of special interest. Our study provides another tool besides phylogenetic analysis to help biologists and conservation managers make decisions about species delimitations.

Single-cell analysis of yeast reveals natural variability in a potential bet-hedging trait

Colin S. Maxwell, Paul Magwene

Saturday, June 21, 2014 -Poster #54

In uncertain environments, organisms may evolve bet hedging strategies, where individuals randomly develop alternative phenotypes specialized for different modes of the environment. Bet hedging is predicted to evolve when there is high environmental variation, where there are strong trade-offs between the phenotypes, and where these tradeoffs are correlated with fitness in alternate environments. Although the evolutionary conditions that favor bet hedging strategies are well understood, the biological mechanisms underlying such strategies are less well known. We have developed an assay to measure both the division-rate and stress-resistance of individual yeast cells using a flow cytometer. We surveyed more than twenty environmental isolates of S. cerevisiae and found extensive differences in both the mean and variance of their division-rate during logarithmic growth in rich media. Furthermore, we found that individuals with a rapid division-rate are more sensitive to mechanical disruption, antibiotics, and reactive oxygen stress than slower-dividing cells. Limited resources available to organisms likely impose a trade-off between growth and stress-resistance, which suggests that bet hedging between quick growth and stress resistance could be a consequence of evolution in environments with highly variable nutrient availability (e.g. feast or famine dynamics). We hope to use the tractable genetics of S. cerevisiae to unravel the mechanisms underlying this trade-off.

The remodeling of the plant vacuole and its role in chloroplast evolution

Amber Paasch, Eunsoo Kim

Saturday, June 21, 2014 -Poster #55

The chloroplast is one of the most important components of life on Earth. Its evolution more than 1.5 billion years ago caused a steep increase in atmospheric oxygen that led to the rise of multicellular aquatic and land organisms, and it continues to be the major producer of oxygen today. The chloroplast, previously a free-living cyanobacterium, was acquired through phagocytosis by a single-celled eukaryote, forming the first plant cell. Today, phagotrophy has been lost in almost all plants and green algae with the exception of the “early-divergent” green alga, Cymbomonas tetramitiformis. Structurally, the permanent nature of phagosome of C. tetramitiformis resembles a plant vacuole more than a traditional transiently-formed phagosome found in animal cells and other protists such as ciliates and amoebozoans. This suggests that the plant vacuole may have prey-digesting origins The goal of this study is to identify whether the plant vacuole originally functioned as an organelle used for phagocytosis. We have sequenced the nuclear and organellar genomes of C. tetramitiformis and used a large-scale comparative approach to map the evolution of the plant vacuole in distant organisms. The plant vacuole proteome was identified and compared in 22 taxa. Our data suggest that the plant vacuole was originally used to digest food in some single-celled eukaryotes and later remodeled to be a digester of cellular garbage in land plants. This study is the first to suggest the organelle used to capture the chloroplast 1.5 billion years ago was a plant vacuole rather than a traditional phagosome.

Investigating natural selection on defense traits in Passiflora incarnata

Aline Waguespack Claytor, Nina Sletvold

Saturday, June 21, 2014 -Poster #56

Most plants exhibit a range of defenses against insect herbivores, but the determinants of this production are still poorly understood. Numerous studies have demonstrated local adaptation of species among populations in plant defense production. One way to better understand plant defenses is to investigate how natural selection acts on plant defense traits.

Passiflora incarnata (‘maypop’) is a perennial vine native to the southeast United States that produces both direct, physical defenses (leaf toughness and trichomes) and indirect defenses (extrafloral nectar in a defense mutualism with ants). To look for differences in expression of these defense traits, we used common garden experiments with plants originating from two different populations. We calculated the heritability of these traits to determine the environmental versus genetic determinants of trait values and looked at genetic correlations between traits. We also used a genotypic selection analysis to investigate how natural selection shapes these traits.

Cascading effects of intraspecific variation in plant subsidies on aquatic and terrestrial ecosystem function

Sara Jackrel, J. Timothy Wootton

Saturday, June 21, 2014 -Poster #57

Cross-ecosystem fluxes can intertwine otherwise disparate food webs, but the effects of biodiversity within species on fluxes across ecosystems boundaries is not known. Fresh leaves, which vary in traits such as defensive compounds against terrestrial herbivores, drop off trees and enter streams, providing a vital resource for riverine organisms. Previously, we found substantial variation among individual red alders in leaf decomposition rates in rivers, and showed that locally derived leaves decompose faster than leaves introduced from trees growing along other riparian zones. These results indicated that aquatic decomposer communities have locally adapted to the specific trees supplying the riparian subsidies at a particularly fine scale. To explore the basis of individual variation in decomposition rate, we studied the effects of induced plant defenses and nutrients on terrestrial herbivore feeding, and on aquatic and terrestrial leaf decomposition through a combination of experimental simulation of herbivory on red alder and measurement of phenotypic leaf traits. The experimental herbivory treatment on red alder trees effectively dissuaded terrestrial insects from feeding on adjacent undamaged leaves. The effects of the induced defense carried over into aquatic ecosystems, where aquatic decomposers fed 60% faster on leaves from controls compared to trees undergoing simulated herbivory. The defense response included a two-fold sharper decline in leaf nitrogen levels compared to controls. This same herbivory treatment had no effect on terrestrial soil decomposers even though these decomposers also showed strong preference for nitrogen rich leaves. These finding illustrate how phenotypic or genetic diversity and the effects of selection in one ecosystem can indirectly shape the structure of other ecosystems through ecological fluxes across boundaries.

Individual growth rate heterogeneity changes population dynamics of perennial plants

Erin Feichtinger, Gordon Fox, Bruce Kendall

Saturday, June 21, 2014 -Poster #58

In plants, size and rate of growth is positively related to reproductive output. Within plant populations, there can be substantial variation in growth rate among individuals of the same age which can change the size structure and in turn, can change the population growth rate and equilibrium size. In natural plant populations, individual heterogeneity results from genetic differences, maternal effects, spatial heterogeneity in resource availability and competition. To examine the effects of variation in among-individual growth rate on the population growth rate and dynamics, we built a stage-structured population model assuming density independence. We used an integral projection model framework where individuals of the same age can grow at different rates. We found that increasing the among-individual growth rates can increase the population growth rate depending on the value of the parent-offspring phenotypic correlation. When the parent-offspring phenotypic correlation is positive, high levels of varition among individuals leads to an increase in the population growth rate, even if the probability of transitioning to the reproductive stage is low. However, if the parent-offspring phenotypic correlation is negative, only some levels of among-individual growth rate variation leads to an increase in the population growth rate. Individual heterogeneity in growth can increase the viability of a population which may be important for estimating probability of persistence, especially for small populations. These results mays have implications for understanding life-history evolution of perennial plants and the evolution of bet-hegding in heterogeneous environments. Future work will include buidling a model with density dependence and investigating trade-offs in variable growth among individuals within a population.

Variation in thermal tolerance in an invasive lizard (Anolis sagrei)

Tamara Fetters, Prabhsimret Dhillon, Joel McGlothlin

Saturday, June 21, 2014 -Poster #59

Biological invasions allow researchers to assess phenotypic responses to novel environments. Anolis sagrei is a tropical lizard that has successfully invaded geographic ranges with climatic variables that differ substantially from its native range. A climate niche shift in this species has been observed between its native range in the Caribbean and an invasive range in the southeastern United States. This shift is expected to lead to population differences in thermophysiological traits such as thermal tolerance between these two ranges. While measures of thermophysiological traits from invasive populations have been recorded, there are no measures of these traits from the native range. This study provides data on such traits from a Bahamian population of A. sagrei. In conjunction with previous work on invasive populations of A. sagrei, our results will be important in further understanding the phenotypic adjustments that often occur in populations exposed to new environments.

Comparing Pieris virginiensis (Lepidoptera: Pieridae) preference and performance on the native Cardamine diphylla and the invasive Alliaria petiolata

Kate Augustine, Joel Kingsolver

Saturday, June 21, 2014 -Poster #60

Invasive and introduced species can have dramatic ecological consequences for native species and communities by altering community interactions and creating new patterns of selection on native species. In environments that have been recently invaded, formerly reliable host plant cues of phytogphagous insects may no longer be associated with adaptive outcomes for female oviposition and larval success. The invasion of Alliaria petiolata (garlic mustard) into the native habitat of Pieris virginiensis (West Virginia White butterfly) and its native host plant Cardamine diphylla (toothwort) in eastern North America is one such example. In New England, P. virginiensis females readily oviposit on the invasive A. petiolata plant, but the larvae are unable to grow and survive. The invasion of garlic mustard has expanded southward, where it is now present in P. virginiensis populations in West Virginia and Virginia but not in North Carolina. We are studying the ecological and evolutionary consequences of this invasion for southeastern populations of P. virginiensis using oviposition preference and larval feeding experiments with toothwort and garlic mustard. Our preliminary studies in North Carolina revealed wide variation among individual females in their oviposition preferences for the two hostplants. Hatching success did not differ between the two host plant species, but larval survival to 3rd instar was much lower on the invasive garlic mustard than on native toothwort. This suggests that the A. petiolata invasion could be a strong force driving selection for oviposition preference in adult P. virginiensis females.

The relative roles of climate and interspecific interactions in determining distribution patterns differ between two species of hybridizing songbirds.

Michael McQuillan, Amber Rice

Saturday, June 21, 2014 -Poster #61
Abiotic factors such as climate are important for determining species distributions. In addition, biotic factors such as interspecific interactions also function to delimit species range boundaries, and may be especially important when closely related species form hybrid zones. Teasing apart the relative contributions of abiotic and biotic factors in shaping species' distributions is thus a longstanding goal in evolutionary biology. Ecological niche modeling provides the unique opportunity to disentangle the relative importance of these factors, and can provide insight into how species' range limits are formed and maintained. Niche models incorporate climatic variables and result in an "actual" range, where a species is known to occur, and a "predicted" range, where a species could potentially occur. Here, we apply ecological niche modeling methods to study range dynamics in two species of parapatrically distributed songbirds, Black-capped (Poecile atricapillus) and Carolina (P. carolinensis) chickadees. These birds overlap in a narrow east to west band stretching from Kansas to New Jersey, and are ideal for ecological niche modeling. The southerly-distributed Carolina chickadees are expanding rapidly northward into territory historically occupied by Black-capped chickadees. If abiotic factors such as climate determine the range limits of these two species, then the actual range of each species should closely match its predicted range. Conversely, if biotic factors are more important in determining range limits, then the predicted range of each species should extend beyond the contact zone. We use this approach to measure the influence of abiotic and biotic factors in shaping species distribution patterns, and discuss the evolutionary implications regarding hybridization and speciation.

The genetic architecture of recombination rate variation in Drosophila melanogaster

Chad Hunter, Nadia Singh

Saturday, June 21, 2014 -Poster #62
Meiotic recombination is an essential biological process, necessary for proper chromosome segregation in many organisms. Despite this importance, rates of recombination are highly variable. The genetic architecture of this variation remains poorly understood, especially in the model organism Drosophila melanogaster. We sought to identify the genetic basis of recombination rate variation using whole genome association mapping. We leveraged the Drosophila Genetic Reference Panel for this purpose and measured rates of meiotic recombination on two chromosomes in 205 fully sequenced inbred lines. Recombination rates were measured using a two-step crossing exploiting recessive morphological markers. We scored over a 500,000 progeny, empowering precise estimation of recombination rate variation among lines. Rates of recombination varied 1.8-3.5 fold among lines on the two chromosomes. Much of this variation is genetic, with estimates of broad-sense heritability exceeding 22% in both cases. We also performed a genome-wide association to identify genetic factors contributing to recombination rate. Our resulting candidate gene list includes a subset of genes possessing multiple C2H2 zinc fingers very similar to PRDM9, which was recently shown to associate with recombination hotspot locations in mice and humans. Other promising candidate genes include genes showing sequence-specific DNA binding transcription factor activity and protein binding functions. Our results thus provide comprehensive insight into the scale and scope of population-level variation in recombination rate in Drosophila. Moreover, our unbiased association mapping approach promises to reveal genes and alleles mediating this variation for the first time. We now stand poised to understand the genetic architecture of an essential biological process in a genetic and genomic model system.

Explaining population dynamics of two threatened prairie orchids through GIS modeling and next-generation sequencing

Andrea Ravelo, Steve Buback, Gavin Conant, J. Chris Pires

Saturday, June 21, 2014 -Poster #63
The prairie fringed orchids, Platanthera praeclara and P. leucophaea, have undergone severe habitat reduction and fragmentation due to the cultivation and development of the prairies of North America. They are currently federally listed as threatened and have been the focus of several initiatives for recovery and reintroduction of viable populations. Despite widespread interest in their conservation status, there are still many unknowns concerning their biological relationship with pollinators and mycorhizal fungi as well as the climatic and environmental factors affecting their populations. This study proposes to create a GIS model that integrates historical population data with several environmental variables in hopes of elucidating the primary factors affecting the orchids' distribution and abundance in the state of Missouri. This study will also look at the soil microbiota community profile associated with these populations by implementing a metagenomic soil study. The symbiotic relationship that Platanthera orchids maintain throughout their lifetime with mycorrhizal fungi is putatively a determining factor in their successful establishment in otherwise adequate habitat. This initiative could establish a baseline representation of the biotic soil characteristics that should be taken into account when evaluating potential habitat for species reintroduction and management.

Evolutionary genetic consequences of a catastrophic event: impacts of Volcan Puyehue on the colonial tuco-tuco

Jeremy Hsu, Eileen Lacey, Elizabeth Hadly

Saturday, June 21, 2014 -Poster #64
The genetic consequences of extreme environmental perturbations are not well understood. Studies of the colonial tuco-tuco (Ctenomys sociabilis) provide a rare opportunity to explore this theme. This herbivorous subterranean rodent is endemic to Neuquen Province, Argentina, where it has experienced ashfall from repeated eruptions of Volcan Puyehue, the most recent of which occurred in June 2011. A robust time series of bone and

tissue samples dating from 10,000 years before present to AD 2012, combined with demographic data from the past 21 years, allows insight into the evolutionary history of the species. Here, we examine the impact of the most recent eruption on genetic structure and polymorphism using both molecular markers and a high-throughput sequencing strategy, the first use in this non-model organism. We compared changes in observed heterozygosity across molecular markers following the June 2011 eruption, and use double digest restriction-site associated DNA sequencing to gain a broader perspective on population level statistics. Finally, we will use a theoretical modeling framework to infer demographic parameters and events from these genetic and genomic datasets.

Comparative Niche Modeling in Common Gartersnake (Thamnophis sirtalis) Subspecies

Kayla Key, Joshua Banta, Andy Gluesenkamp, Marsha Williams, John Placyk

Saturday, June 21, 2014 -Poster #65

The common gartersnake, Thamnophis sirtalis, is known for its extensive geographic distribution that ranges farther north than any other snake species in the Western Hemisphere and from the Atlantic Coast to the Pacific Coast of the USA. Given the wide geographical range of T.sirtalis, it often displays morphological characters that differ from one geographic range to the next and this has resulted in 11 subspecies being described. Although there is much information on the evolution, ecology, and life-history of Thamnophis sirtalis, as a species, information on specific subspecies can be vague or non-existent. In Texas, three of Thamnophis sirtalis subspecies (T. s annectens, T. s. parietalis, and T. s. sirtalis sirtalis) occur in relatively close proximity often times having range overlap. T. s. annectens was initially described in 1950 based on morphology and geographic distribution that differ from T. s. parietalis and T. s. sirtalis. No further work has been conducted to verify its taxonomic status or explore its specific habitat requirements. This information is pertinent to conservation efforts as T. s. annectens has recently been listed as state imperiled in Texas. By comparing ecological niche models for T. s. annectens, T. s. parietalis, and T. s. sirtalis, we can examine the different environmental variables that may be important to each subspecies and explore the potential use of niche modeling as a tool for species delimitation.

Updating the phylogeny of Rhagoletis: Relationships of the North American species groups

Daniel Hulbert, Jim Smith

Saturday, June 21, 2014 -Poster #66

Flies in the genus Rhagoletis (Diptera: Tephritidae) are of interest to evolutionary biologists as models for studying speciation processes, and their coevolutionary relationships with braconid (egg, larval) and diapriid (pupal) parasitoids. Despite several analyses based on morphology, allozymes, and mitochondrial DNA, the phylogenetic relationships of Bush's five North American Rhagoletis species groups (pomonella, tabellaria, cingulata, suavis, and ribicola) remain unresolved. Further, the North American Rhagoletis taxa apparently do not represent a monophyletic group. For example, the Palearctic R. flavigenualis and R. batava are members of a well-supported clade that contains the North American species groups. Thus, the main goals of research presented here were to determine phylogenetic placements within and relationships of the North American Rhagoletis species groups, and to identify monophyletic groups within the genus. Our work to date includes sequences of the mitochondrial COI barcode region, plus two nuclear genes (ribosomal 28S rRNA gene and CAD). While largely congruent, the mitochondrial COI phylogeny has areas of incongruence with respect to the CAD phylogeny. For example, the unplaced Nearctic cherry-infesting R. fausta is strongly supported as sister to the juniper-infesting R. juniperina in the COI tree, while it is basal to all of the Nearctic species in the CAD tree. Interestingly, juniper may have served as an ancestral host for a number of Nearctic Rhagoletis species. The Palearctic juniper-infesting R. flavigenualis is supported as sister to R. juniperina in the CAD tree and is allied with R. juniperina and the dogwood-infesting R. tabellaria group in the COI tree. Nuclear 28S sequences are currently being incorporated into the analyses and key taxa that are missing from our current analyses, for example R. ribicola and the buffaloberry fly, are on our collection list for 2014.

Investigating the molecular basis of female-to-male sex change in fish

Hui Liu, Melissa Slane, John Godwin, Kim Rutherford, Neil Gemmell

Saturday, June 21, 2014 -Poster #67

Socially-induced sex change is a common phenomenon in marine fishes. The Caribbean bluehead wrasse (Thalassoma bifasciatum), for example, exhibits female-to-male (protogynous) functional sex change based on social context: when the dominant male disappears, the largest female initiates sex change to replace him. This process entails a series of radical alterations at morphological, behavioral and physiological levels, which makes the bluehead wrasse a good experimental model for understanding plasticity of sexual development in response to the environment. Recent research suggests that, during sex change, social cues gathered by the brain are likely transduced into a cascade of physical signals that travel through the hypothalamic-pituitary-gonadal axis to the gonads, where they mediate steroid hormone synthesis and promote the gonadal transition. We still know little about the details, especially of how this process is regulated at the molecular level. My PhD research uses next generation sequencing approaches to detect what genes are expressed and at what level they are expressed in the brain and gonads at different time points across the sex change process in bluehead wrasses. By analyzing the expression pattern of these genes using downstream bioinformatics tools, we hope to gain a better understanding of how sex change is controlled at the most fundamental level in fish. In a more general sense, we anticipate this study will also provide important insights into the sex differentiation mechanisms, as well as behavioral and phenotypic plasticity in response to the environment.

Postmating Prezygotic Barriers to Gene Exchange in Rapidly Speciating Hawaiian Laupala Crickets

Jon Lambert

Saturday, June 21, 2014 -Poster #68

Speciation biologists want to know what kinds of speciation phenotypes tend to evolve first, initiating lineage divergence. Postmating prezygotic (PMPZ) barriers are a potentially common initial barrier to gene exchange as they often represent the outcome of continual intra- and inter-specific sexual conflict, their underlying mechanisms (reproductive proteins) evolve rapidly, and an incompatabiliity between males and females at any point in the PMPZ timeline results in decreased mating success. Testing hypotheses about which barriers evolve first requires investigating rapidly speciating systems, where it might be possible to disentangle which phenotypes diverge first. Here we test for PMPZ isolation between two sister species of Hawaiian Laupala crickets, a rapidly speciating complex. Laupala species are primarily differentiated by male calling song, female preference for song, and cuticular hydrocarbonsm, but PMPZ barriers have never been tested. Here, we find evidence of PMPZ isolation, suggesting future work looking within species, among population could yield insight into the relative origin of PMPZ barriers and other Laupala speciation phenotypes.

Genomic clines and admixture in a natural primate hybrid zone

Marcella Baiz, Liliana Cortes Ortiz

Saturday, June 21, 2014 -Poster #69

Studies of speciation seek to understand the genomic basis of reproductive isolation. Identifying the loci that drive divergence and maintain isolation in natural populations can reveal the importance of different mechanisms that operate during the speciation process. Previously, several studies have identified a “large X effect” in the genetics of animal speciation. Loci that maintain isolation in the face of gene flow (i.e., barrier loci) can be identified by looking at differential patterns of introgression of genomic markers. Here, I examine patterns of genomic concordance and introgression at X-linked markers in a natural primate hybrid zone (Alouatta pigra x A. palliata) and compare them to other types of loci. Among admixed males, X haplotypes were highly concordant with ancestry at other markers and showed evidence for reduced introgression. These lines of evidence suggest that the X chromosome might be driving reproductive isolation in these species, supporting the idea of a large X effect across taxa. Consistent results in future analyses with greater coverage in genomic data and more extensive sampling will strengthen this interpretation.

Mechanisms by which phenotypic plasticity promotes and hinders ecological speciation

Etsuko Nonaka, Richard Svanbäck, Xavier Thibert-Plante, Göran Englund, Åke Brännström

Saturday, June 21, 2014 -Poster #70

Adaptive phenotypic plasticity can both promote and hinder ecological speciation by altering selection and gene flow. Several conceptual models emphasize the roles of plasticity in promoting diversification and speciation in populations exhibiting resource polymorphism. These models predict that plasticity plays a critical role in the early stages of speciation by facilitating fast phenotypic divergence, prior to genetic divergence. The ability to express plastic alternative phenotypes may, however, interfere with the early phase of the formation of reproductive barriers, especially in the absence of geographic barriers. Here, we quantitatively investigate the mechanisms under which plasticity can promote and hinder ecological speciation. We use a stochastic individual-based model of predator-prey that incorporates sexual reproduction and mate choice in the predator. The results show that evolving plasticity promotes ecological speciation when habitat choice is adaptive and there is an intermediate level of mate choice. Plasticity can also hinder ecological speciation when adaptive habitat choice is weak or absent. Plasticity facilitates speciation by accentuating phenotypes in adaptive directions and by facilitating adaptive habitat choice and assortative mating. High phenotypic differentiation appeared early in the diversification process. We conclude that the major role of plasticity contributing to ecological speciation is to accelerate the evolution of a reproductive barrier through enhanced phenotypic differentiation between emerging locally adapted phenotypes.

Genomic regions of intraspecific divergence in a homoploid hybrid species

Cassandra Trier, Glenn-Peter Sætre

Saturday, June 21, 2014 -Poster #71

The Italian sparrow (Passer italiae) is a hybrid species that has arisen from past hybridization between Spanish sparrows (Passer hispaniolensis) and house sparrows (Passer domesticus). The Italian sparrow maintains the same number of chromosomes as its parent taxa, making it one of the few documented cases of homoploid hybrid speciation in animals. Homoploid hybrid speciation is thought to be a difficult process because the hybrid must develop reproductive barriers against both parents and recent evidence has shown that mito-nuclear and sex-linked incompatibilities may play a principal role in reproductive barriers in this system. However, sharp shifts in genomic clines and a gradual shift in plumage traits has also been exhibited within the Italian sparrow’s range. Though sex linked and mito-nuclear incompatibilities are the most likely drivers of interspecific divergence between the taxa, areas of intraspecific adaptive divergence in the Italian sparrow may be more likely to evolve on autosomes where there is a lower likelihood of linkage to incompatibility genes. This paper aims to examine which genomic regions are involved in intraspecific variation in the Italian sparrow and if autosomes more likely to hold the genes underlying local adaptation in this system. We plan to utilize a population genomics approach to investigate genomic divergence in three geographically distant and phenotypically distinct populations of the Italian sparrow.

Genomic signatures of rapid adaptive divergence in the Swamp Sparrow

Petra Deane-Coe, Steven Bogdanowicz, Irby Lovette, Rick Harrison

Saturday, June 21, 2014 -Poster #72
A subspecies of swamp sparrow restricted to the tidal marshes of Delaware and Chesapeake Bays (Melospiza georgiana nigrescens) differs from its widespread sister taxon (M. g. georgiana) in a number of adaptive traits associated with tidal marsh habitats. The two subspecies have diverged recently, probably since the last postglacial maximum (

Hybrid songbirds employ intermediate routes in a migratory divide

Kira Delmore, Darren Irwin

Saturday, June 21, 2014 -Poster #73
Migratory divides are contact zones between populations that use different routes to navigate around unsuitable areas on seasonal migration. Hybrids in divides have been predicted to employ intermediate routes that are inferior to those of parental forms. We provide the first direct test of this hypothesis, using light-level geolocators to track birds breeding in a hybrid zone between Swainson's thrushes in western Canada. Compared to parental forms, hybrids exhibited increased variability in their migratory routes, with some using intermediate routes that crossed arid and mountainous regions, and some using the same routes as one parental group on fall migration and the other on spring migration. Hybrids also tended to use geographically intermediate wintering sites. Analysis of genetic variation across the hybrid zone suggests strong selection against hybrids. These results indicate that seasonal migratory behaviour might be a source of selection against hybrids, supporting a possible role for migration in speciation.

It's inner beauty that counts: ecomorphological diversification of feeding morphologies in the Neotropical fish superfamily Anostomoidea

Benjamin Frable, Brian Sidlauskas

Saturday, June 21, 2014 -Poster #74
The hyper-abundant Neotropical freshwater fish superfamily Anostomoidea contains two groups with seemingly disparate evolutionary strategies. The first, Anostomidae, represents ~150 species with wide variation in body coloration, mouth position, tooth shape and trophic strategies ranging from herbivory to insectivory and even freshwater spongivory. The other major group, families Curimatidae, Chilodontidae and Prochilodontidae, contains around the same number of species but its members are generally silvery with little pigmentation, limited variation in mouth position and reduced dentition. All feed mostly on detritus, or decaying organic matter and associated microorganisms. Although the detritivores may be superficially similar, they vary among at the familial and generic levels in the arrangement of the gill arches, which are used in processing food. We investigate 1) how a group that presumably feeds on the same resource can exhibit similar species diversity to the ecomorphologically diverse Anostomidae, 2) whether detritivore gill arches are more diverse than anostomids, 3) whether the shape of detritivore gill arches evolves faster than anostomid gill arches and finally 4) if there is a relationship between ecomorphological diversity and lineage diversification rates. To answer these questions, we generated the first time-calibrated phylogenies for the Anostomoidea, collected multivariate morphometric data of ventral gill arch shape for over 70% of known species, and determined rates of phenotypic evolution and diversification. This system provides a crucial example for investigating the role of ecomorphology in diversification and whether detritivory encompasses a spectrum of morphological and ecological specialization.

Importance of Museum Specimens versus Literature Data for Distribution Records, a Case Study with Cicadas

Kreshnik Jusufi, Geert Goemans, Chris Simon

Saturday, June 21, 2014 -Poster #75
The importance of the maintenance and further addition of biological specimens to museum collections is demonstrated by comparing distribution records of museum specimens of three species of cicadas from the tribe Zammarini (Hemiptera:Cicadidae); Zammara smargdina, Z. smaragdula, and Z. tympanum, with distribution as recorded in the available literature. Stored museum specimens present researchers with valuable taxonomic information that literature records alone cannot provide and help to improve databased museum specimen distribution records. The implementation of new digital systematic techniques makes museum collections all the more useful to researchers and illustrates one of the many values of continued funding of science museums and technology centers across the globe. Accurately databased museum specimens can be an invaluable source of information to scientists and researchers across all biological disciplines.

---

anyFish: a free, open-source software platform for generating animated fish models to study behavior

Spencer Ingley, Chengde Wu, Mohammad Rahmani Asl, Mahmoud Islam Abdelhay Gadelhak, Rongfeng Cui, Jon Simpson, Jerald Johnson, Wei Yan, Gil Rosenthal

Saturday, June 21, 2014 -Poster #76
Experimental approaches to studying behaviors based on visual signals are ubiquitous, yet these studies are severely limited by the inability or difficulty of combining realistic models (e.g., live fish) with the manipulation of signals in isolation. Recently, computer animations have become a promising way to break this trade-off by allowing controlled manipulation of a single visual cue while holding the rest of the stimulus constant. However, computer

animations are often prohibitively expensive, difficult, and time consuming, thus limiting their utility in behavioral research. Here, we present a free, open-source software called ‘anyFish,’ which allows end-users to create realistic animated 3D fish models on a user-friendly platform. Both the physical appearance and behavior of the model can easily be modified by the end-user to suit virtually any specific needs. In addition to providing a powerful experimental tool for studying animal behavior, anyFish serves as a model for transparency, repeatability, and collaboration unmatched by other tools in animal behavior research.

The Generation of Ontology: negotiating the organism's place in evolutionary theory

Max Dresow, Emilie Snell-Rood

Saturday, June 21, 2014 -Poster #77

Amid calls for a “new” or “extended” evolutionary synthesis, great importance attaches to issues of ontology. Accordingly, recent years have seen problems of ontogenesis and organism attacked with renewed vigor, by biologists and philosophers alike. No consensus and few trends have yet emerged from these investigations. Notwithstanding, it is possible to discern two background assumptions that have served to structure much of the inquiry. The first is that reproduction consists, at bedrock, in the transmission of hereditary material, however packaged. Thus species and genes, as well as organisms, reproduce in an evolutionarily meaningful sense. The second is that “fitness” represents a propensity or probabilistic disposition of individuals. In other words, measures of fitness pick out some objective characteristic of an individual, such as its propensity to produce n offspring in a given environment. These background assumptions – while they encode important insights – are heavily informed by modeling conventions and engrained modes of speech. Here, I begin to develop a complementary perspective, which uses a philosophical approach to explore information and reproduction in their material aspects. Such an approach represents a useful supplement to the formal dimensions of evolutionary theory, and may help situate concepts of organism and ontogeny within the familiar channels of evolutionary thought.

Keywords: constraints, evolution, individual, information, ontology, organism

---

Using microsatellite loci to distinguish detween members of the Peromyscus leucopus species group

Hayden Pehl, Sean Beckmann, Lauren Hyser

Saturday, June 21, 2014 -Poster #78

Among rodent taxa it is frequently difficult to distinguish between sister taxa in areas of sympatry utilizing morphological characteristics. Within the Peromyscus leucopus species group, range overlap and morphological similarity are particularly burdensome when distinguishing between, P. leucopus and P. gossypinus. Further, identification of a rapid, low cost, reliable genetic marker to distinguish between these sister taxa has been difficult. To date, presence/absence assays have been proposed to distinguish between the species electrophoretically. However, these assays are prone to misidentification due poorly/non-amplifying specimens. Microsatellites provide the opportunity for markers that will amplify in both species and distinguish between them. In this study specimens of both P. gossypinus and P. leucopus were genotyped at 26 microsatellite loci developed in other Peromyscus species. Specimens were collected throughout the range of both species, including sympatric areas, and genotypes were compared electrophoretically on 3% agarose gels. Among these a single locus (Bw4-5) reliably distinguished between P. leucopus and P. gossypinus while successfully amplifying in both species. This has valuable applications for both rapid identification of morphologically intermediate field specimens as well as identification of museum specimens to species when current identifications are unknown or questionable. Finally, this marker has potential applications for the identification of hybridization between these two species in the wild.

Keywords: Microsatellite, Sister Taxa, Peromyscus

Applications of Circos beyond genomics

Christopher Campbell, Peter Larsen, Christopher Blair, Anne Yoder

Saturday, June 21, 2014 -Poster #79

The Circos software package allows for the visualization of data in circular layouts and it is especially useful for depicting relationships within complex data, specifically genomic datasets. Though Circos diagrams have frequently been used to depict genomic data the popularity of the software has grown and more disciplines (outside of genomics) are using Circos for data visualization. Nevertheless, of the greater than 500 manuscripts that have utilized Circos, relatively few are focused on research topics familiar to evolutionary biologists (e.g. phylogeography, systematics, natural history, etc.). Here we show how our lab has utilized Circos to visualize datasets originating from studies focused on lemur evolution. The Circos diagrams that we have generated allow for the visualization of patterns within an array of datasets, ranging from natural history and systematics to eco-immunology and molecular evolution. There are endless applications for the Circos software package, including an array untapped of possibilities within Evolutionary Biology.

FlatNJ: A Novel Network-Based Approach to Visualize Evolutionary and Biogeographical Relationships

Monika Balvociute, Andreas Spillner, Vincent Moulton

Saturday, June 21, 2014 -Poster #80

We introduce FlatNJ, a new method for producing a special type of phylogenetic networks known as planar split networks. Properties of these networks will be discussed by showing a few application examples followed by an overview of the method itself, which generalizies the popular NeighborNet method.

Planar split networks are a type of phylogenetic networks that can be drawn in the plane without edge crossings, facilitating exploratory data analysis. They can be used to detect and visualize potential relationships between sequence evolution and other aspects of a data set such as, for example, the geographic distribution of the corresponding organisms as well as indicate possible conflict in the data (e.g., in case of recombination). The main advantage of using planar split networks instead of phylogenetic trees is their ability to provide a more complete overview of the data when a single tree is not appropriate.

Phenotypic Plasticity of the Pharyngeal Jaw in the Parachromis Managuensis Cichild Fish

Carson Cope, Brian Langerhans

Saturday, June 21, 2014 -Poster #81
ABSTRACT

Cichlid fishes represent a remarkable case of adaptive radiation, as the majority of the African members of the family evolved around half a million years ago in response to the forming of the Great Rift Valley's lakes. Cichlids have also diversified into hundreds, or even thousands of species with a wide range of lifestyles and span four continents. Diet-induced phenotypic plasticity of the pharyngeal jaw is suspected to represent a key trait facilitating much of this diversification. The ability to develop appropriate pharyngeal jaws to exploit locally under-utilized resources—even food items typically difficult to consume, such as hard-shelled prey—would enhance colonization of novel environments and shifts to novel resources, helping to explain their diversification and wide range. But the extent to which this ability occurs throughout the family is unknown. Here, we conducted a feeding experiment to test for diet-induced pharyngeal jaw plasticity in the Central American cichlid Parachromis managuensis, which typically consumes fishes and macroinvertebrates in the wild. We fed two similar sized and aged fish two different diets: hard-shelled prey (Physa sp. snails) and soft prey (fish flakes). Both prey were readily eaten by the fish, and the shells were crushed with the pharyngeal jaws despite the fish being only ~80 mm standard length. In only six weeks, we found that the snail diet induced a heavier, shorter, and wider pharyngeal jaw, matching predictions and previous empirical findings in other species known to enhance shell-crushing ability. These findings suggest that such plasticity might be widespread throughout the family and represent a key innovation facilitating rapid diversification.

Population variation in age and size at metamorphosis in different morphs of spadefoot toads

Katrina Pfennig, Elsa Pfennig, David Pfennig, Karin Pfennig

Saturday, June 21, 2014 -Poster #82
Spadefoot toad tadpoles occur as different morphs: carnivores and omnivores. Carnivores eat shrimp and smaller tadpoles, whereas omnivores eat algae and detritus. Past research has shown that carnivores develop faster and are bigger than omnivores once they develop. However, this past research was based on only one population. We tested whether or not this pattern was in only one population, or various populations.

Analysis of the genetic adaptation of two Arabidopsis strains to high concentrations of heavy metals

Maggie Lassiter, Alex Ludwig, Hari Madhu, Cere Poovey

Saturday, June 21, 2014 -Poster #83
The experiment is designed to test the effects of heavy metal pollutants on different Arabidopsis strains. This is important because heavy metals are often found in high levels in storm water runoff (45-90 µg/L) which would negatively affect the growth of plants. Once the heavy metal has settled into the soil tests can be conducted to determine which strand of Arabidopsis will grow most successfully. Since the Arabidopsis strand Santa Clara is naturally found in areas with high concentrations of heavy metals is should have genetic variations due to adaptations that would allow it to grow more successfully in soil with high concentrations of heavy metals. Hypothetically, Santa Clara will be affected less than the Columbia control strain in the presence of copper powder. In order to test this, both Santa Clara and Columbia strains will be exposed to levels of copper powder often found in runoff and compared to both a control and each other to determine with strain is the most able to grow in areas with heavy metal toxicity. The genetic differences will then be compared by analyzing the expressed proteins in the plant in an attempt to determine if there is a genetic adaptation that allows Arabidopsis to withstand heavy metal toxicity. If there is a genetic difference, then this will indicate that the heartier strain has evolved to live in an environment that is less than ideal.

Citizen Science: Engaging Students in Authentic Scientific Research

Lea Shell, Kristin Bedell

Saturday, June 21, 2014 -Poster #84
Through this poster presentation, viewers will gain the knowledge and confidence needed to effectively introduce citizen science projects to students and families. Incorporating citizen science into the classroom allows learners from pre-K to adult to participate in low-cost, authentic scientific research, providing a context for scientific discussions that extend beyond the classroom walls into the homes of students and families.

We will examine ways in which protocols available from the Your Wild Life team and Dunn Lab at NC State University are implemented in classrooms in order to help students reach the levels of understanding set by the National Research Council Disciplinary Core Ideas in Life Science. Through this poster session, attendees will learn the protocols and receive information about access to materials to use with students and their families. In addition, participants will consider practical applications for citizen science protocols in the classroom by considering one district's journey and viewing samples of elementary student work. Finally, participants will learn about ways to use Your Wild Life's citizen science projects to foster discussion around biodiversity and interdependence.

Analysis of Cancer-Related Genes in the Wnt Signaling Pathway

Tingzhou Meng

Saturday, June 21, 2014 -Poster #85
This experiment analyzed effects of four Wnt-signaling genes, APR-1, BAR-1, LRP-2 and MOM-5, on embryonic development of the model system, Caenorhabditis elegans, using RNA interference to inhibit their gene expressions. The goal of this research was to determine the importance of these genes and thus to infer the probability and severity to cause cancer when their human orthologs mutate, since the Wnt-signaling pathway is usually dysregulated in cancer cells. Two different genetic backgrounds of C. elegans were utilized: wild-type (N2) strain and double-mutant (ced-9/end-3) strain. A significantly higher percent of embryonic lethality in a silenced gene than the negative control indicated that the gene is essential on the Wnt-signaling pathway. In the normal screen, embryonic lethality of APR-1, BAR-1, and LRP-2 were all 0%, and MOM-5 was 24.24%. In the sensitized screen that used the double mutant, embryonic lethality of APR-1 was 8%, and BAR-1 0.28%, LRP-2 6.81%, MOM-5 67.42%. This experiment reports, for the first time, that silence of APR-1 or LRP-2 causes significant embryonic lethality in C. elegans. This experiment reports, also for the first time, that silence of BAR-1 does NOT cause significant embryonic lethality in C. elegans due to gene duplication, which is surprising because its ortholog CTNNB1 in human is known to cause cancer. Chi-square tests statistically support our findings. Further research should be conducted to determine during which stage of embryonic development APR-1, LRP-2 and MOM-5 play important roles, and whether their human orthologs can become new targets for molecular targeted cancer therapy.

The effect of population size on the genetic drift of eye color in Drosophila melanogaster

Jaye Sudweeks, Richard Romano

Saturday, June 21, 2014 -Poster #86
This experiment was preformed to explore the effects of population size on allelic frequencies inside of a population. Fourteen populations of Drosophila were established, half with a population size of 2, and the other with a population size of 16. The allelic frequency of the trait controlling eye color was monitored over 4 generations. Genetic drift occurred, with surviving populations showing different allelic frequencies at the end of four generations.

Female mate choice based on male morphology in Poecelia reticulata

Anjalique Knight, Na'Briya Ware, Etinosa Obanor, Emily McGuirt

Saturday, June 21, 2014 -Poster #87
Sexual selection in guppies (Poecelia reticulata) has been shown to occur via female-choice (Bischoff et al, 1985). Variations in male morphologies (tail size, tail shape, color and coloration patterns) were compared in effectiveness at attracting females. Females were allowed to "choose" males by visual inspection, and time spent in proximity to males with different characteristics was measured. Chi-square analysis was performed to determine significance. Current results are inconclusive.

Effects of UV radiation on survival and reproduction of S. cerevisiae strains with and without DNA-repair mechanisms

Amanda Glen, Abby Blaine, Sydney Cole, Cailee Ladd

Saturday, June 21, 2014 -Poster #88
S. cerevisiae cells deficient in DNA-repair enzymes were used to quantify the extent of damage caused by exposure to UV radiation in comparison to wild-type strains. The evolution of repair mechanisms to combat DNA damage by UV in eukaryotes is of interest, as levels of UV-A and UV-B reaching the earth's surface may be changing in the future due to variation in stratospheric ozone. The effectiveness of various methods of blocking exposure to UV was compared, including physical sunscreens, chemical sunscreens, fabric, plastic and glass. Cells were plated on YEPD and exposed to either natural sunlight or an artificial UV source. A chi-square analysis was performed to determine significance. Current results are inconclusive.

Adaptation for salinity tolerance in two mutant strains of Arabidopsis

Michael Li, Shuyi Wang, Maggie Knostman

Saturday, June 21, 2014 -Poster #89
This experiment tests the salinity tolerance of two mutations of the Col-0 strain of arabidopsis. The first, SOS-1, is known as a salt shock tolerant gene. The other, Abi-5, codes for a transcription factor as part of a signaling network for stress response. Both are exposed to 1M NaCl solution. Measuring the way both respond to the same conditions will tell us which is better adapted for conditions of intense salinity.

The complete mitochondrial genomes of two species of Orconectid crayfishes

Dyani Sabin, Angela Roles

Saturday, June 21, 2014 -Poster #90
Due to it's conserved structure and rapid rate of evolution, the mitochondrial genome is very informative for phylogenetic analyses, including relationships between closely related species. We are studying the interaction between the native Orconectes sanbornii and the invasive O. rusticus, species known to hybridize in rivers invaded by O. rusticus. Hybridization of O. rusticus is also known to occur with another congener, O. propinquus. In previous phylogenetic reconstructions based on mitochondrial loci, neither of the native species is sister to O. rusticus, suggesting great potential for this invader to hybridize with fourteen other closely related congeners. We have sequenced the complete mitochondrial genome of both O. rusticus and O. sanbornii to provide greater insight into the relationship between these species

as well as identify mitochondrial fixed differences between them, which may be useful in studies of hybridization, especially in assessing directionality. We compare our full mtDNA genome sequences to the three other complete mitochondrial genomes available for crayfish, and examine specific mitochondrial loci for which data is available for a broader sample of crayfish species. Gene order and number are conserved relative to other crayfish in the Cambaridae family. Our focal species exhibit 92.4 percent mitochondrial genome identity and about 1200 base differences that are candidates for species-diagnostic variation.

CHARACTERIZATION AND EVOLUTIONARY ANALYSIS OF THE HIGHLY DIVERSE LATROTOXIN VENOM GENE FAMILY FROM THE COMMON HOUSE SPIDER GENOME

Kerry Gendreau, Robert Haney, Jessica Garb

Saturday, June 21, 2014 -Poster #91

Animal venoms attract wide scientific attention because of their biomedical applications and are an excellent model for understanding the origins and diversification of ecologically important genes. Black widow spiders (Latrodectus spp.), infamous for their potent venom, produce an assortment of toxic proteins that alter neuronal function and signaling. One such protein is α-latrotoxin, the molecule responsible for the extreme pain, paralysis, and death occurring in vertebrates injected with Latrodectus venom. While most studies of black widow venom have focused on α-latrotoxin, little is known about the diversity and evolution of the latrotoxin gene family. Accordingly, we used bioinformatics tools to investigate latrotoxin evolution from the recently sequenced genome of the house spider Parasteatoda tepidariorum, a close relative of the black widow. We have identified forty-five latrotoxin genes from the P. tepidariorum genome, many of which are arranged in tandem clusters on two genomic scaffolds, providing evidence of gene family expansion through non-homologous recombination. Bayesian phylogenetic analysis of latrotoxin protein translations indicates that Parasteatoda and Latrodectus species possess distinctly different sets of latrotoxin genes, due to significant lineage specific gene duplications since the divergence of these genera. Structural analyses of latrotoxins predicted from the house spider genome indicate they contain a greater diversity of functional domains than previously seen in latrotoxins, including differing numbers of ankyrin repeats, transmembrane regions, and coiled-coils. This suggests that latrotoxins substantially differ in their activities as neurotoxins, and in their affinities for extra-organism cellular targets. Current work is focused on relating house spider transcriptional data to its genome to determine how latrotoxin venom expression differs between the house spider and black widow species.

Notung 2.7: Software platform for reconciling gene and species trees to infer duplications, losses, and transfers

Minli Xu, Han Lai, Maureen Stolzer, Dannie Durand

Saturday, June 21, 2014 -Poster #92

Gene events, including gene duplication, transfer and loss, are three major forces driving the evolution of genetic novelty. The history of events in a gene family can be inferred by comparing the gene tree with the corresponding species tree to find the series of gene events that best explains the incongruence between them. This process is called reconciliation. Previous reconciliation software focused on models of duplication and loss only for eukaryotes or transfer and loss only for prokaryotes. However, accumulating evidence suggests that, in some species, both duplication and transfers are active processes. To answer the need for a new model for inferring all three gene events, we introduce Notung 2.7, Java-based software incorporating a novel algorithm to infer duplication, transfer and loss in gene tree and species tree reconciliation. It can also distinguish between the incongruence caused by gene events and the incongruence caused by incomplete lineage sorting, therefore reducing over-estimation of gene events. When both duplication and transfer are considered, there can be more than one optimal event history. Notung2.7 also provides an option to generate all such event histories and guarantees that the histories are temporally feasible, i.e., do not include transfers that travel backwards in time. A graphical user interface allows the user to visualize the event history on the gene tree and explore how various parameter choices can influence the inferred evolutionary history. High-throughput analysis can be accomplished under a command-line mode where Notung2.7 can automatically analyze genome-scale phylogenetic datasets and also summarize the events over all optimal event histories of all gene trees. The software package is free to download at http://www.cs.cmu.edu/~durand/Notung/index27.html. The distribution package also includes a detailed manual and working examples with sample gene and species trees.

Complete mitochondrial genome sequences reveal that independent control region duplications (usually) result in identical gene orders in parrots

Jessica Eberhard, Erin Schirtzinger, Timothy Wright

Saturday, June 21, 2014 -Poster #93

Mitochondrial genomes are generally thought to be under selection for compactness, due to their small size, consistent gene content, and a general lack of introns, gene duplications or intergenic spacers. As more animal mitochondrial genomes are fully sequenced, rearrangements resulting from tandem gene duplications are being identified with increasing frequency, particularly in birds. Understanding the underlying mechanisms, evolutionary dynamics, and fitness consequences of these duplications remains an ongoing challenge. In this study, we investigate the evolutionary history of mitochondrial control region states within the avian order Psittaciformes (parrots and cockatoos, hereafter ‘parrots’). To this aim, we reconstructed a comprehensive multi-locus phylogeny of the parrots, used PCR of three diagnostic fragments to classify the mitochondrial control region state as single or duplicated, and mapped these states onto the phylogeny. Ancestral state reconstruction using a range of weighting schemes identified six independent origins of mitochondrial control region duplications within the parrots. We further investigated gene order by sequencing the complete mitochondrial genomes of 10 parrots species and comparing these to complete genomes of 12 other parrots downloaded from Genbank, including a representative of each of the six clades with independent duplications. All sixteen taxa with the presumably ancestral single control region state showed the same gene order. Likewise, with only one exception, the six species with independently derived mitochondrial control region duplications had similar gene orders around and within the area of tandem duplication. There was, however variation among these taxa in the degree of degradation of the duplicated genes and tRNAs, and in the level of sequence similarity in the duplicated control regions. Further investigations into the fates of duplicated genes, the potential costs and benefits of having a second control region, and the complex relationship between evolutionary rates, selection, and time since duplication are needed to fully explain these patterns in the mitochondrial genome.

SimPhy: Comprehensive simulation of gene, locus and species trees at the genome-wide level

Diego Mallo, Leonardo de Oliveira Martins, David Posada

Saturday, June 21, 2014 -Poster #94

We present SimPhy, a new fast and flexible simulation tool to simulate gene family evolution with incomplete lineage sorting (ILS), gene duplication and loss (GDL) and horizontal gene transfer (HGT) at the genome-wide level. The core of this new tool is a generative model based on the recently coined 3-tree paradigm – species tree, locus tree and gene tree. SimPhy has been explicitly designed to implement comprehensive realistic simulation scenarios, with several sources of branch length heterogeneity. A typical SimPhy simulation study is first parameterized with a certain number of species tree replicates and prior distributions for the species tree simulation (including birth and death rates, number of individuals per species, ingroup/outgroup distance, generation time, population size and related sources of heterogeneity), locus tree simulation (including number of gene families; birth, death and transfer rates and locus-specific rate heterogeneity) and gene tree simulation (including gene tree branch-specific rate heterogeneity).Then SimPhy starts the simulation of species, locus and gene trees, sampling the parameters from prior statistical distributions, and generating trees, reconciliations and sequences (the latter using Indelible), saving all the information directly to a database. Thus, SimPhy could be used not only to perform classical grid-like simulation studies, accepting fixed parameters, but more importantly, is able to generate simulations under continuous parameter landscape. SimPhy could be used to study the interaction between the processes that generate species tree / gene tree incongruence and to perform thorough evaluations of phylogenomic methodologies.

Student-centered active learning curriculum in evolutionary biology

Andrew Martin, Sarah Seiter

Saturday, June 21, 2014 -Poster #95

Evolutionary biology is often taught in a large-enrollment, lecture-style format. I have developed student-centered active learning lessons for teaching evolutionary biology. I highlight various features of the curriculum, including the learning goals, measures of learning gains, and various tools for advancing student's science process skills. The purpose of the poster is to stimulate conversation on how to best accomplish educating students to become effective citizen science with a good understanding of the principles of evolution and the ability to apply the principles across diverse contexts. All materials for the course are available on request.

Increasing student engagement in STEM through an authentic research introductory biology laboratory course

Jane Indorf, David Janos, Michael Gaines

Saturday, June 21, 2014 -Poster #96

A Howard Hughes Medical Institute-funded introductory biology laboratory course at the University of Miami (UM) exposes students to authentic scientific research during their first year as undergraduates. Instead of a traditional ‘cookbook’ style lab in which a particular outcome is expected, students perform inquiry-based group research projects led by a multi-generational team consisting of a research faculty mentor, a graduate student, and an advanced undergraduate peer facilitator. The research projects are based on the faculty mentor’s research area, but allow students to investigate their own hypotheses with their own experiment designs. This creates a sense of ownership of their research and connects each student on a personal level with the process of genuine scientific inquiry. Student research projects have focused on topics such as population genetics, symbiosis, gene expression, and behavioral ecology.

Based on 10 years of data, we have found that students who take these labs are twice as likely to have subsequent individual research experiences as students with matched SAT scores who take our traditional introductory biology labs. Each semester we use David Lopatto’s Classroom Undergraduate Research Experience (CURE) survey to evaluate UM’s authentic research biology labs. Students who take the authentic research laboratory course report greater gains in research-related skills than the aggregate scores of all students surveyed. Both formative and summative data show that these labs are highly successful in increasing student engagement in STEM. With this success, our next step is to expand these labs to serve additional students and to integrate the lab course with chemistry in order to expose students to the interdisciplinary nature of scientific research.

DNA barcoding gap: Reliable species identification over morphological and geographical scales

Klemen Čandek, Matjaz Kuntner

Saturday, June 21, 2014 -Poster #97

The philosophical basis, and utility of DNA barcoding has been a subject of numerous debates. While most literature embraces it, some studies continue to question its use in dipterans, butterflies, and marine gastropods. Here, we explore the utility of DNA barcoding in identifying spider species that vary in taxonomic affiliation, morphological diagnosibility and geographic distribution. Our first test searched for a "barcoding gap" by comparing intra- and interspecific means, medians and overlap in more than 75,000 computed Kimura 2 parameter (K2P) genetic distances in three families. Our second test compared K2P distances of congeneric species with high versus low morphological distinctness in 20 genera of 11 families. Our third test explored the effect of enlarging geographical sampling area at a continental scale on genetic variability in DNA barcodes within 20 species of nine families. Our results generally point towards a high utility of DNA barcodes in identifying spider species. However, the size of the barcoding gap strongly depends on taxonomic groups and practices. It is becoming critical to define the barcoding gap statistically more consistently, and to document its variation over taxonomic scales. Our results support models of independent patterns of morphological and molecular evolution by showing that DNA barcodes are effective in species identification regardless of their morphological diagnosibility. We also show that DNA barcodes represent an effective tool for identifying spider species over geographic scales, yet their variation contains useful biogeographic information.

Linking to Literature to Increase Understanding and Decrease Fear about Evolution and Science

John Niedzwiecki, Wyeth Burgess

Saturday, June 21, 2014 -Poster #98

Two of the greatest obstacles to teaching science in a general education curriculum are a lack of understanding of the practice of science and a fear of the change it may force upon us through its ideas or technologies. One way to address those fears is by providing a venue for exploring those fears as well as the potential impacts of science on our lives. Science over the past few centuries, and at an acelerting pace over the past few decades, has wrought great changes to our world and our view of ourselves in that world.The Humanities, and Literature in particular provide a way to understand or place in the world, especially in a rapidly shifting world.The general education curriculum or Bell-Core at Belmont University, provides an opportunity to link classes in disparate disiplines through "linked" Learning Communities. The goal of the Learning Community to allow students to see connections between disiplines in their liberal arts education, but it also allows for professors to increase understanding of content specific content, through mutual support and motivation between "linked" class content. Over the past three years, we have linked Biology 1010, a lab science survey course with an english literature course focusing on dystopian writing based on scientific and technological advancements over the past 100 years. Asssignments, linking literature and writing with the scientific process, have aided students in seeing the importance of scientific literacy, have provided a forum to directly discuss the powers and limits of science and perhaps counterintuitively reduce fear of science through this process. In literature, the science content contributes a new perspective to understand the human condition and human fears. Ancedotal evidence suggest that these classes improve student engagement and performance in both classes. We are currently constructing instruments to test this hypothesis.

SDMtoolbox: a python-based GIS toolkit for landscape genetic, biogeographic, and species distribution model analyses

Jason Brown

Saturday, June 21, 2014 -Poster #99

Species distribution models (SDMs, also known as ecological niche models) are broadly used in ecological and evolutionary studies. Almost all SDM methods require extensive data preparation in a geographic information system (GIS) prior to model building. Often this step is cumbersome and if not properly done, can lead to poorly parameterized models or in some cases, if too difficult, prevents the realization of SDMs. SDMtoolbox is designed to facilitate many complicated pre- and post-processing steps commonly required for species distribution modelling and other geospatial analyses. SDMtoolbox is a free comprehensive python-based toolbox to be used in ArcGIS 10.1 (or higher) with the Spatial Analyst extension. The toolkit simplifies many GIS analyses required for species distribution modeling and other analyses, alleviating the need for repetitive and time consuming climate data pre-processing and post-SDM analyses. SDMtoolbox also facilitates advanced modeling in MaxEnt. Spatial jackknifing (or geographically structured k-fold cross-validation) tests evaluation performance of spatially segregated localities. SDMtoolbox splits the landscape into 3-5 regions based on Voronoi polygons and spatial clustering of occurrence points. Models are calibrated with all permutations of the groups using occurrence points and background data from n-1 spatial groups and then evaluated with the withheld group. SDMtoolbox also enables testing different combinations of the five model feature class types and regularization multipliers to optimize model performance.

Mating prescription, proscription, and the time since a common ancestor; a coalescent approach

Russell Campbell

Saturday, June 21, 2014 -Poster #100

The expected time since a common ancestor of two genes in a diploid individual which is 4N+2 (where N is the number of mating pairs, hence 2N is the number of individuals, hence 4N is the number of genes) is initially increased by approximately 4 for each generation that inbreeding is proscribed. This approximation breaks down as the the number of generations inbreeding is proscribed approaches the number for maximum avoidance of inbreeding. The expected time since a common ancestor under maximum avoidance of inbreeding (which entails two progeny per mating pair) is 8N-2, which is also the expected time for random mating with two progeny per mating pair. Hence progeny distribution is a significant component of mating structure for determining the expected time since a common ancestor of two genes in an individual.

Phylogeny of urban ants in North America: Does relatedness predict ant success in cities?

Amy Savage

Saturday, June 21, 2014 -Poster #101

The world is becoming increasingly urban, and evidence is accumulating that non-human species are key to many ecosystem processes and services in cities. However, we have a poor understanding of the ecology and evolution of those species that survive and/or thrive in urban environments. Employing a phylogenetic approach could provide important information about urban diversity and allow us to make predictions about the relative roles of different ecological factors and evolutionary history in structuring urban communities. Because species can vary widely in their contribution to ecosystem services and processes, such differences in urban biodiversity could have cascading, ecosystem-wide consequences. An important step toward gaining an understanding of the phylogeny of urban success will be to assess patterns of phylogenetic relatedness within a taxonomic group that is diverse, widespread, ecologically important, and is commonly found in cities.

In this study, we examined ants across North America. Ants are important to ecosystems worldwide, influencing community structure and ecosystem processes from the tops of canopy trees to the soil underfoot. Furthermore, we have a relatively good understanding of the diversity of ants-particularly in North America, and many species are well-described. Finally, recent work suggests that cities can support diverse ant assemblages. Some species appear to survive in cities, but are restricted to urban parks or forests embedded within complex urban habitat mosaics. Other species apparently thrive in high stress urban habitats, such as street medians. Here, we present findings from phylogenetic analyses of ant occurrences across the United States using data collected by participants in The School of Ants citizen Science project. Importantly, these samples span urban – rural gradients but focus on those species that live near humans and are attracted to human foods. Because cities are comprised of heterogeneous habitat mosaics, we also assessed the phylogenetic relatedness patterns of ants living in habitats with varying levels of chronic environmental stress in three US cities: Raleigh-Durham, Chicago, and New York City. These findings not only inform urban ecology and city planning, but also provide key insights into the role of evolutionary history in determining the diversity of an ecologically important group in urban ecosystems. Such insights are likely to become increasingly relevant as the world becomes more and more urban.

Genome-wide patterns of isolation by time associated with life cycle shifts in the European corn borer

Gabriel Golczer, Brad Coates, Erik Dopman

Saturday, June 21, 2014 -Poster #102

Heritable differences in the timing of reproduction can reduce gene flow and ultimately produce patterns of genetic Isolation By reproductive Time (IBT). We tracked genome-wide patterns of genetic variation across seasons in areas of overlap between populations of Ostrinia nubilalis (European corn borer) displaying two generations per year and one generation per year. At two different sites in Minnesota U.S.A., we found significant genetic differentiation (FST) and shifts in coefficients of membership ( ) as a function of seasonal mating flights and these patterns were repeated across years. In contrast, genetic differentiation was absent at three sites consisting of strictly two-generation populations. Evidence for genome-wide patterns of isolation by time between moth populations differing in life cycle suggests the possibility of widespread but cryptic population genetic structure in insects with variable numbers of generations per year.

Patterns of ecological selection and geographic divergence within a neotropical fruit fly

Kristina Ottens

Saturday, June 21, 2014 -Poster #103

Determining how biodiversity is generated and maintained is crucial to understanding the evolutionary histories of ecological communities. Ultimately, biodiversity results from the evolution of barriers to gene flow, which can result from geographic isolation and/or from divergent ecological selection. We are interested in disentangling the role of geographic isolation and ecological selection in the diversification of a species-rich genus of tropical Tephritid fruit flies. Blepharoneura are highly specialized and host specific flies; most species specialize on a single plant host and flower sex although multiple species may exploit the same resource. At one location in Peru, two plant species (two sexes; four plant niches) are host to 14 Blepharoneura species. Even though many Blepharoneura species overlap in the same host plant, they do not show niche overlap when these niches are defined by lethal interactions with their parasitoids. A recent study by Condon et al. (2014) suggests that diversification in Blepharoneura may be driven by shifts onto new host plants and/or parasitoid pressure (divergent ecological selection). However, phylogenetic analyses based on mitochondrial and nuclear sequences suggest that historical patterns of speciation could also be a result of geographic divergence. To parse apart the ecological and geographic signals underlying the history of Blepharoneura speciation, more rapidly evolving molecular markers are required. Here, I use microsatellites to address this question for three Blepharoneura species (sp21, sp28, and sp30) characterized by differing patterns of host-plant use, parasitism rates, and geographic distribution. Preliminary microsatellite data indicates patterns of ecological divergence associated with host use in one species while the other two species do not show ecological or geographic patterns.

An Integrative Approach to Detecting Cryptic Wild Tomato Species (or How Many Tomato Species Live in the Atacama Desert?)

Andrew Raduski

Saturday, June 21, 2014 -Poster #104
Evidence for the presence of two cryptic tomato species is presented. Solanum chilense, as currently described, occupies a disjunct range on the western slopes of the Andes in northern Chile and southern Peru. Data from disparate sources support the hypothesis that S. chilense is actually composed of two cryptic species corresponding to distinct groups of populations. Biosystematic, morphological, and genetic data are presented and ongoing and future research plans are discussed.

Imaging Kleptoplasty in the Marsh Foraminifera of South Carolina

Megan Cevasco

Saturday, June 21, 2014 -Poster #105
The phenomenon of kleptoplasty in which the plastids of algal prey are sequestered by predators/hosts and are kept functional (photosynthetically active) for an extended period of time (weeks/months), is examined in foraminiferal taxa collected from tidal lagoons habitats along the SC coast. Evidence of the kleptoplastic condition within select taxa is presented using confocal imaging and PCR amplification of plastid sequences retained within the host. The taxonomic identities of both the hosts and the sequestered plastids are determined using sequence data. This investigation supports the existence of and specificity within the kleptoplastic condition in the foraminifera of coastal South Carolina.

The effects of social environment and predation risk on the emergence of personality: an experiment

Tamás Urszán, János Török, Attila Hettyey, László Garamszegi, Gabor Herczeg

Saturday, June 21, 2014 -Poster #106
Understanding the evolutionary background of behavioural consistency (animal personality, behavioural syndrome) is a major challenge in current evolutionary behavioural ecology. While the main focus is on adaptive vs. nonadaptive genetically based mechanisms, less is known about how environmental challenges experienced during ontogeny contribute to the emergence of the phenomenon. Here, we tested how social environment and predation risk affect behavioural consistency of agile frog (Rana temporaria) tadpoles reared in a factorial common garden experiment. We recorded activity and risk-taking in tadpoles reared alone or in groups and in the presence or absence of chemical cues from their predators. We found that both individual behavioural means (representing behavioural type) and individual behavioural variation (representing behavioural precision) were influenced by our treatments. Our results emphasize the importance of direct environmental effects for the emergence of behavioural consistency both within and across behaviours.

Mitochondrial hot spots: recombination, mutation, or selection?

Meggan Alston, Stephen Jensen, Sarah Bradburn, Halie Andersen, Carina Marón, Sílvia Pérez-Espona

Saturday, June 21, 2014 -Poster #107
Multiple substitutions often occur at individual synonymous sites in large samples of conspecific mitochondrial DNA sequences, with a few sites having unexpectedly large numbers relative to the mean. Occasional recombination events between distantly related mitochondrial genomes have been considered as a possible cause of this pattern, as have elevated site-specific mutation rates ("hot spots"). Selection could also simultaneously increase the frequencies of many lineages carrying independent occurrences of a given mutation, especially in a large population with abundant standing variation. An incipient soft sweep of this kind would be hard to distinguish from an elevated site-specific mutation rate. Here we analyze site-specific substitution frequencies in some large data sets for the cox1 genes of several species of marine invertebrates (whale lice and krill). Some very hot synonymous sites are found in all of the data sets, but they occur in different places, even in closely related species (as seen in the nad2 sequences of primates by Galtier et al. 2006). Coalescent simulations suggest that such patterns could be caused by selection, possibly induced by complex epistatic effects of synonymous substitutions on rates of translation (Chevance et al. 2014), which could be sensitive to varying environmental factors such as temperature.

Exploration of conditions favoring the evolution of superfetation using a state dependent life history model

Ashley Edwards, Rebecca Hale

Saturday, June 21, 2014 -Poster #108
Superfetation, the simultaneous development of two or more broods in vitro, is found in a variety of species including marsupials and rodents; however, none are as clearly demonstrated as that of the Heterandriini, a subfamily of poeciliid fish. Superfetation appears to have evolved independently several times within this group, allowing us to explore mechanisms of its evolution. We investigate the effects of resource availability as a factor influencing selection for superfetation using a state-dependent life history model of the least killifish (Heterandria formosa). We manipulate resources availability and evaluate allocation to offspring, fitness consequences conferred on the female, and the model conditions under which the female will fertilize new embryos before the birth of a current brood. This model is designed to generate testable predictions of superfetation occurrence in the field.

Habitat transitions in insects and associated molecular evolutionary patterns

T Fatima Mitterboeck, Sarah J. Adamowicz, Jinzhong Fu

Saturday, June 21, 2014 -Poster #109
Growing public databases of DNA sequence data present new opportunities for broad-scale investigation of patterns of molecular evolution and macroevolution across life. Insects are a species-rich group with diverse biological and ecological traits. Within this group, the evolutionary shift between terrestrial and freshwater habitats has occurred numerous times for both larval and adult life stages. Due to habitat discontinuity in the freshwater realm, we predict that, on average, effective population size of freshwater insects is lower than for species inhabiting the terrestrial realm. If this is true, we would predict genome-wide higher ratios of non-synonymous-to-synonymous (dN/dS) substitutions in freshwater insects; moreover, differing selection regimes between environments may yield marker-specific differences in molecular rates. Using publicly available DNA sequence data, we investigated patterns of molecular evolutionary rates, including overall nucleotide substitution rates and dN/dS ratios, associated with these habitat shifts within the orders Coleoptera, Diptera, Lepidoptera, Hemiptera, Mecoptera, Trichoptera, and Neuroptera. We did not detect any significant overall differences in the relative pace of molecular evolution among paired lineages inhabiting these broad habitat categories. Further work will consider specific habitat categories that more closely associate with connectivity and dispersal ability differences.

Analysis of QTLs for dietary influences on body weight in Drosophila

Ayse Cigdem Tunckanat

Saturday, June 21, 2014 -Poster #110
Metabolic Syndrome (MetS) is a complex disease with several symptoms such as insulin resistance, obesity, increased risk of type-2 diabetes and cardiovascular diseases, elevated blood pressure, and higher concentrations of circulating triglycerides.

It is known that the prevalence of MetS has been increasing due to Westernized dietary habits and increased rates of sedentary life. We used Drosophila model for sharing great homology to humans. QTL maps and tissue specific expression profiles of 1700 recombinant inbred lines reared in two different types of food (high fat food and normal food) were analyzed and nine genes were selected for further analyses. The nine genes we selected might have significant effects on an important endophenotype body weight and thus, might induce metabolic syndrome.

Detecting novel instances of meiotic drive in wild populations of Mus

Lorraine Provencio, Matt Dean

Saturday, June 21, 2014 -Poster #111
According to Mendel’s laws two alleles at a genetic position should be transmitted to progeny at equal probability. However, transmission bias of a particular allele is a frequent phenomenon termed transmission ratio distortion. This type of bias can be partially explained by meiotic drive. Meiotic drive occurs when one chromosome carrying the drive element is preferentially inherited due to the distortion of gametes carrying the homologous chromosome. Meiotic drive elements target male gametes leading to impairment of fertilization via manipulation of spermatogenesis. Though meiotic drive elements are ubiquitous in nature many occurrences of drive may be overlooked due to the difficulty of detecting this phenomenon. Here, we propose a method to detect novel instances of drive by doing whole genome analysis on both motile and non-motile populations of sperm taken from wild populations of mice. We predict that regions underlying drive will segregate preferentially with motile sperm.

Structure and Decay of a Proto-Y Region in Tilapia, Oreochromis niloticus

Will Gammerdinger

Saturday, June 21, 2014 -Poster #112
Sex-determination genes can leave a distinct footprint on the genomic architecture of an organism. Sexually antagonistic alleles can find resolution through tight linkage with sex-determination genes, which is often accomplished by chromosome inversions. We used pooled sequence data from families of the Nile tilapia, Oreochromis niloticus, to characterize variants within a previously mapped region associated with sex. We found an 8.8Mb block of differentiation, indicative of an inversion surrounding the sex-determination locus. This region also shows a substantially increased number of functionally relevant mutations. The transcriptome in this region is substantially female-biased compared to the rest of the transcriptome, suggesting a lack of dosage compensation mechanisms. The Nile tilapia provides a stimulating perspective on sex chromosome evolution, because it represents an intermediate stage of sex chromosome evolution. Recombination has been suppressed through an inversion and genes have begun to accumulate deleterious mutations through Muller’s Ratchet, but dosage compensation mechanisms have yet to take hold.

Naturally occurring deletions of Hunchback binding sites in the even-skipped stripe 3+7 enhancer

Arnar Palsson, Natalia Wesolowska, Michael Ludwig, Martin Kreitman

Saturday, June 21, 2014 -Poster #113
Changes in regulatory DNA contribute to phenotypic differences within and between taxa. Comparative studies show that many transcription factor binding sites (TFBS) are conserved between species whereas functional studies reveal that some mutations segregating within species alter TFBS function. Consistently, in this analysis of 13 regulatory elements in Drosophila melanogaster populations, single base and insertion/deletion polymorphism are rare in characterized regulatory elements. Experimentally defined TFBS are nearly devoid of segregating mutations and, as has been shown before, are quite conserved. For instance 8 of 11 Hunchback binding sites in the stripe 3+7 enhancer of even-skipped are

conserved between D. melanogaster and Drosophila virilis. Oddly, we found a 72 bp deletion that removes one of these binding sites (Hb8), segregating within D. melanogaster. Furthermore, a 45 bp deletion polymorphism in the spacer between the stripe 3+7 and stripe 2 enhancers, removes another predicted Hunchback site. These two deletions are separated by ~250 bp, sit on distinct haplotypes, and segregate at appreciable frequency. The Hb8 deletion is at 5 to 35% frequency in the new world, but also shows cosmopolitan distribution. There is depletion of sequence variation on the Hb8 deletion carrying haplotype. Quantitative genetic tests indicate that Hb8 deletion affects developmental time, but not viability of offspring. The Eve expression pattern differs between inbred lines, but the stripe 3 and 7 boundaries seem unaffected by Hb8 deletion. The data reveal segregating variation in regulatory elements, which may reflect evolutionary turnover of characterized TFBS due to drift or co-evolution.

The Status and Populations Genetics of the Flattened Musk Turtle

Peter Scott

Saturday, June 21, 2014 -Poster #114

The Flattened Musk Turtle (Sternotehrus depresss) is a federally threatened and IUCN listed (critically endangered) freshwater turtle endemic to the upper reaches of Black Warrior River basin in north-central Alabama, USA. We conducted a large scale study on the current physical status, conservation genetics, and assessment of possible deleterious genetic introgression from S. minor to S. depressus. Our current work shows that the range of S. depressus is greatly reduced from its historic distribution. Additionally, mtDNA and morphological data shows strong signal of unidirectional gene flow from S. minor into S. depressus. Although useful for initial inferences, the low genetic diversity in the turtle mitochondrial genome, and general limitations due to the nature of mtDNA render it less than ideal for assessing hybridization throughout contact zones. Expanding on mtDNA work, preliminary RAD-seq based genomic sequencing of a subset of individuals show cytonuclear discordance in genetic signal. This suggests that strong signals of mtDNA introgression may result from a mtDNA sweep rather than ongoing introgression between species. This research has major implications for the long-term survivorship of S. depressus in two ways: 1) inference genetic population structure between S. depressus populations; 2) identification of pure S. depressus populations without S. minor alleles. Additional samples in our genomic dataset combined with our current work on the physical status of S. depressus will continue to provide a comprehensive assessment of S. depressus in the wild providing a framework for conservation priorities to ensure the long-term survivorship of S. depressus.

Eye size sexual dimorphism and interspecies variation in Daphnia

Stephen Walterhouse

Saturday, June 21, 2014 -Poster #115

Vision is important because it provides a means by which organisms can “construct” a representation of their environment through visual stimuli. The genus Daphnia is comprised of small crustaceans commonly referred to as “water fleas”. Adults contain a single compound eye. Daphnia have mostly translucent bodies, decreasing their chances of detection by predators. The major exception to this is their eye, which is why eye size is important in Daphnia. Whatever purpose they have for taking in more light must benefit them more than the cost of being more easily detectable by potential predators on top of the cost of manufacturing and maintain a larger eye. We know based on their level of eye development that Daphnia can utilize vision to perform tasks involving things like: predator avoidance, locating mates, or finding food sources. However, despite knowing the stage of visual function Daphnia’s eyes are at and as a result the processes that can be conducted with them, the processes they do use them for are currently unknown. We investigated the evolution of eye size in the genus Daphnia with the objective of determining which potential functions might potentially drive eye size evolution. The eye diameters and body lengths of adult females in thirty four species, and also in males of twenty nine of those species were measured. We found that eye size varied widely across the genus, and was strongly correlated to body size. We also found that, for all species, males had larger eyes for a given body size, compared to females. The existence of which would suggest mate detection as a possible conducted process by Daphnia. The data for female eye size (adjusted for body size) was mapped to the phylogeny of Daphnia and tested for phylogenetic correlations to habitat characteristics. We conclude that evolution of visual capabilities is likely driven by foraging and mating, but is constrained by visual predators. This information is important because not only does it provide more insight into the behavior of Daphnia, but it also provides insight into their evolutionary history and a justification for Daphnia’s energy expense in order to develop and maintain an eye at their current level of visual function.

Genomic impacts of sex-ratio meiotic drive in stalk-eyed flies

Josephine Reinhardt

Saturday, June 21, 2014 -Poster #116

Populations of stalk-eyed flies (Teleopsis dalmanni) regularly exhibit frequencies of an X chromosome that distorts the sex-ratio of offspring (XSR) approaching 30% in the wild. Males carrying XSR parent mostly daughters, and unlike in other species where sex-ratio meiotic drive has become suppressed, XSR appears to have been maintained as a stable polymorphism in T. dalmanni over 25 years of collections and across multiple populations. This long term association with a driving chromosome raises the question of what impacts meiotic drive may have had on the genome of these flies. We combined deep transcriptome sequencing of XSR and standard testes from one population of stalk-eyed flies with genomic resequencing of pools of XSR and standard individuals from two populations. We found that the majority of differentially expressed transcripts were X-linked, implying the effects of meiotic-drive on gene expression are largely in-cis to the driving chromosome. Hundreds of X-linked transcripts also contained fixed differences within the transcriptome data between standard and sex-ratio transcript pools. In addition, the degree of genetic differentiation (FST) was found to be elevated across most of the X chromosome between XSR and standard samples. Furthermore, within-population FST between drive and standard samples was significantly higher than between-population FST, supporting the notion that XSR has persisted within these populations for some time prior to their separation. Using these data, we were also able to confirm that the complete loss of expression in some drive-associated genes is most likely caused by XSR -specific deletions in these genes. XSR is associated with a wide array of phenotypic changes in these flies, making these genes interesting candidates for further phenotypic study.

Male fertility costs of sex-ratio meiotic drive and rates of female remating in Drosophila neotestacea

Cheryl Pinzone, *Kelly Dyer*

Saturday, June 21, 2014 -Poster #117

Selfish genetic elements bias their own transmission into the next generation, often at the expense of the fitness of its carrier. X-chromosome meiotic drive, also known as sex-ratio (SR) drive, occurs when an X-chromosome causes Y-bearing sperm to die during spermatogenesis such that only female offspring are produced. Theoretically, its large transmission advantage may allow SR to spread very rapidly and ultimately cause its host population to go extinct due to a lack of males. Despite many decades of study, it is currently unknown how SR is maintained as a stable polymorphism in the absence of any costs to female carriers or of genetic suppressors. To better understand how this may occur, we use the SR drive system in the mushroom-feeding fruit fly Drosophila neotestacea. The prevalence of SR chromosomes exists between 0 – 30% throughout the species range and this polymorphism has been stable for at least 20 years. Here we investigate the fertility cost that SR males bear relative to standard males, examine sperm competitive ability of SR males, as well as investigate the rates of female remating in the wild.

Cryptic sex? Estimates of gene exchange between sexual and asexual mole salamanders (Ambystoma sp.)

H. Lisle Gibbs, *Robert D. Denton*

Saturday, June 21, 2014 -Poster #118

Cryptic sex has been argued to explain the exceptional longevity of certain gynogenetic asexual vertebrate lineages yet direct measurements of the levels of gene exchange between sexual and asexual forms are rare. Female unisexual mole salamanders (Ambystoma sp.) are the oldest known unisexual vertebrate lineage, arising approximately 5 million years ago. One hypothesis for their persistence is that allopolyploid female unisexuals periodically exchange genomes with males from sympatric sexual species during gynogenetic reproduction. Here we use genome-specific microsatellite DNA markers to estimate rates of gene exchange between sexual males and unisexual females in two ponds in NE Ohio and test the prediction that levels of gene flow should be higher for "sympatric" (sexual males present) and "allopatric" (sexual males absent) portions of unisexual genomes. We analyzed this process as multiple populations with unidirectional gene exchange from sexuals to unisexuals using a model testing framework in the coalescent-based program MIGRATE. As predicted, our results show positive levels of gene flow between sexuals and sympatric genomes but that allopatric genomes are not replaced. Our results provide direct evidence that gene exchange between sexual and unisexual Ambystoma occurs but that the magnitude depends on which sexual species are present. They also raise the possibility that allopatric genomes in unisexuals may accumulate mutations at a greater rate than sympatric genomes.

Recombination load caused by multiple chromosomal rearrangements

Spencer Koury, *Walter Eanes*

Saturday, June 21, 2014 -Poster #119

Recombination is an important force in genome evolution; in particular, suppression of recombination is an initial step in major transitions such as speciation and sex chromosome evolution. Chromosomal inversions suppress recombination in the heterozygous state because crossing-over in inverted regions results in acentric and dicentric meiotic products. In Drosophila melanogaster these aberrant chromosomes are shunted into the polar bodies; thus, no additional genetic load is incurred by the segregation of a single chromosomal inversion. However, there is recombination load associated with segregation of multiple overlapping inversions in a population. We provide evidence that recombination can occur in homosequential regions of inversion/inversion heterozygotes resulting in meiotic products with a single centromere. Recombination also generates large segmental duplications and deletions (> 9 Mbp) by fusing one inversion's proximal breakpoint to the distal breakpoint of the other. We conducted experimental test-crosses to quantify 1) the extent of recombination suppression in standard/inversion heterozygotes, 2) the rate of recombination in inversion/inversion heterozygotes, and 3) the fitness effects of the resulting segmental duplications and deletions. Consistent with previous work we found recombination rate was suppressed in inversion/standard heterozygotes. We also found recombination in homosequential regions of inversion/inversion heterozygotes occurred at reduced, but experimentally detectable, rates. The duplication/deletion recombinants were viable in the heterozygous state but had severely reduced homozygous fitness. This form of frequency-dependent selection against new chromosomal rearrangements is consistent with classical population cage experiments on invasion fitness of new inversions. In contrast to the prevalent co-adaptation and local adaptation interpretation of geographic distribution of inversions, we present recombination load associated with overlapping inversions as a simple non-adaptive mechanism for this well-known pattern.

B Chromosome Maintenance in Cichlid Fishes

Frances Clark

Saturday, June 21, 2014 -Poster #120

While every species has its own typical set of chromosomes refered to as A chromosomes (As), some species have B chromosomes (Bs) which are supernumery, nonessential chromosomes found in some but not all members of a population. Bs do not follow the typical ploidy rules nor go through mieosis and mitosis in the same manner as A chromosomes. The molecular details of the mechanisms that allow Bs to be maintained in this unique way are unknown. A common mechanism often utilized in conjunction with others that is seen across many B-carrying species is non-disjunction, which leads to variation in B-copy number within and among individuals. A peculiar case of B chromosomes has been found in several species of Lake Malawi cichlids, where Bs are found solely in females. This study aimed to identify the mechanism by which Bs are maintained in these fishes. Finclips were collected from wild individuals from 3 time periods across 8 years and genotyped for B-presence using B-specific and A-specific primers. qPCR was performed for relative quantification within and among populations to ascertain B copy number. PCR genotyping confirmed the absence of B chromosomes from all male individuals. We found variation in B copy number between populations, but intra-population variation in B copy number is lacking. This suggests that non-disjunction is not occurring to increase individual B copy number between generations. Future directions for this project include quantifying transmission ratios of Bs and the impact of B-presence on sex ratio within families. It is also a future goal to identify any functional sequence of the B chromosome that may play a role in B maintenance.

Local adaptation of the eastern oyster: evidence from a reciprocal transplant experiment

Martha Burford Reiskind

Saturday, June 21, 2014 -Poster #121

We examined the role of local adaptation in structuring the stable, genetic step-cline of the eastern oyster (Crassostrea virginica) along an environmental gradient in the lagoon system of eastern Florida, USA. Reciprocally transplanted progeny produced by a 10 x 10 genetic cross of wild brood stock from northern and southern genetic lineages of the eastern oyster, yielded significant evidence of local adaptation (G x E) in variables related to fitness, including survival, wet meat weight, and reproductive maturation. The strength of local adaptation was asymmetric, with greater effects on the northern compared to the southern genetic lineage. To a lesser extent, we found evidence of both the role of environment, in particular adverse effects on both genetic crosses in the southern region, and the role of genetic differences between the two crosses independent of environment, with higher initial growth of the southern genetic lineage and higher condition of the northern lineage. These differences suggest that maintenance of the genetic step-cline involves natural selection. We discuss the potential role of temperature and phytoplankton community composition between the northern and southern regions. Our study is the fist to determine the genetic basis for fitness-related phenotypes and relate this to local adaptation of the eastern oyster. Understanding the role of the environment in structuring the eastern oyster throughout its range is critical for effective management and the results of this study also suggest that small environmental changes may have significant effects on conservation of the eastern oyster, particularly in the northern genetic lineage.

The influence of plasticity and evolution on information use during resource exploitation with variable competition

Sarah Jaumann, *Emilie Snell-Rood*

Saturday, June 21, 2014 -Poster #122

Animals use information from the environment to identify high-quality resources. Personal information entails direct, individual exploration of the environment while social information is acquired from conspecific cues. Both sources of information involve costs such as intraspecific competition. Furthermore, competition varies across seasons, years, habitats, and species communities, and such variation may be especially pronounced in areas experiencing anthropogenic change. How, then, do animals decide which source(s) of information to follow when locating resources? The goal of this work is to understand the degree to which plastic and evolutionary mechanisms interact and influence the type of information animals use to find resources in environments with fluctuating competitive costs. Cabbage white butterflies are an ideal system in which to address this question because competition significantly affects fitness. To confirm that cabbage whites use personal and social information, adult information use was assessed using a host plant search assay. The results suggest that butterflies pay attention to both social and personal information. To build on this finding, butterflies from different populations were exposed to high or low conspecific density as adults and juveniles, and their subsequent information use was determined using the search assay. I predict that plasticity and selective history are both important. If plasticity is important, butterflies exposed to high conspecific densities will rely more on personal information and social avoidance rather than social attraction compared to butterflies exposed to low conspecific densities. Differences between populations and individual genotypes would suggest a role for selective history. These experiments will pave the way for a framework that seeks to understand the evolutionary maintenance of diverse information use strategies and the evolution of social information. Understanding the mechanisms that allow animals to find resources in variable environments is also critical in predicting the rate of adaptation to habitat disturbance and thus survival of species in the face of human-induced change.

Evolutionary relations and population differentiation of Acipenser gueldenstaedtii Brandt., Acipenser persicus Borodin and Acipenser baerii Brandt.

ALEXEY SERGEEV, Nikolai Mugue

Saturday, June 21, 2014 -Poster #123
Russian (Acipenser gueldenstaedtii), Persian (Acipenser persicus)and Siberian (Acipenser baerii) Sturgeons - are closely related Ponto-Caspian species. Research on its population genetic structure is an important task, which determines measures for conservation of these species. This study analyzed the frequency of 'baerii-like' mitotypes of Russian Sturgeons of the Volga River, the Ural River, the Caspian and the Azov Sea and Persian Sturgeons from the Caspian Sea. 'Baerii-like' mitotype was found in 35% of individuals of Russian Sturgeon from the Caspian Sea (Volga, Ural), and in 2% from the Azov Sea and wasn't found in the Persian Sturgeons. AFLP method reveals that Caspian Russian Sturgeon is closer to Persian Sturgeon from the Caspia Sea than to the Russian Sturgeon from the Azov Sea. The Siberian Sturgeon (from the Ob' river) has formed a separate branch to the common Persian-Russian sturgeons cluster. The data confirms genetic isolation of Persian sturgeon from Russian sturgeon in the Caspian Sea, but the nuclear DNA markers show that the Persian Sturgeon is a young species. RAD sequencing of these two very close species allowed verifying discrimination between Russian and Persian Sturgeons. We found 7346 candidate SNPs across the two samples of which 43.9% were estimated to be polymorphic in Russian, 64.5% in Persian and 9.2% estimated to be fixed between Russian and Persian sturgeons (alternate homozygotes). The discovery of molecular genetic markers that show differences between Russian and Persian sturgeons is very important. Until now, these two taxa, while widely recognized as valid species, have been impossible to separate, using standard phylogenetic markers, such as mtDNA. Now it is possible to combine new genetic approaches, morphological and ecological features for more effectivediscrimination between these two closely related species.

Rapid visual pigment evolution in a radiation of freshwater anchovies

Alex Van Nynatten, Devin Bloom, Belinda Chang, Nathan Lovejoy

Saturday, June 21, 2014 -Poster #124
The divergent spectral composition of marine and freshwater habitats imposes substantial visual challenges on marine derived freshwater species. This makes for an ideal natural system for studying evolutionary adaptation in light sensitive opsin proteins. We have sequenced rhodopsin, the dim-light sensitive opsin protein, from 36 anchovy species, representing distinct marine and freshwater clades. Applying maximum likelihood models for detecting positive selection to our dataset revealed a highly significant increase in molecular evolutionary rates in the freshwater clade of anchovies, a pattern not observed in other nuclear and mitochondrial genes. This evidence indicates that the dimmer more spectrally deficient freshwater environment is driving visual adaptation at a molecular level in the marine derived freshwater lineage of South American anchovies.

Investigating the role of candidate genes PIN1 and BRC2 in shaping resource allocation tradeoffs and life history evolution in diverged popula

Bishwa Giri

Saturday, June 21, 2014 -Poster #125
Understanding the mechanistic and physiological basis for costs of reproduction could be an important approach to understanding life history evolution in a whole. We have been studying diverged natural populations of evolutionary model A. lyrata, one from European gene pool (A. lyrata ssp. petraea) and another from North American gene pool (A. lyrata ssp. lyrata). These two populations show local adaptation and strong phenotypic differentiation including nature of resource allocation characterized by differences in flowering time, length of flowering and number or inflorescence produced during reproductive season. These adaptive features closely tie with variation in shoot architecture these two populations exhibit; the North American population produces more inflorescence and allocates resource relatively more into reproduction. QTL study suggests that candidate genes contributing to these adaptive differences lie in linkage group 2 of the A. lyrata genome. Two potential candidates in this region include PIN1 and BRC2. PIN1 is an efflux auxin transporter protein involved in shaping shoot architecture through the process of apical dominance while BRC2 is related to the maize lateral shoot repressor and major domestication gene tb1.

To test these hypotheses we are assaying variation in auxin transport between populations and investigating quantitative variation in gene regulation using ASE (allele specific expression) approach in F1 hybrid.

The role of evolution for the invasion of salt cedar (Tamarix ramosissima) across Western United States

Soo-Rang Lee, Matthew Olson

Saturday, June 21, 2014 -Poster #126
Invasive species provide opportunities to study evolution in action, yet the role of evolution during biological invasion has been understudied. Because colonizers face environmental challenges during colonization, selection might favor increased physiological tolerance to environmental demands. Genetic variation in a trait is required for a response to selection, but its presence does not prove that there has been adaptation. Genetic variation can be measured using common garden studies, and past adaptation can be inferred or assessed in several ways including reciprocal transplant studies, detection of correlations between the environment and genetic variants, and comparisons between quantitative trait divergence (Qst) and divergence of neutral genes (Fst). Since it escaped from cultivation in the late 1800's, salt cedar (Tamarix ramosissima) has become major threat to riparian ecosystems in the western U.S. Understanding the role of adaptation during its spread will provide insight into both the

evolutionary process and management strategies for its control. The primary goals of my research are to: 1) assess whether T. ramosissima populations harbor genetic variation for traits related to drought tolerance, 2) determine whether drought tolerant phenotypes are correlated with annual precipitation at the sites origin, and 3) assess whether T. ramosissima harbors signatures of variation that are consistent with past adaptation in drought tolerance.

Population genetic structure and fitness of Daphnia pulicaria across a pH gradient in three North American lakes

<u>Billy Culver</u>

Saturday, June 21, 2014 -Poster #127
Natural selection on standing population genetic variation is known to result in adaptive responses among a plethora of organisms. Here, we look at how the aquatic keystone species, Daphnia pulicaria has adapted to its environment, specifically looking at three North American lakes across a pH gradient: Madison Lake, MN (average annual pH 8.6), Hill Lake, MN (average annual pH 7.6), and Frenchman lake, Ontario, CN (average annual pH 6.5). Genotypes (clones) were subjected to a common garden experiment in which the following proxies for fitness were measured: survivorship and juvenile growth rate (JGR). Further, population genetic structure was determined for daphniids from each lake using 17 microsatellite loci, and genetic structure was correlated with fitness results. Survivorship results showed that Daphnia from Frenchman Lake had a significantly higher survivorship at the medium to low end of the pH gradient, while Daphnia from Hill and Madison Lakes had significantly higher survivorship over the medium to high end of the pH gradient. Significant within-population (lake) clonal differences in JGR were observed for all populations. In addition, at the between-population level, Frenchman Lake Daphnia showed significantly lower JGRs across the whole pH range, as compared to Madison and Hill Lake Daphnia. Population genetic structure analyses showed that Hill and Madison Lake Daphnia are more similar genetically, as well as physiologically (i.e. similar fitness responses across the pH gradient). In contrast, Frenchman Lake Daphnia were significantly different genetically and showed significantly different fitness responses across the pH gradient. There are a number of anthropogenic and natural phenomena that have altered pH in aquatic and marine environments; therefore it is critical to understand how organisms, such as Daphnia, respond with regards to fitness in these changing environments in order for conservation managers to understand how to properly manage these aquatic and marine systems.

Host before Habitat? Assessing congruency in patterns of gene flow in an imperiled freshwater mussel and its vertebrate host.

<u>Mason Murphy</u>, *David Weisrock, Steven Price*

Saturday, June 21, 2014 -Poster #128
Freshwater mussels (order Unionoida) are one of the most threatened groups of taxa within the United States and worldwide. Freshwater mussels exhibit a distinctive lifestyle, in which they disperse via fish hosts as larvae. Although the causes for freshwater mussel declines are numerous, the requirement of a fish host for larval development and dispersal has direct implications for mussel conservation. Few investigations have assessed the role of host dispersal as it relates to mussel population decline, yet long-term population viability is not only dependent on local survival and recruitment, but also on host population sizes and host dispersal. I will employ powerful population genetic data to understand this unique lotic host/parasite relationship and aid in the conservation of freshwater mussel populations. Specific objectives include: 1) assessment of population structure and gene flow in both an imperiled host (Necturus maculosus) and mussel (Simpsonaias ambigua) at multiple hierarchical scales; 2) assessment of congruency in genetic structure of mussel and host at multiple hierarchical scales; and 3) relating habitat conditions within sampled streams and rivers to mussel population genetic parameters. I will estimate population structure of both species using genetic clustering methods that assign individuals to genetic clusters based solely on their multilocus genotypes. I will then perform a hierarchical analysis of molecular variance (AMOVA) to estimate gene flow. I will use a coalescent-based analytical approach, performing model-selection among a set of alternative models of demography and gene flow to determine the one that best explains our data. Importantly, this approach will allow me to directly compare models of gene flow between the mussel and salamander systems. Furthermore, I will estimate demographic and gene flow parameters in the program MIGRATE. For each taxon, I will use both Bayesian and likelihood approaches to estimate population parameters under a full model that allows for all sampling locations to have their own estimate of population effective size and separate rates of migration, allowing for the assessment of population structuring across the geographic range of our study area, and comparison of specific gene flow estimates at different hierarchical levels of stream structure. I expect that the two species will exhibit generally congruent systems of gene flow and population structure. However, I do believe populations of S. ambigua will have lower gene flow and more entrenched isolation than N. maculosus due to a more pronounced reaction to both abiotic factors and hierarchical structuring.

Population genetics of non-LTR retrotransposons in lake and oceanic populations of three-spine stickleback

<u>Jayson Slovak</u>, *Stephane Boissinot*

Saturday, June 21, 2014 -Poster #129
Non-long terminal repeat (LTR) retrotransposons (nLTR-RT) constitute the dominant category of transposable elements in vertebrate genomes. The diversity and abundance of nLTR-RT differ consideraby among vertebrate genomes. At one extreme, mammalian genomes are littered with 100,000s of copies resulting from the activity of a single type of nLTR-RT, the L1 clade, whereas fish genomes contain a much more diverse repertoire of nLTR-RT, represented by numerous active clades and families. The number of nLTR-RT in fish is however two orders of magnitude smaller than

in mammals. The vast majority of insertions appear to be very recent, suggesting that nLTR-RT do not accumulate in fish genomes. The chance of fixation of nLTR-RT insertions depends on the strength of selection against deleterious insertions and the effective size of populations. Theory predicts that, in large populations, selection will efficiently eliminates deleterious insertions from the gene pool but in small populations, drift can counter-act the effect of selection, resulting in the fixation of slightly deleterious alleles. Thus, in small populations nLTR-RT may reach fixation leading to an increase in genome size. We tested the respective role of drift and selection on nLTR-RT insertions in fish populations that differ in population size. We compared the frequency of insertions in oceanic (i.e. large) and lake (i.e. small) populations of threespine stickleback. We found that, consistent with our prediction, insertions tend to accumulate at a faster rate in lake populations.

Phylogeography of the Malagasy ant species Odontomachus coquereli.

Jason Jackson, Brian Fisher, Brice Noonan

Saturday, June 21, 2014 -Poster #130
The Malagasy ant species Odontomachus coquereli inhabits much of the eastern coast of Madagascar, and of the 32 species in its genus, is the only one to lack winged queens. The reduced migration potential of this species makes it amenable to phylogeographic study, as does its location. Madagascar's ants are a diverse (c.a. 1000 species, 8 subfamilies), highly endemic (~96%) assemblage derived from colonizing lineages from mainland Africa and Eurasia. Such radiations promise to make phylogeographical studies of endemic species, like O. coquereli, particularly fruitful for investigating historical processes giving rise to evolutionary diversification. We analyzed 6 anonymous nuclear loci from specimens spanning the entire range of O. coquereli in our analyses to investigate population structure, divergence times, and levels of genetic diversity.

We found O. coquereli to be divided into three main populations by latitude, and that these were likely the product of successive southward expansion. The timing of expansion and differentiation among population clusters offers, perhaps, the greatest insight as to why such a strong pattern was recovered. The first southward expansion and subsequent isolation coincides with the Illinoian glacial period (130-200 kya) and the second pulse of expansion about 80k years later with the Wisconsin glacial period (12-110 kya). Though Madagascar's equatorial location prevented temperature from falling to levels not tolerated by this species, Madagascar did experience a substantial precipitation shortfall during these glacial periods. We hypothesize that species took refuge in high elevation moist areas (there are two main high elevation areas in the species range, one in the north and one located centrally) during glacial periods and expanded south subsequently, leading to the genetic patterns observed today.

Macro- and micro-scale phylogeny of Japanese hynobiid salamanders: implication of genetics to conservation of H. tokyoensis

Hirotaka Sugawara, Tamotsu Kusano, Fumio Hayashi

Saturday, June 21, 2014 -Poster #131
The comprehensive phylogenetic relationship of Japanese hynobiid salamanders, Hynobius, has been investigated using DNA variations. However, the monophyly of several species is not supported based on mitochondrial DNA, and the phylogentic relationships among species are still left unsolved. The Tokyo Salamander, Hynobius tokyoensis, has been shown to be monophyly in this genus, but a fine-scale population genetic structure of this species is uncertain. H. tokyoensis is a lowland lentic breeder and endemic to Kanto District, central Japan. This species has low dispersal ability and a narrow distribution range. The current distribution pattern is strongly affected by human activities in urban areas, and there are growing concerns between habitat fragmentation and population decline. Several populations are threatened with extinction. In this study, to contribute to the future conservation of this species including the genetic factors, we assessed the current population genetic structure and genetic diversity among 16 populations using a mitochondrial cytochrome b gene (650 bp) and microsatellite DNAs (5 loci). In Kanto District, populations were separated into northern and southern groups based on mitochondrial DNA analyses, but fine-scale genetic structure of each group were ambiguous. Based on microsatellite DNA analyses, isolation of northern and southern groups was also clear, and southwestern populations were genetically different from the other populations of the southern group. A positive correlation were detected between the genetic diversities of mitochondrial and nuclear DNAs in 16 populations. However, there was a possibility that the strong bottleneck effects on females occurs in not only urban areas but also marginal areas of this species distribution range. We would like to discuss how should we apply the population genetics into the conservation activities in the future.

Where do introduced populations learn their tricks? Searching for the geographical source of a species introduction to the Galápagos archipelago.

Adrienne Cheng, Sarah Pangburn, Jasmine Gums, Adrian Troya, Andrea Sequeira

Saturday, June 21, 2014 -Poster #132
We are exploring the genetic reasons behind the ecological success of species introductions. The genetic richness underlying such success can either be imprinted in the genetic patterns at the source location, or gained in situ through demographic expansion and multiple introduction pulses. The weevil Galapaganus howdenae howdenae, introduced to Galápagos from mainland Ecuador, is an example of an introduced species with an expanding geographic range. Our observations confirm that G. h. howdenae has expanded into the moist highlands of Santa Cruz Island, now sharing habitats with highland specialists (G. ashlocki). Previous

microsatellite analyses of island populations support a single introduction pulse, high genetic diversity and large population sizes (compared to long-established endemics), and no significant genetic structure across the introduced range. We are now incorporating populations from a portion of the source range to characterize the geographic patterns of genetic variability and historical demography in the continental populations of G. h. howdenae. Specifically, we aim to answer questions such as: Do the patterns of genetic variation differ between source and introduced populations? Do the source continental Ecuadorian populations show significant genetic structure across their range? Is it possible to pinpoint the exact geographical source of the introduced populations? The results of these investigations can help us obtain a more complete picture of the introduction history of an insect species into the Galápagos archipelago: an ecosystem that is hailed as an example for conservation efforts, while under increasing pressure from tourism and development. If our analyses were to detect higher levels of genetic variability in the introduced range compared to the source areas, then that might indicate that introduced populations have the genetic potential to successfully colonize other areas from Santa Cruz. In the short term, the results could inform measures that attempt to control accidental inter-island transfer. In the long-term, our results could provide insight into the genetic background of biological invasions.

Genetic variation in a fungal entomopathogen Pandora neoaphidis and the evolution of symbiosis in pea aphid populations

Narayan Wong, Jacob Russell, Andrew Smith

Saturday, June 21, 2014 -Poster #133

Symbiotic bacteria are known to mediate a wide range of interactions between their insect hosts and the environment. An organism's fate when challenged by natural enemies such as parasitoid wasps, viruses, and fungal pathogens may be bolstered by the presence of defensive bacterial endosymbionts. In populations of the pea aphid, Acyrthosiphon pisum, the prevalence of defensive symbiont species and their component strains can vary temporally and spatially. Such variation in symbiont types may result from variability in the genetic composition of natural enemies in the environment. Conversely, the presence of diverse types of symbiotic bacteria in an insect population may promote genotypic variation in natural enemies. Previous studies have demonstrated that different symbiont species and strains vary in their ability to protect aphids against a single isolate of the fungal pathogen Pandora neoaphidis. It has also been demonstrated previously that genetic variation exists between Pandora isolates, but little work has been done to characterize the variation that exists over time and space. If sufficient genetic variation exists in both the defensive symbiont and fungal pathogen, reciprocal adaptations may result in coevolution between symbiont communities and natural enemies. We are developing molecular approaches to survey the genotypic variation of Pandora neoaphidis infecting wild populations of the pea aphid throughout the year and combining these data with previously collected information on symbiont prevalence and diversity.

A SINE-based tool for studying population structure of Coilia nasus

Dong Liu, Wenqiao Tang

Saturday, June 21, 2014 -Poster #134

Short interspersed nuclear elements (SINEs) are one type of retroposons. They are short DNA sequences (80-400 bp) that inserted into host genomes via copy-and- paste transposition. SINEs often are used as molecular markers in phylogenetics and population studies, because they are abundant (103-106 copies) in host genomes and ineffaceable signal can always be found at their insertion sites. In the present study, we used biotinylated beads to capture and isolate SINEs from genome of Coilia nasus, a clupeiform fish. Firstly, an AFLP library of DNA was constructed. Then, a probe designed from previously obtained SINE sequences, was used to screen the clones in the DNA library. A total of 316 positive clones have been detected from 1248 clones screened. Finally, SINE sequences were determined from 72 of the 316 clones. The SINEs isolated from C. nasus are composed of two conserved regions, box A and box B. The SINEs can be categorized into six types according to their related- tRNA genes, tRNA-Ala, tRNA-Val, tRNA-Thr, tRNA-Pro, tRNA-Arg and tRNA-Ser, indicating multiple original of SINEs in C. nasus. Nevertheless, most SINE clones are tRNA-Ala related, suggesting that there might have been selective preference since those SINEs were transposed into the host. The flanking sequences of all 72 SINEs were used to design PCR primers to study population structure of C. nasus sampled from six sites in China: Xiangshan in Zhejiang province, Jingjiang in jiangshu province, Chongming in Shanghai, Lake Taihu, Lake Poyang and Lake Dongting. Five primer pairs produced absence/presence data that are concordant with the sampling localities, suggesting the usefulness of these SINES-inserted sites as a tool to study the population structures of C. nasus.

Effects of geography, climate and host plant association on population genetic differentiation of a specialized mediterranean grasshopper

Víctor Noguerales, Pedro J. Cordero, Joaquín Ortego

Saturday, June 21, 2014 -Poster #135

The dramatic environmental changes of the Quaternary, particularly the climatic conditions prevailing since the Last Glacial Maximum (LGM; ca. 21 ka bp), have strongly influenced the demographic history, genetic diversity, and distribution of many organisms. Understanding the role of current and past climates on shaping dispersal routes and spatial patterns of genetic variability can provide important insights into the processes driving species diversification and distribution. In addition to the effects of current and/or past dispersal routes, isolation-by-ecology (IBE) can also play an important role on genetic differentiation. Populations established in different environments or using different resources (e.g. host plants in herbivorous organisms) may evolve local adaptations to the particular conditions that they experience and this can ultimately reduce realized gene flow due to divergent selection against immigrant genotypes.

In this study, we combine microsatellite genetic data, climate niche modeling, circuit theory, and host plant-animal association information to investigate the factors explaining contemporary patterns of genetic variability in Chorthippus binotatus (Charpentier 1825), an oligophagus mountain grasshopper that exclusively feeds on some species of bush legumes (tribe Genisteae). Specifically, we employed a Multiple Matrix Regression with Randomization (MMRR) approach to analyze the potential influence of 1) Euclidean geographical distance (i.e. isolation-by-distance, IBD); 2) LGM-, current- and climatic stability-based resistance distances (i.e. isolation-by-resistance, IBR); and 3) the use of different host plants on contemporary patterns of genetic structure.

Pair-wise FST values ranged from 0.001 to 0.309 and most pair-wise comparisons were significant after sequential Bonferroni correction. Structure analyses and the statistic ΔK indicated an optimal value of K = 3, but populations generally showed a considerable degree of genetic admixture. MMRR analyses showed that genetic distance was correlated with geographical distance and climatic stability-based resistance distance when these variables were included alone into different models. However, only geographical distance was retained into the final model and no other variable remained significant after it was included. Overall, our analyses indicate a predominant effect of geographic distance on contemporary patterns of genetic structure. In the near future we aim to use a larger panel of microsatellite markers and more detailed information on the species ecology (e.g. phylogenetic distance among host plants) to get a better understanding on the relative role of geography, ecology and current and past dispersal routes on structuring genetic variation in this grasshopper species.

Geographic and genetic variation in an acoustically-orienting parasitoid fly

Marlene Zuk, Susan Balenger, Henry Kunerth, David Gray

Saturday, June 21, 2014 -Poster #136

Obligate parasitoids are by definition restricted to the same geographic range as their host species. The distribution of Ormia ochracea, a North American parasitoid fly, however, is widespread due to its ability to utilize multiple cricket species as hosts even though many of its hosts have limited ranges. This ability to utilize multiple hosts is particularly interesting because O. ochracea finds its host via their sexual signals; gravid females use male cricket calling song to locate individuals upon which they can release their larvae. Thus, not only must the larvae be capable of developing within a variety of cricket species, but adult females must be able to detect and locate hosts with sometimes extremely divergent songs in different parts of their range. Earlier work found that female flies from across the distribution not only have a preference for their local host calling song, but also vary in their ability to detect the songs of crickets from other parasitized populations. The ability of O. ochracea to utilize multiple host species across its range suggests the possibility of on-going genetic isolation between populations that use different hosts. We used 17 highly polymorphic microsatellite loci to 1) determine the phylogenetic relationships of populations of flies between the 6 regions sampled, 2) evaluate the population structure of each in order to determine whether gene flow is occurring between regions, and 3) identify the likely mainland source population of the O. ochracea population recently established in the Hawaiian Islands. We found strong support for a Florida-Texas sister-group, while Mexico-Arizona and California-Hawaii form less well-supported groupings. Structure analysis shows a clear divide between the genetic identities of individuals found on either side of the continental divide. It is unlikely that much gene flow, if any, is occurring across these regions. It is, however, still unclear whether this is primarily driven by geographic barriers or due to adaptation to local host species making immigration unlikely. Unsurprisingly, we found that Hawaiian populations have reduced allelic diversity compared to other populations, but do exhibit variation at all loci examined. Allelic composition suggests a California source for the Hawaiian introduction.

Heat shock transcription factor regulates differential responses to acute heat stress in conspecific populations of Tigriopus californicus

Sumaetee Tangwancharoen, Ron Burton, Gary Moy

Saturday, June 21, 2014 -Poster #137

Temperature is one of the main environmental factors that influences local adaptation of conspecific populations along the latitudinal gradients. However, the molecular mechanisms underlying local adaptation to temperature gradients are not well understood. The intertidal copepod Tigriopus californicus is a good model for studying acute heat stress response and thermal adaptation. Populations of T. californicus inhabit high intertidal rock pools along the west coast of North America from Baja California to Alaska. These pools present extreme thermal environment and previous studies have shown evidences of thermal adaption of T. californicus populations along the latitudinal gradient. Southern populations survive acute heat stress at higher temperatures than northern populations. Transcriptome studies have shown that thermal tolerance is associated with levels of expression of numerous heat shock protein (Hsp) genes. We hypothesize that genetic variation in the heat shock transcription factor (HSF) underlies differential responses to acute heat stress among different populations of T. californicus. There is one copy of the HSF gene with 529 amino acids in the T. californicus genome. For example, we found 8 amino acid substitutions in the HSF gene between Santa Cruz and San Diego populations. This suggests functional differences of HSF from different populations along the latitudinal gradient. HSF is activated by heat stress and it subsequently induces transcription of Hsp genes. However the heat shock regulatory network has not been well studied in the ecological and evolutionary context. Here we investigate differential regulations of heat stress responses by comparing the activation temperatures of HSF from different populations of Tigriopus californicus.

Horizontal gene transfer enables rapid evolution and decline of the legume/rhizobia mutualism

Benjamin Gordon, Christie Klinger, Dylan Weese, Patricia Burke, Jennifer Lau, Katy Heath

Saturday, June 21, 2014 -Poster #138

Understanding the drivers of mutualism evolution in a changing environment will be essential for anticipating the long-term impacts of global change, including increased nitrogen (N) deposition. Specifically, bacterial mutualists have a proclivity to evolve rapidly, thanks to short generation times and horizontal gene transfer (HGT). We have formerly shown that long-term N-deposition caused the evolution of rhizobia that are less-beneficial to their clover hosts when compared with rhizobia from control (C) plots. Here, using quantitative genetic and phylogenetic analyses of 63 rhizobium strains isolated from N and C plots, we determine whether host phenotypic variance is attributable to phylogenetic relationships among strains or microevolutionary change caused by N-deposition. We provide strong evidence for the latter, suggesting HGT of the symbiosis plasmid has contributed to mutualism decline. Our results illustrate that N-deposition fuels evolutionary change in an essential mutualism and more broadly provides insight into the mechanisms behind bacterial adaptation in response to environmental change.

Population specific differential thermal stress response in Drosophila melanogaster in a lab versus field setting

Vinayak Mathur, Paul Schmidt

Saturday, June 21, 2014 -Poster #139

Background/Question/Methods

Temperature is an important physical factor that affects the life-history strategies and range distributions of ectothermic insects . Photoperiodic cues also play an important role in enabling insects to predict long-term changes in temperature and adjust their development, physiology and behavior. Studies that focus on modulating temperature and other environmental parameters aim to interpret the results in the context of the environmental conditions that the organism is expected to meet in the field. However, the physiological and ecological responses usually investigated under controlled laboratory conditions may not capture the true complexity of the natural environment. In order to resolve this discrepancy, we compared laboratory and field results of temperature manipulation on Drosophila melanogaster.

For the purpose of our study we chose three natural populations of D. melanogaster collected from Maine, Pennsylvania and Florida and set up population cages using one hundred isofemale lines from each location. Virgin females were collected and placed in cages for a five day outdoor treatment in a common garden experiment. Flies were also placed in incubators in the laboratory under fixed temperature and photoperiod regimes. After the initial field or lab treatment flies were assayed for heat shock tolerance, chill coma resistance and starvation tolerance.

Results/Conclusions

Phenotypic stress response results from the lab show that northern and southern populations of flies respond differentially to environmental cues. The data demonstrates that southern populations are generally more starvationtolerant, whereas northern populations are more resistant to heat shock. In the outdoor experiments we see similar patterns of differential response, with the Northern populations performing better in the chill coma and heat shock assay in certain months of the year. The most striking result is that the variation in response correlates with the high variation in the temperature cycle and not the absolute hot or cold treatment as indicated by the lab results. Our results suggest that it is important to consider the variation in temperature when testing for thermal tolerance in flies. The response that we get under laboratory conditions at fixed temperatures is highly variable when compared to the field experiments. The Northern populations of flies which have been exposed to a certain temperature regime perform better i.e. have higher survivorship, because of the underlying genetic mechanism to cope with extreme environmental conditions. Thus, we show that experiments done in the field can detect subtle differences in thermal performance not evident in simple laboratory tests.

Acclimation and adaptation in a marine invertebrate, Tigriopus to common marine pollutants

Patrick Sun, Helen Foley, Suzanne Edmands

Saturday, June 21, 2014 -Poster #140

Ecological risk assessment is complicated by variation in chemical tolerance among populations of the same species. It is particularly important to know whether this variation is a result of physiological acclimation or evolutionary adaptation to determine whether a period under common conditions can normalize chemical tolerance among populations. This study examined variation in chemical tolerance within and among species of the marine copepod Tigriopus, a proposed ecotoxicological model system. Specifically, we assessed whether chronic exposure of laboratory populations elicited an acclimation or adaptation response and whether variation in tolerance in natural populations is a result of acclimation or adaptation. We focused on two common marine pollutants, copper (Cu) and tributyltin oxide (TBTO). Tigriopus has been exposed to Cu, which occurs naturally at low concentrations, throughout its evolutionary history and uses it as an essential micronutrient. In contrast, TBTO is anthropogenically-generated and has only recently been introduced into marine environments. Examining reproductive output as a measure of tolerance, a laboratory population of Tigriopus chronically exposed to Cu showed a response consistent with acclimation (fast gain/loss) while chronic exposure to TBTO showed a response consistent with adaptation (slow gain/loss). Using another metric of tolerance, median lethal dose (LC50), we found variation in tolerance to Cu and TBTO among natural populations of two species of Tigriopus. This variation was still present after 5 generations of maintenance under common conditions indicating that tolerance differences among natural populations are not strictly a result of acclimation. Maintenance under common conditions may not be sufficient to normalize chemical tolerance when comparing populations of Tigriopus.

Cryptic Diversity in Ethiopian Highland Amphibians Revealed Through Molecular Data

Megan Smith, Brice Noonan, Timothy Colston

Saturday, June 21, 2014 -Poster #141

Cryptic diversity in Ethiopian Highland amphibians revealed through molecular data

Megan Smith1, Brice P. Noonan1, Timothy J. Colston1,2

1Biology Department, University of Mississippi, University, MS 38677 USA

2Department of Zoology, Addis Ababa University, Addis Ababa, Ethiopia

The Ethiopian highlands harbor high levels of endemism and are characterized as a world biodiversity hotspot. There are more than 63 described amphibian species in Ethiopia, and, of these, 40 percent are considered endemic. The Ethiopian central plateau is divided into the Harar Massif on the East and the Abyssinian Massif on the West. While these massifs are characterized by a temperate, wet climate, the Great Rift Valley, which divides the two, is hot and dry and may serve as a dispersal barrier for highland species. We used molecular techniques to investigate diversification patterns in two widespread amphibian taxa (one frog and one toad) in the Ethiopian highlands. The genus Ptychadena is thought to have experienced an evolutionary radiation in the Ethiopian highlands and Freilich et al. studied the molecular diversity of highland Ptychadena. They identified eight distinct species, including P. cooperi, P. nana, P. erlangeri, and five cryptic species in the P. neumanni species complex. We collected molecular data for 55 additional individuals and previously unsampled localities, including the first molecular data for the rare species P. harenna. Our results highlight further undiscovered cryptic diversity in this species complex. The genus Amietophrynus consists of 38 species of toads native to Africa and has a complex, unresolved phylogeny. The molecular diversity of A. regularis has not previously been studied in the Ethiopian highlands and may represent a cryptic species complex. To investigate this, we collected molecular data from 53 individuals spanning the species range in Ethiopia Our results revealed cryptic diversity within this species complex and broaden our understanding of the hidden diversity contained in Ethiopian highlands. Lastly, we use biogeographic tools to investigate patterns and timing of diversification within these two taxa.

Natural variation in freeze tolerance between the yellow monkeyflowers Mimulus tilingii and M. guttatus

Alexis Caldwell, Clifford Smith, Kevin Kurack, Carrie Wu

Saturday, June 21, 2014 -Poster #142

Plants that are restricted to alpine environments frequently encounter freezing temperatures, which can pose a particularly strong environmental stress. Because cold-acclimation and freezing tolerance has been found to be metabolically costly, it may pose a negative fitness cost for plants if they rarely experience freezing stress. As closely related members of the Mimulus guttatus (yellow monkeyflower) species complex in western North America occupy a variety of ecological niches, including alpine habitats, they provide an ideal opportunity to test for this type of specialization to environmental stresses. We have developed an electrolyte leakage assay (ELA) to quantify tissue damage due to subfreezing temperatures, and determined that lowland M. guttatus plants show substantially greater tissue damage at temperatures below -6°C than alpine M. tilingii. Our findings suggest that the differences in freeze-tolerance between the two species likely have an important role in their habitat divergence. We also found an additional, compelling trend: populations from the southern range of M. tilingii appear to suffer slightly greater freeze damage than do plants from northern populations. This differentiation is consistent with variation in morphological traits that may confer freeze-tolerance through different mechanisms, most notably via secretions of glandular trichomes in the southern populations. Any protective benefits of these secretions on the leaf surface would not be detected by our ELA.

Exploration of the Evolutionary Landscape of Chemical Sequestration Using a Model System from the Southern United States

Katherine Bell, Chris Nice, Premal Shah, James Fordyce

Saturday, June 21, 2014 -Poster #143

Chemical sequestration, the acquisition of toxic material from plants by insects for defensive use, is fundamental to many ecological and evolutionary phenomena. The maintenance of chemical sequestration involves tri-trophic ecological interactions and antagonistic selection. Evidence from tri-trophic interactions demonstrates that variation in plant chemistry will not only affect herbivores but also their natural enemies, and thus the influence of plant chemistry will extend to higher trophic levels. Sequestration may affect fitness in two ways: it can increase fitness through defense against predators, but it can also decrease fitness through increased development time and reduced energy reserves. The balance of these fitness consequences are typically related to the amount of toxin that is sequestered. Estimates of the fitness response surface of sequestration must involve consideration of predator response as well as potential fitness costs to herbivores. In Lepidoptera, there remains a gap in our knowledge of the behavioral response of invertebrate predators to prey toxicity. Using a model system for sequestered defenses, the pipevine swallowtail butterfly (Battus philenor), we examined the effect of variable prey toxicity on predator efficacy, explicitly linking predator behavior to prey toxicity. Additionally, we assessed the stage specific fitness costs of sequestration in the pipevine swallowtail butterfly. We used these results to estimate fitness parameters and carry out model validation for a conceptual framework developed to explore the benefits and costs of chemical sequestration. Our framework includes two models, the first simple model that allows for a single predator encounter per group of caterpillars and a second expanded model that allows for multiple encounters. The results from the parameterized models reveal the complex evolutionary trade-offs and fitness consequences involved with the maintenance of chemical sequestration. In the future these models have the potential for broad application to other systems, providing valuable information about the role that chemical sequestration may play in many ecological and evolutionary phenomena.

Reproductive isolation in sympatry & allopatry: Gene expression/sequence analysis of courtship traits and male sterility in Hawaiian Drosophila

Donald Price, Eva Brill, Thomas Fezza, Anne Veillet, Elizabeth Stacy, Pawel Michalak

Saturday, June 21, 2014 -Poster #144

One of the grand challenges in evolutionary biology is determining how the phenotypic mechanisms and genetic factors evolve to create and maintain species. The Hawaiian picture-winged Drosophila offer an excellent opportunity to examine species at different stages of the speciation process that are isolated by pre-reproductive courtship behaviors and post-reproductive hybrid male sterility. We are investigating the courtship behavior, epicuticular hydrocarbons and hybrid male sterility between three species, the sympatric D. silvestris and D. heteroneura on Hawaii Island and their close relative D. planitibia from Maui. D. silvestris and D. heteroneura are sympatric and known to hybridize in nature but exhibit differences in epicuticular hydrocarbons and behavioral reproductive isolation. In contrast, D. silvestris and D. planitibia are allopatric and produce viable but sterile hybrid males. We are utilizing the recently sequenced genomes of these species to analyze the genomic sequence and gene expression differences of backcross males in these species that are associated with differences in male mating ability, epicuticular hydrocarbons and male sterility. These results will allow us to examine the genomic changes associated with behavioral isolation, epicuticular hydrocarbons and hybrid male sterility. This research will advance our understanding of the genetic and phenotypic basis of early stages of pre-reproductive and post-reproductive isolation that are important in Hawaiian Drosophila speciation.

Divergence and gene flow in a cosmopolitan lineage of dabbling ducks

Joel Nelson, Kevin McCracken, Jeffrey Peters

Saturday, June 21, 2014 -Poster #145

The shovelers (genus Anas) are a globally distributed dabbling duck lineage comprising four species, each found on a different continent. Although these species are widely allopatric, high dispersal abilities potentially make gene flow likely. We obtained samples from the Holarctic northern shoveler (Anas clypeata; N = 50), African Cape shoveler (A. smithii; N = 28), South American red shoveler (A. platalea; N = 23), and Australasian shoveler (A. rhynchotis; N = 13) from widely distributed locations throughout their respective ranges. We sequenced five nuclear introns and the mitochondrial control region to examine phylogenetic relationships and to test for gene flow. Phylogenetic relationships inferred from mitochondrial (mt) DNA and nuclear (nu) DNA were concordant, recovering northern and Australasian shovelers as sister taxa and the red shoveler as the basal lineage. Coalescent analyses revealed significant evidence of gene flow from the northern shoveler into the Australasian shoveler and perhaps into the Cape shoveler, but not into northern or red shoveler. We conclude that the migratory behavior of northern species, relative to the sedentary behavior of the southern species, facilitates gene flow, and that this species complex is an excellent candidate for divergence with gene flow models of speciation.

The molecular basis of novel phenotypes in hybrids: transgressive segregation in heat-tolerance

Madoka Krick, Ricardo Pereira, Felipe Barreto, Ron Burton

Saturday, June 21, 2014 -Poster #146

Hybridization may lead to genetic incompatibilities (hybrid breakdown) or to the manifestation of novel phenotypes that are extreme relative to parental taxa. The latter process is called transgressive segregation, and the resulting phenotypes may colonize new ecological niches and become established as new taxa of hybrid origin. The molecular basis of transgressive phenotypes is largely unknown; they may result from the combined action of different genes that are uniquely expressed in parental taxa (complementary gene action), or be a consequence of extreme up-regulation in genes that are normally expressed in both parentals (over-expression). Here, we test which of these mechanisms underlies increased thermal tolerance in hybrids of the copepod Tigriopus califonicus. Using trancriptome data from thermal tolerant populations, we chose candidate genes based on significant up-regulation during heat stress in either both or only one parental taxa, and use real time quantitative PCR (qPCR) to validate these categories. We generated 200 recombinant inbred lines (RILs), characterized by random assemblages of the parental genomes. Subsequently, we classified RILs as transgressive or intermediate, according to their survivorship to 36.5°C heat stress, which is nearly lethal to parental taxa (survival 10% and 35%). Finally, we used qPCR to quantify gene expression of the candidate genes in transgressive and intermediate hybrids and distinguished the underlying mechanisms of transgressive segregation in heat tolerance. Learning more about the genetic basis of transgressive phenotypes will contribute to our understanding of a possible mechanism of speciation by hybridization.

Characterization of Newly Discovered Interspecific Hybrids in the Drosophila affinis Subgroup

Amanda Abrams, Ryan Mulqueen, Spencer Koury

Saturday, June 21, 2014 -Poster #147

That the D. affinis subgroup follows Haldane's rule is based on observation of four interspecific hybrids. Here we report on several newly discovered viable hybrid crosses. We established multiple inbred lines of five species from the D. affinis subgroup: D. affinis, D. athabasca, D. narragansett, D. azteca and D. algonquin. Of the 20 possible interspecific crosses (reciprocal crosses included), five viable crosses have been previously published, and we documented eight newly observed viable hybrids. These new successful interspecific hybridizations include: two reciprocal crosses for previously known hybrids, one new hybrid (D. affinis x D. algonquin) where reciprocal crosses yield viable offspring, and four newly observed crosses that are successful in only one direction. After establishing viability of the hybrids, we examined sex ratios and fertility of the F1 generation to re-evaluate Haldane's Rule in light of the newly discovered hybrids. We also characterize these hybrids by examining the quantitative genetics of sex comb morphology which is the species diagnostic trait for the D. affinis subgroup. The emerging picture is that all species in the D. affinis subgroup can form interspecific hybrids with each other, and adhere to Haldane's Rule. We propose D. affinis subgroup is an a particularly interesting study system for the different theories of Haldane's Rule, especially given the prevalence of sex-linked meiotic drive and sex linked-suppressors in this subgroup.

The genomic landscape of a homoploid hybrid species

Tore Oldeide Elgvin, Glenn-Peter Sætre, Cassandra Trier

Saturday, June 21, 2014 -Poster #148

The Italian sparrow (Passer italiae) has been shown to be of hybrid origin resulting from hybridizations between the house sparrow (P. domesticus) and Spanish sparrow (P. hispaniolensis). Homoploid hybrid speciation is thought to be rare in animals with just a handful of well documented cases, and we aim at understanding more of the underlying genetics of this mode of diversification. Recently, we have assembled a denovo reference genome and constructed a linkage map for the most ubiquitos of the parent species, the house sparrow. With subsequent re-sequencing of reference populations, we are doing a whole genome landscape analysis of the hybrid Italian sparrow and its parents. Results from the house sparrow assembly and a roadmap for the population genomic analysis of the three taxa will be presented.

Diversifying selection on candidate genes involved in postcopulatory reproductive incompatibilities between Drosophila mojavensis and D. arizonae

Jeremy Bono, Luciano Matzkin, Kim Hoang, Laurel Young

Saturday, June 21, 2014 -Poster #149

Traits involved in postcopulatory interactions between the sexes may evolve rapidly as a result of sexual selection and/or sexual conflict, leading to postmating-prezygotic (PMPZ) reproductive isolating barriers between diverging lineages. Although the importance of PMPZ isolation is recognized, the molecular basis of post-copulatory incompatibilities is not well understood. Here, we investigate molecular evolution of 24 previously identified genes potentially involved in PMPZ isolation between Drosophila mojavensis and D. arizonae, reasoning that genes under divergent selection between the species are most likely to generate incompatibilities. These analyses revealed four particularly strong candidates for involvement in PMPZ isolation based on patterns of molecular evolution and functional annotations. Transcripts of all four genes are transferred from males to females during copulation. Three of the four genes belong to the Sperm Coating Protein (SCP)-like family, including an ortholog of antares, which influences female fertility and receptivity in D. melanogaster. The transfer and persistence of male transcripts in the reproductive tract of mated females, coupled with evidence for divergent selection across species, point to a potentially novel mechanism generating PMPZ reproductive incompatibilities.

Trade-off between the reproductive and anti-competitor roles of a bacterial symbiont of insect-parasitic nematodes

Farrah Bashey-Visser, Sofia Bertoloni Meli

Saturday, June 21, 2014 -Poster #150

Microbial symbionts have been shown to have dramatic, beneficial effects on their eukaryotic hosts. Do different symbiont functions come at the expense of each other? Is it possible for symbiont traits to be beneficial in one context, but costly to the host in other contexts? We investigated these questions using Xenorhabdus bacteria, which are mutualistic symbionts of the obligately killing, entomopathogenic nematode (Steinernema spp.). Some Xenorhabdus bacteria produce an anti-competitor toxin called a bacteriocin that can restrict the growth of other genotypes of Xenorhabdus bacteria that may be present within the insect. Bacteriocin production can be beneficial to the producing bacterial genotype, and in the case of competition between different nematode species, to the nematode. Nevertheless, in nature both non-producing and producing genotypes appear to coexist. We examined in a non-competitive context the reproductive traits of sympatric nematode isolates associated with either producing or non-producing genotypes of Xenorhabdus. We found that nematodes associated with bacteriocin-producing bacteria were slower at killing their insect host and less successful reproducing than nematodes associated with non-bacteriocin producing bacteria. In future work we plan to decouple the nematode-bacterial associations to determine the mechanistic underpinnings of this trade-off. Our work demonstrates that various roles of a mutualistic symbiont can conflict with each other, which may maintain genetic diversity within the symbiont population.

Host-Parasite Interactions: The Cuckoo Catfish and Non-Sympatric Hosts

Anna Vinton

Sunday, June 22, 2014 -Poster #1

The cuckoo catfish (Synodontis multipunctatus) from Lake Tanganyika in Africa parasitizes mouth-brooding cichlid fishes (catfish eggs get picked up and incubated in the mouths of cichlid females, where the catfish young feed on cichlid eggs). I examined the impact of parasitism by the cuckoo catfish on an allopatric (not naturally co-occurring) mouthbrooding cichlid, the red zebra (Maylandia estherae) relative to that of a previously characterized sympatric (naturally co-occurring with the parasite) host species (Ctenochromis horei). The red zebra was parasitized significantly more than the sympatric C. horei, which suggests that the sympatric host has evolved strategies to minimize cuckoo catfish parasitism. Early development of the red zebra did not differ significantly from that of the C. horei, indicating no early developmental adaptations to deter the catfish young from eating the host young. While the courtship behaviors of C. horei were also similar to that of the red zebra, C. horei was clearly more aggressive, which may be an adaptation to avoid brood parasitism. I also examined levels of parasitism between the red zebra and a closely related, also sympatric albino zebra cichlid (Maylandia zebra). Due possibly to its lower visual acuity, the albino zebra morph was parasitized significantly more than the red zebra. Lastly, the catfish was found not to parasitize hosts at random, but to prefer to parasitize female cichlids of an intermediate size.

Assessing Genotypic Bias in Neotropical Army Ant Caste Determination

Andrea Thompson

Sunday, June 22, 2014 -Poster #2

Ection burchellii, more commonly known as army ants, is one of the most well known species of predatory ants. Ection burchellii is a top Neotropical predator that has great ecological importance. Ection burchellii parvispinum colonies can have 10,000 to 2 million adult individuals that are divided into four casts: minors, media, submajors, and, majors. These four casts exhibit strong polymorphism; minors being the smallest in size and majors being the largest with giant sickle shaped mandibles that are used for defense of the colony against predators. Ection Burchellii parvispinum is highly polyandrous, with only one queen that mates with up to 17-20 males to produce her sterile workers. This study seeks to examine if there is a genetic component to cast determination of a worker. 18 colonies from the tropical dry forest Area de Conservacion Guanacaste (ACG) in Central America were sampled in this study. 12 microsatellites were amplified from DNA extracts and used to infer parentage of each Ection colony to determine if there is a genotypic bias in caste determination. This information can be used to infer effective population size and potential for relative inbreeding.

Inferring parentage in Eciton burchellii colonies

Gabriel Trujillo

Sunday, June 22, 2014 -Poster #3

Apex predators are often thought of as charismatic vertebrate megafauna. Despite the small size of an individual army ant, the top Neotropical predator Eciton burchellii is of equal ecological importance as more familiar vertebrates occupying the highest trophic levels. Given their abundance in Neotropical ecosystems and the variety of their prey, these nomadic social insects could be critical for maintaining diversity, and thus understanding genetic variation and reproductive dynamics is important for shaping conservation policy. E.burchellii parvispinum is highly polyandrous, but each colony only has one queen. Through collections sampled from the Area de Conservacion Guanacaste, I was able to analyze 18 colonies of E. burchellii parvispinum with 12 microsatellites to infer parentage of each colony. This information can be used to infer effective population size and potential for relative inbreeding.

The role of Agouti isoforms in the evolution of pigmentation differences in deer mice

Tess Linden, Ricardo Mallarino, Catherine Linnen, Hopi Hoekstra

Sunday, June 22, 2014 -Poster #4

The search for mutations that contribute to adaptive phenotypic variation has generally focused in two areas: protein-coding changes and cis-regulatory mutations. For the latter, few mutations have been identified and therefore the underlying mechanisms driving gene regulatory evolution have remained elusive. Here, we provide a novel example for the role of isoform variation in adaptive evolution. Previous studies in a population of deer mice (Peromyscus maniculatus) living in the Nebraska Sand Hills have shown that multiple mutations at the pigmentation locus Agouti are associated with light fur coloration that camouflages these mice from visual predators. Here, we identify two novel upstream regulatory exons of Agouti that are expressed at high levels in the ancestral dark deer mice found off the Sand Hills, but down-regulated in light mice carrying the Sand Hills allele. We found that one of these novel exons contains three alternative start sites that each reduces the efficiency of protein translation. Therefore, down-regulation of this isoform may represent a mechanism for increasing the strength of the Agouti expression that leads to lighter pigmentation. These findings demonstrate that the alternative splicing of regulatory elements of a gene transcript can be a mechanism by which to modulate protein expression at both the transcriptional and translational levels in order to create a novel adaptive phenotype.

Cryptic diversity of Melanochlamys sea slugs (Gastropoda, Aglajidae) in the North Pacific

Samantha Cooke, Angel Valdes

Sunday, June 22, 2014 -Poster #5
Melanochlamys is a relatively small group of nine valid species of aglajid sea slugs (Gastropoda, Cephalaspidea, Aglajidae), typically found crawling on mud and other soft sediments. Very little is known about the ecology of these organisms, but at least one species is known to prey upon polychaetes and nemerteans (Rudman 1972). In this study, North Pacific specimens of Melanochlamys sea slugs were examined morphologically (including the male reproductive morphology, shell, and external coloration), and were sequenced for 3 genes (mitochondrial COI and 16S and nuclear H3) to determine the evolutionary relationships and species diversity. Both molecular and morphological data revealed an unexpected high level of cryptic diversity. At least four distinct species occur on the Northwestern Pacific. Melanochlamys ezoensis occurs in Russia and temperate and cold areas in Japan. Three additional undescribed species occur in Japan and South Korea. One of the undescribed species occurs both in South Korea and in Japan, but only in Tokyo Bay, suggesting that it could be non-native in Japan. Two distinct species occur on the Northeastern Pacific coast; Melanochlamys diomedea, widespread from Southern California to Alaska, whereas M. ezoensis was found only in San Francisco Bay, suggesting a human-mediated introduction. This was further supported by the absence of records of M. ezoensis in San Francisco prior to 2001. The species diversity of Melanochlamys in the Northwestern Pacific is much greater than in the Northeastern Pacific; it is hypothesized that differences in geographic and ocean current system complexity might account for different responses to glacial extinction and postglacial expansion.

Discordance Among Geographical, Morphological, and Genetic Data May Indicate Interspecific Hybridization in the Peromyscus leucopus Species Group

Jennifer Brannon, Sean Beckmann

Sunday, June 22, 2014 -Poster #6
Hybridization between sister taxa has been identified in numerous animal groups. Within the Peromyscus leucopus species group, hybridization has been observed in controlled laboratory settings and has been suggested in the wild. Given the high degree of morphological variation within this species group, identification of hybrids in the wild has been largely speculative. In this study, the D-loop of the mitochondrial control region was sequenced in several museum and field caught specimens of P. gossypinus, the sister taxon of P. leucopus. All specimens were from coastal South Carolina, within the allopatric range of P. gossypinus, and were morphologically identified as P. gossypinus in the field. Museum skin identifications were verified by museum personnel. Sequences were compared to those of both P. gossypinus and P. leucopus retrieved from GenBank. Phylogenetic reconstructions were performed using maximum parsimony, maximum likelihood, and Bayesian methods, with P. maniculatus as an outgroup. Resulting phylogenies identified that several specimens form a monophyletic group with GenBank sequences from P. leucopus. Given that mitochondrial DNA is maternally inherited, these data do not provide a complete picture but do suggest two distinct possibilities. The first is that the range of P. leucopus has greatly expanded in South Carolina. The second is that hybridization occurs within the P. leucopus species group in the wild and that coastal South Carolina supports several such organisms and/or their descendants. Genotyping of nuclear loci is needed to distinguish between these hypotheses.

Testing the Coalescent with Whole Genome Data

Amie Settlecowski, John Kelly

Sunday, June 22, 2014 -Poster #7
Here, we test the fit of the neutral coalescent, allowing recombination, to observed sequence variation along the first chromosome of the Mimulus guttatus genome. The parameters and are estimated from sequences collected from ten individuals of different inbred lines of one M. guttatus population. Using the estimated theta and rho, we simulate whole genome sequences, reiterating the data structure under the coalescent. We partitioned the observed and simulated sequences using the four-haplotype rule into ‘loci.’ For each locus, we inferred a genealogy, the tree length and the Pybus-Harvey gamma statistic. We measured discordance (Robinson-Foulds weighted and un-weighted distances) between neighboring loci. Analysis of the distribution of these measurements over both the real and simulated data revealed a difference in the mean of the gamma statistic. Since the model is parameterized from the data, the good fit of observed to predicted distributions of the other measurements is not unexpected. Observing that patterns of linkage disequilibria and other aspects of tree structure (frequency of polytomies) also mismatch the coalescent, we discuss reasons why the natural population may deviate from the assumptions of the coalescent.

Evolution of Biased Chemotaxis in Escherichia coli

Austin Cole

Sunday, June 22, 2014 -Poster #8
Cellular information processing is poorly defined. Few model systems offer ease of manipulation and precise measurement necessary for rigorous investigation of signal acquisition and response. With a defined genic network, protein architecture, and readily observable phenotype, chemotaxis in Escherichia coli (E. coli) coherently integrates both criteria. Although chemotaxis functionality is well understood, its evolution is unexplored. Our repeatedly selected cells preferentially scavenge Aspartate or Serine. Sequencing revealed a number of genes plausibly responsible for the observed change in functionality.

The effect of eye size and habitat on scleral thickness in mammals

Sophie Wang, Lars Schmitz

Sunday, June 22, 2014 -Poster #9

Marine mammals and reptiles are characterized by an array of morphological features that are considered to be adaptations towards secondary aquatic lifestyles. One of such features is found in the eye: it has been noted since the 19th century that the sclera, the fibrous protective outer layer of the eye, is unusually thick in marine mammals and reptiles. However, while the role of the thick sclera has been hypothesized about, differences in the thickness of sclera across different mammals have never been rigorously quantified. Here we show that the sclera of aquatic and semiaquatic mammals is thicker than the sclera of terrestrial mammals even when eye size is accounted for, using a sample of 70 species and 128 individual specimens. This is true for both the sclera at the posterior pole of the eye and sclera near the cornea. We also saw that phylogeny has a strong effect on this relationship, and therefore must be accounted for when determining variance in scleral thickness between habitat groups. We argue that the most plausible hypothesis is that increasing intraocular pressure as a method of visual accommodation causes increased scleral thickness, though other aspects of aquatic life like temperature and pressure may play small roles.

The impacts of floral features on pollinator landing success

Michael Rivera, Anna Dornhaus

Sunday, June 22, 2014 -Poster #10

Foraging bumblebees can visit upwards of one hundred flowers per trip, and landing on these flowers is the most costly part of foraging, both energetically and in terms of time. Here we quantify how floral traits affect how difficult it is for bees to land on flowers. We show that bumble bees are not always successful: around 20% of landing attempts fail even in experienced individuals. Given these limitations, how have flowers adapted to reduce the costs associated with pollinator foraging? We looked at two aerodynamic features of flowers, overall orientation and the presence of a ‘landing platform’, called a labellum. Flowers display a huge variety of shapes and orientations. Variation in the angle can drastically change the approach a bee needs to take when landing. Comparing horizontal and vertical landing surfaces, we saw no difference in the preference or success of foragers. When testing the effects of a labellum, we found that larger bumble bees land successfully more often with a labellum than without. However, this increase in success decreases with body size of the forager. Not only are flowers under selective pressure to ease the difficulty of pollinator landings, but they also could select for pollinator size, through their morphology

Floral and Pollinator Evolution in Light of a Near-complete Phylogeny for Polemoniaceae

Jacob Landis, Margarita Hernandez, Douglas Soltis, Pamela Soltis

Sunday, June 22, 2014 -Poster #11

The wide diversity of floral variation results in part from pollinator-mediated selection. Flowers are often characterized by a given suite of traits, historically coined pollinator syndromes, which are associated with certain types of pollinators. These traits can include characters such as flower size, color, and overall morphology. Although a correlation between certain floral characters and specific pollinators is still debated, it is clear that understanding morphological traits, such as flower color and size, and their association with pollinators will deepen our understanding of the biology of specific interactions and will ultimately contribute to a refined view of pollinator syndromes. Furthermore, a strong phylogenetic framework will provide a solid foundation on which to map floral characteristics and establish relationships between morphological adaptations and genetic mechanisms. Here we present a new phylogenetic analysis of Polemoniaceae, with samples from 92% of the nearly 400 species. Using this phylogeny, we evaluate the evolution of flower color and flower size in the context of known pollinators. Analyses suggest over 40 transitions in flower color, with both color gains and losses observed. Flower size (length and width) was measured from herbarium specimens, with several accessions used per taxon when available. Analyses were conducted using continuous data, as well as binning into discrete groups. Many transitions result, with overall flower size increasing and decreasing in certain genera. Further analyses are needed to investigate the role that flower size plays in attracting specific pollinators. This project lays the foundation for ongoing projects on the genetic mechanisms involved in the evolution of flower color and flower size in Polemoniaceae.

Migratory birds carry plant diaspores in their feathers

Emily Behling, Lily Lewis, Hannah Gousse, Emily Qian, Chris Elphick, Jean-François Lamarre, Joël Bêty, Ricardo Rozzi, Bernard Goffinet

Sunday, June 22, 2014 -Poster #12

Migratory birds are commonly invoked as vectors for transequatorial dispersal of plants, but supporting evidence is largely circumstantial. Birds disperse plant units internally via ingestion or externally. Internal dispersal plays a significant role in the dispersal of seeds and invertebrates. External dispersal may play an important role in dispersal across extreme bipolar disjunctions and for organisms for which dispersible units (diaspores) are not adapted to animal mediated dispersal. However, it remains unknown if birds carry plant diaspores externally. Here we show that transequatorial migrant birds captured in their arctic breeding range harbour a diversity of plant diaspores in their plumage. Three of the recovered units represent wind-dispersed lineages (mosses and liverworts). Our observations indicate that bird mediated dispersal plays a role in the dispersal of lineages that lack adaptations for animal mediated dispersal. The frequency with which we recovered diaspores suggest that entire migratory populations may be departing their northern breeding grounds laden with potentially viable plant parts and thereby play a significant role in bipolar range expansions.

Documentation of Female Song in the Tropics: The Case of the Puerto Rican Oriole

Susanna Campbell

Sunday, June 22, 2014 -Poster #13

Evolutionary biologists often assume that elaborate traits that cause sexual dimorphism evolve through male competition for females. However, recent work from our lab showed that the males and females of the common ancestor of all song birds both sang. Therefore, the dimorphism that is observed in many temperate breeding songbird species is due to loss of female song and not the gain of song by males (Odom et. al 2014, Nature Communications). We investigated whether Puerto Rican Orioles (Icterus portoricensis), a tropical songbird, exhibits both male and female song. For this project we marked individuals with sex specific color bands and collected DNA samples. We successfully isolated CHD, a gene that is present in different lengths on either of the sex chromosomes in birds and determined the sex of our banded individuals. In March 2014, we repeatedly observed and recorded female song as well as male song of the Puerto Rican Oriole. Our findings show that both male and female Puerto Rican Orioles sing. This information helps show that the common ancestor to the oriole genus had both male and female song and that dimorphism has evolved due to loss of female song.

Species delimitation and genetic diversity among populations of Etheostoma raneyi (Yazoo Darter) in northern Mississippi.

Andrew Brown

Sunday, June 22, 2014 -Poster #14

Abstract

The Yazoo Darter, Etheostoma raneyi (Percidae; subgenus Ulocentra) is a small, freshwater fish species endemic to tributaries of the Yocona and Tallahatchie rivers of the upper Yazoo River basin, North Mississippi. The two populations are allopatric and isolated by unsuitable habitat (i.e. lakes and unsuitable downstream areas) which lies between the two river drainages. It is possible that after being physically isolated for an extended period of time that the two populations have diverged into separate species. The goals of this study were to (1) determine whether the two populations of E. raneyi are genetically distinct from one another and the extent of gene flow (if any), (2) estimate the divergence time of the populations using sequence divergence and known mutation rates, (3) determine what event(s) may have caused the split, and (4) address the need for conservation. Both nuclear (S7) and mitochondrial (cytb) DNA data were obtained from 66 individuals, representative of the distribution of E. raneyi. The distribution of genetic lineages was analyzed using Bayesian and network-based frameworks. Nucleotide divergence values, as a measure of genetic distance, were used to estimate the time since divergence based on known mutation rates. We found that the two populations are genetically isolated and significantly distinct from each other. There is strong support for two monophlytic clades, restricted to the two river drainages. Based on the divergence time estimates, we conclude that the separation of these populations must have occurred in the Pleistocene, and was likely due to headwater stream capture caused by the climatic and geological changes occurring at that time. These findings strongly support the need for a re-evaluation of the current taxonomic classification of the species and highlight the need for conservation of these highly vulnerable, endemic fishes.

Developing and evaluating novel nuclear markers for phylogenetic reconstruction in the myrrh genus,Commiphora Jacq.using multiplexed target enrichment

Kiera Coy, Andrea Weeks, Morgan Gostel

Sunday, June 22, 2014 -Poster #15

To date, widely available nuclear genetic markers (e.g., ETS, ITS) have not provided sufficient variation to fully resolve the evolutionary relationships among the ca. 200 species of Commiphora. Here we use freely available genomic resources to expand the range of genetic markers that can be used for comparative phylogenetic analyses and are optimized for parallel enrichment and sequencing. This poster describes the development and evaluation of these markers from a target pool of about 950 putative shared single-copy nuclear genes using Madagascan species of Commiphora to test them. These closely related species have radiated relatively recently and are a good model for selecting the most informative markers across the genome. Development of these markers followed a bioinformatics pipeline we developed that compares a draft transcriptome of Bursera simaruba against a pool of putative single-copy, orthologous nuclear genes shared across angiosperms. Our analysis identified a subset of approximately 240 genes that aligned to the Bursera simaruba transcriptome and our target gene pool. We demonstrate the effectiveness of a subset of markers for comparative phylogenetic analyses and propose criteria for future research that will consist of primer optimization, size standardization of target products, and sequencing the targets using microfluidic PCR and multiplexed next-generation sequencing. Sequences from these new markers will allow us to better understand the rapid diversification of Commiphora in Madagascar. These gene regions may be useful for phylogenetic analysis in resolving challenging species-level relationships in other angiosperm groups beyond Commiphora and Burseraceae. We will develop test these markers more broadly in other angiosperm lineages for comparative phylogenetics at broad and shallow-scales.

Effect of chronic infection on resource allocation

Sarah Khalil, Moria Chambers, Brian Lazzaro

Sunday, June 22, 2014 -Poster #16

Previous research on infection in fruit flies focuses on the effect of acute infections, which cause moderate to high levels of mortality and significantly reduce lifespan. However, humans routinely face infections which persistent throughout their life-time with little clinical symptoms. We use Drosophila melanogaster to investigate chronic infection's effect on resource allocation. A chronic infection occurs when a pathogen persists in the host without causing mortality. Flies chronically infected with the bacterium Providencia rettgeri have increased resistance to secondary acute infections, as well as decreased starvation resistance. These findings suggest an underlying physiological tradeoff between host immunity and metabolism. My project determined how chronic infection affects Drosophila resource allocation by measuring several aspects of its immune and metabolic systems.

During the chronic infection, bacterial numbers are relatively constant. We hypothesize that this equilibrium is due to active proliferation of bacteria countered by simultaneous bacterial killing by the fly's immune system. To test whether chronically infected flies maintain immune activation, we measured antimicrobial peptide induction, an instrumental part of the Drosophila immune response. Infected flies have a higher transcription of the defensin, dipterecin, attacin, and metchnikowan anti-microbial peptides genes.

An actively cycling equilibrium could also put strain on the host's energy stores. To test whether chronically infected flies have reduced energy stores, we measured triglyceride and soluble protein levels one week post infection using biochemical assays. Metabolite levels were normalized to wet weight to account for natural variation in body size. Chronically infected flies have decreased triglyceride and increased protein levels seven days post infection.

This study will improve our understanding of how chronic infection adjusts Drosophila's investment in energy stores and immunity. We are preparing to knock down immune function after establishment of chronic infection in order to determine whether this causes an acute outbreak. In the wild these tradeoffs have important implications for the organism's fitness – survival to secondary infections will impact lifespan and resource availability will impact ability to invest in reproduction.

Remarkable colonization from West Indies to Neotropical mainland in weevils supported by phylogenetic and biogeographic analyses

Usmaan Basharat

Sunday, June 22, 2014 -Poster #17

Sampling ~100 species and six gene fragments, we conducted a molecular phylogenetic analysis and reconstructed the biogeographic history of broad-nosed weevils (Insecta: Curculionidae: Entiminae) in the Exophthalmus genus complex from the West Indies (a.k.a. the Caribbean) and Central America. We revealed a remarkable colonization event from the West Indies to the Neotropical mainland. We also investigated the diversification and biogeographic history of weevils within the West Indies.

Past and current debates on the origin of the West Indian fauna have centered on three alternative hypotheses: late cretaceous vicariance, over-water dispersal, and a recent theory coined as mid-Cenozoic GAARlandia land bridge (GAAR = Greater Antilles + Aves Ridge). In comparison, less attention has been devoted to the biogeographic scenarios of and inter-relationships within the West Indian islands. Comprising more than 65,000 described species, Weevils are a mega-diverse lineage of insects. The Exophthalmus genus complex contains >110 described species, distributed on both the West Indian islands and the Neotropical mainland, therefore providing an ideal opportunity for testing the origin of the West Indian fauna, its relationship to the mainland, and the diversification history within the islands.

In the current study, we sampled ~100 species, with representatives from all major islands in the Greater Antilles, part of the Lesser Antilles and Central America (Panama, Costa Rica and Nicaragua). Based on six gene fragments (28S, 16S, 12S, COI, EF1-alpha and Arginine Kinase; >4,000bp), we reconstructed a dated molecular phylogeny incorporating fossil calibration points. We performed model-based statistical biogeographic analyses. We found a remarkable colonization event of weevils from the West Indies to the Neotropical mainland during the Miocene. We also inferred multiple inter-island vicariance/dispersal events in the West Indies.

Elemental Defense in Alyssum murale: Effect on a Specialist Herbivore, Pieris rapae

Alexandria Igwe, Mary McKenna

Sunday, June 22, 2014 -Poster #18

Alyssum murale (Brassicaceae) is a nickel-hyperaccumulating plant from serpentine habitats in the Mediterranean region. The "elemental defense hypothesis" (Martens & Boyd 1994) suggests that metal hyperaccumulators benefit by reduced herbivory on tissues with high levels of heavy metals. Generalist herbivores may gain protection against elemental defenses by a dilution effect since small amounts of dietary toxins may not have significant negative consequences. A previous study (Kissell and McKenna, 2008) showed that elemental defense does not protect A. murale seedlings from generalist herbivores (slugs, Gastropoda) under field conditions. This study examines the response of a specialist herbivore (Pieris rapae) to an elemental defense (nickel) in A. murale. We focused on two questions: Do high levels of soil nickel protect Alyssum murale against herbivory by a specialist herbivore (Pieris rapae)? and Does plant nickel concentration affect growth of the specialist herbivore Pieris rapae?

A. murale seeds were germinated in soils at 0 ppm, 100 ppm, 500 ppm, and 2000 ppm Ni. Plants were transplanted after 4 months to grow singly in small pots at each nickel level for 8 weeks. Initial plant size (leaf number) was measured before placing 4 plants in a "no choice" array with one P. rapae larvae. Arrays were covered with a plastic lid containing a mesh top that prevented herbivores from escaping, but allowed airflow, light penetration, and watering. After one week, we removed the larvae for analysis and took final plant size measurements.

We found high herbivory in controls; significantly fewer leaves remained after exposure to the herbivore for one week (p = 0.003). There was no difference in plant size (leaf number) after exposure to the herbivore for plants in 100 ppm and 500 ppm nickel. Plants in soil with 2000 ppm nickel showed significantly greater leaf number after exposure to the herbivore (p=0.04), suggesting net increase in biomass over the one week period. High nickel concentrations appear to interfere with larval growth; high nickel levels resulted in smaller P. rapae larvae. In addition, we recovered fewer larvae from plants with highest nickel levels. This study adds to our understanding of the potential selective advantage of heavy metal accumulation in protecting plants against specialist herbivores. Further long-term studies on the interactions between specialist and generalist insects with metal-accumulating plants are needed to explore the relative selective advantages of physical, chemical, and elemental defenses in these species.

Consequences of terrestrial egg laying in amphibians: a comparison of embryonic oxygen sensitivity in two Ambystomatid salamanders

Natrieifia Miller, Emily Saxe, Rebecca Hale, Caroline Kennedy, Robert Francis

Sunday, June 22, 2014 -Poster #19
Natrieifia Miller, Emily Saxe, Rebecca Hale, Caroline Kennedy

Many amphibians lay their eggs in seasonal ponds and fast growth both reduces the amount of time larvae face the intense resource competition typical in these ponds and ensures that larvae metamorphose before ponds dry. In addition, female size at metamorphosis can be positively correlated with fecundity. As a result, natural selection should favor individuals that develop faster and are larger at metamorphosis. However, selection on these two traits can be antagonistic, as metamorphosing earlier is often achieved by metamorphosing at a smaller size. Low DO concentrations should heighten this antagonism. For example, larvae whose growth is prolonged by unfavorable conditions often reach typical metamorphic size later. Therefore, they may respond by either taking longer to metamorphose yet reaching a favorable size, or by metamorphosing smaller, but leaving the highly competitive pond environment sooner. One solution to this problem may be for species that develop in low oxygen environments to evolve greater metabolic efficiency such that, for a given level of DO, low oxygen-adapted embryos and larvae develop faster and/or are larger at metamorphosis than those of closely related species that typically develop in high DO environments. We test this hypothesis in two closely related salamanders, Ambystoma opacum and A. maculatum. A. maculatum, like most Ambystomatids, lays its eggs aquatically. In contrast, A. opacum lays its eggs terrestrially, in moist soil. The aquatic and terrestrial environments differ considerably in oxygen availability and it is possible that A. opacum's ability to develop with lower oxygen availability is lessened compared to that of A. maculatum. We examine embryonic development of these two species under laboratory conditions, comparing growth, development, and hatching success under a range of dissolved oxygen concentrations as well as in a moist, terrestrial environment.

Development of microsatellite primers and population genetics of an arctic-alpine species, Toefiledia pusilla

Daniela Zarate

Sunday, June 22, 2014 -Poster #20
The objective of this study is to understand how past and current climate change affects the phylogeography and genetic diversity of Tofieldia pusilla. T. pusilla is an arctic-alpine plant species whose geographic range distribution is characterized by a significant separation between the core of its species distribution and a few disjunct populations present in more southern latitudes, such as Isle Royale, Michigan. Disjunct populations offer a valuable window to study the effects of climate change on the population's diversity and evolution as these populations are often subject to extreme geographical isolation and divergent environmental conditions that can leave the species prone to extinction. Analogs like this are relevant to conversations of the effects of modern, anthropological-driven, climate change on the population genetics of endangered species. In order to assess genetic diversity and population genetic structure of T. pusilla, I developed polymorphic microsatellite markers and am currently analyzing the population genetic structure in Isle Royale National Park (Michigan) and two populations in Newfoundland (Canada). Isle Royale National Park is a protected national park and as such, any changes in population are likely due to measured shifts in weather patterns or a change in biotic interaction, not simply human interference.

Population genetic analysis of golden eagles (Aquila chrysaetos) killed at the Altamont Wind Pass Resource Area in California

Nadia Fernandez, Jacqueline Doyle, Todd Katzner, J. Andrew DeWoody

Sunday, June 22, 2014 -Poster #21
The Altamont Pass Wind Resource Area (APWRA) in west-central California is one of the largest and oldest operational wind farms in North America. Raptors, including many species of conservation concern, are often killed in collisions with wind turbines. We obtained golden eagle (Aquila chrysaetos) carcasses killed at APWRA in 2012 and 2013 and asked whether they were comprised of distinct population segments (e.g., migrants and residents) or if they represented a single gene pool. We extracted DNA from feather, tissue, and bone samples (n=45). We then genotyped these eagles at 9 microsatellite loci and we sequenced a ~700 bp portion of the mitochondrial DNA control region. There was no evidence of population structure and our results suggest that the eagles killed at APWRA constitute a single panmictic population. These data will be important to future modeling efforts that will determine if wind turbine mortality is compensatory or additive.

Biogeographical Patterns of Two Phoenicurus Redstarts Across Eurasia

Anna Blick, Gary Voelker, Sergei Drovetski

Sunday, June 22, 2014 -Poster #22

The avian genus Phoenicurus (redstarts) are widely distributed across Eurasia and Northwest Africa. Many species are migratory and have widespread distributions, while a few species are more restricted geographically. Recent studies have found genetic and geographic structuring within a number of species distributed across eastern, western, and southern Eurasia. An interspecific biogeographic study of Phoenicurus has also indicated that both Phoenicurus auroreus and Phoenicurus ochruros have deeply divergent clades; this was however based on very limited sampling of geographically disjunct populations. In this study, we elucidate the biogeographic patterns of Phoenicurus through phylogenetic and phylogeographic analysis of Phoenicurus ochruros and Phoenicurus auroreus, using 2 independent molecular loci: mitochondrial NADH dehydrogenase 2 and intron 9 of the Z chromosome specific ACO1. Bayesian, maximum likelihood, and molecular dating methods are used to assess patterns of diversification within each species. We then compare phylogenetic structure between these species in order to determine possible causative links between genetic structuring and vicariant events, such as desertification and glacial cycles of Eurasia that have been linked to widespread speciation patterns in Eurasian birds.

Rhagoletis juniperina in the Great Lakes region: A bridge to Old World Rhagoletis?

Megan Frayer, Daniel Hulbert, Jim Smith

Sunday, June 22, 2014 -Poster #23

Rhagoletis juniperina Marcovitch (Diptera: Tephritidae) infests Eastern Red Cedar (Juniperus virginiana L.) and other North American junipers. R. juniperina is of interest both as a representative of the genus Rhagoletis, but also because it may tie together evolutionarily the Nearctic and Palearctic Rhagoletis fauna. Our goal in this study was to test two competing hypotheses first proposed by Bush (1966): i) that R. juniperina is more closely related to the Nearctic dogwood-infesting R. tabellaria, to which it is morphologically similar; or ii) that R. juniperina is more closely related to the Eurasian juniper-infesting R. flavigenualis. To study R. juniperina, which is rarely collected, we first established a local study site by collecting juniper berries from several sites in the Lansing, MI vicinity in fall 2010, finding a heavily-infested juniper tree on the Michigan State University campus. Mitochondrial COII sequences of reared pupae matched the R. juniperina COII sequence in GenBank, and the morphology of adults reared from these pupae the following spring and summer matched R. juniperina, as well. Phenological attributes of this population were determined via weekly fruit collections in fall 2011 and 2012, and “peak” larval infestation was found to occur during the first part of October, while mean post-diapause eclosion time was found to be approximately 110 days. R. juniperina adults were also reared from infested junipers found in Wisconsin and North Carolina (a new state record), indicating that the geographic range of R. juniperina is broader than previously thought. Hymenopteran parasitoids of R. juniperina were also observed; both a new pupal parasitoid (Coptera n. sp.) and an egg parasitoid (presumably Utetes juniperi) were collected at the MSU campus site. Phylogenetic analysis of mitochondrial COI sequences from R. juniperina indicates a sister relationship with R. tabellaria, with the sole R. flavigenualis individual in our sample basal to these two taxa. Interestingly, the analysis also revealed within-species haplotype variability in R. juniperina, with a 3.8% nucleotide sequence difference observed between COI sequences from MI, WI, and NC compared to the Ontario R. juniperina sequences in the Barcode of Life database.

Reproductive incompatibility within a woodland strawberry species

Rebecca Dalton

Sunday, June 22, 2014 -Poster #24

Hybrid incompatibility between individuals from isolated populations may be asymmetrical if there is a conflict between mitochondrial and nuclear genes, and this incompatibility could lead to hybrid breakdown, playing a role in speciation. Recent data suggests that there are a number of genetic differences (in chloroplast, mitochondrial, and nuclear genomes) between two populations of gynodioecious Fragaria vesca subsp. bracteata, suggesting that crosses between populations could exhibit genetic conflicts and thus hybrid incompatibilities. To determine if there is evidence of asymmetrical reproductive isolation between two geographically distinct populations, we produced ~1500 progeny from inter and intrapopulation crosses. We crossed female and hermaphrodite maternal donors by hermaphrodite paternal donors for each population. Using seed set, germination, and male fertility as measures for hybrid fitness, we found some indication of asymmetrical reproductive barriers for male fertility measures in progenies derived from female maternal donors, but not for early measures of progeny fitness when either sex is the maternal donor. These results suggest that post-zygotic barriers for reproductive incompatibility may not prevent introgression of novel genes from other populations, and male fertility measures in the hybrid might be indicative of incipient cyto-nuclear interactions.

Duplicated Mitochondrial Genes in Whip-Tail Lizards

Jose Maldonado

Sunday, June 22, 2014 -Poster #25

Animal mitochondrial genomes are invariably compact (~15 kilobases in length), perhaps due to selection pressure to maintain an efficient genome. Having a smaller mitochondrial genome reduces the time and energy it takes to replicate. Parthenogenetic lizards, however, have large tandem duplications, making their mitochondrial genomes some of the largest in vertebrates. My research aims to use parthenogenetic whiptail lizard to determine how these duplications originated, what gene are involved, and how they are evolving. Using next-generation sequencing technology, I sequenced 30 complete mitochondrial genomes from whiptail lizards by employing a newly developed protocol that avoids many of the pitfalls of traditional, PCR-based methods.

Using a bioinformatics pipeline, I have assembled and annotated all of the genomes sequenced thus far. My preliminary results indicate that parthenogenetic lizards are all related to each other based on the mitochondrial genome sequences. Once additional genomes are sequenced, I will employ molecular evolutionary tools and theory to investigate how the duplications evolve.

The influence of community biodiversity on coevolution: Drosophila and their parasitoid wasp as a model system

Chia-Hua Lue, Jeff Leips, Matthew Buffington

Sunday, June 22, 2014 -Poster #26

Ecological interactions among species are one of the most important processes driving adaptive evolution and diversification. Strong and persistent interactions within communities can lead to the co-evolution of species and indeed, co-evolution has been proposed as one of the most important processes organizing biodiversity on earth. Communities are not homogeneous, and the diversity of species in communities can vary both temporally and geographically. Variation in community composition can produce variation in both the strength and nature of species interactions that will in turn influence the genetic characteristics of the interacting species. As such, variation in community composition can directly influence the evolutionary outcome of species interactions.

The geographic mosaic theory of coevolution (GMTC) provides a conceptual framework for studying coevolutionary processes in a community context and provides a foundation for my research. I am using Drosophila species (Insecta: Diptera: Drosophilidae) and their Eucoilinae parasitoid wasps (Insecta: Hymenoptera: Figitidae) as a study system for this work. My dissertation research is focused on describing host and parasitoid species and documenting patterns of variation in Drosophila host-parasitoid communities both temporally and geographically. I will then use this information to test how community diversity impacts the coevolutionary process in host-parasitoid interactions. I propose three objectives integrating both field surveys and laboratory experiments. The objectives are: 1) to describe clinal geographic and temporal variation in host-parasitoid community structure in seven locations along the east coast of North America; 2) to characterize local trophic interactions through the construction of quantitative food webs; and 3) to carry out laboratory transplant experiments and investigate how community composition influences patterns of local adaptation of coevolved traits. These objectives will help us understand how spatial and temporal variation in the community composition of hosts and their parasitoids influences host-parasitoid coevolution.

Population structure in Egyptian geese and their heamosporidian parasites

Tim Kawsky, Leah Shurte, Graeme Cumming, Jeffrey Peters

Sunday, June 22, 2014 -Poster #27

Egyptian geese (Alopochen aegytiacus) are found throughout southern Africa, along the Nile Valley, and in isolated areas along the southern and eastern coasts of the Mediterranean Sea. They potentially serve as vectors for the dispersal of diseases, such as avian malaria and avian influenza, which can have detrimental effects on other birds, including livestock. To resolve the geographic and genetic relationship between Egyptian geese and their haemosporidia parasites (including avian malaria), we screened 716 individuals for avian malaria and genotyped 54 individuals from five southern African populations using five nuclear loci. Egyptian goose populations had comparable levels of genetic diversity and weak to no genetic differentiation (mean Fst = 0.021). Forty-three (6.0%) individuals were positive for haemosporidia infections, forty-two of which were found in Strandfontein (STR) and Barberspan (BAR), South Africa. Overall, 19.3% of the total genetic variation in haemosporidia sequences was partitioned between these sites. This variation mostly resulted from frequency differences in infection rates between Haemoproteus spp. and Plasmodium spp. (BAR: 61.1% Haemoproteus; STR: 89.7% Haemoproteus (Fisher's Exact Test, P = 0.030)). Within genera, differences between sites were not significant (Haemoproteus, Fst = 0.0005; Plasmodium, Fst = 0.002; P > 0.4). Thus, population structure within genera of haemosporidia is concordant with that of their Egyptian goose hosts, which is consistent with these hosts serving as vectors for the dispersal of avian malaria.

Do ecology, habitat, life history or social behaviour influence disease risk in squirrels?

Mirjam Ansorge, Natalie Cooper

Sunday, June 22, 2014 -Poster #28

Squirrels are ubiquitous and share our parks and forests. Therefore they are likely to have close contact with humans and could be possible vectors for infectious diseases like plague. Understanding how disease risk is influenced by life history, ecology or squirrel behaviour can help us to predict which kinds of squirrels may pose the highest risk of infection for humans. Here we review records of disease carrying squirrels in North America and collected data on life history traits such as body size, life span and population density. We also included information about colonial behaviour, whether the squirrels hibernate, and whether they mainly life on the ground or in trees. As a measure of infection rate we used squirrel parasite species richness. We then used phylogenetic generalized least squares (PGLS) models (corrected for sampling effort) to investigate which of these traits bests predicts parasite species richness in squirrel species. We found no significant relationships between the mentioned parameters and parasite species richness of squirrels. Instead more idiosyncratic factors appear to be involved.

Who's your chipmunk? Co-divergence, host-switching, and diversification in a widespread pinworm

Kayce Bell, John Demboski, Joseph Cook

Sunday, June 22, 2014 -Poster #29

Unraveling the history of host and parasite associations is a fundamental first step to investigate the evolutionary consequences of climate change and host history on these interspecific associations. Recent phylogenetic analyses of chipmunks (Rodentia: Tamias) indicate multiple instances of mitochondrial introgression and suggest a complex and dynamic history underlies contemporary diversity (25 nominal species), distribution, and interactions. We generated mitochondrial and nuclear phylogenies for a pinworm (Heteroxynema cucullatum) associated with a diverse assemblage of western North American chipmunks (23 species) to address questions about the history of this host-parasite complex. In particular, does this system have a history of strict host-parasite codivergence? Is there evidence of host-switching, possibly due to patterns of recurrent expansion and isolation events in host populations across varying spatial and temporal scales? Phylogenetic and phylogeographic relationships suggest that pinworm lineages are primarily associated with host lineages or clades, but secondarily structured geographically. Multiple instances of pinworm host-switching in areas of host geographic overlap are also evident. Divergence among the 4 major pinworm lineages suggests that this nominal species of pinworm consists of 4 distinct taxa, possibly specific-level differentiation. This is further supported by instances of geographic and host sympatry of multiple pinworm lineages. Exploration of parasite and host biogeographic histories in tandem provides a foundation for additional insight into the complexity of biotic interactions over time.

Influence of sex and habitat on the size and shape of anal and dorsal fins of the blackstripe topminnow, Fundulus notatus

Daniel Welsh, Rebecca Fuller

Sunday, June 22, 2014 -Poster #30

In fish, the anal and dorsal fins serve multiple functions, including those related to swimming, display, and reproduction. As such, they are likely to be targets of both natural and sexual selection. Many fish species occupy different habitats, yet how environmental differences influence multi-use traits is largely unknown. Here, the size and shape of the anal and dorsal fin in the blackstripe topminnow, Fundulus notatus, from lake and stream habitats across multiple ages and sexes was examined. Differences in the size and shape of anal and dorsal fins were sex-specific, and not related to habitat differences. Males have longer and more pointed anal fins and longer, larger, and more pointed dorsal fins than females. These sex differences occur predominantly in the older age class. The angle (i.e. pointedness) of the dorsal and anal fins is tightly correlated suggesting that fins follow a similar growth trajectory as individuals become sexually mature.

Squash bugs host multiple endosymbiotic Burkholderia sp.

Gregory Fricker, Justine Garcia, Tarik Acevedo, Nicole Gerardo

Sunday, June 22, 2014 -Poster #31

Endosymbiotic interactions, in which one organism resides within a host, are common among true bugs. Many different microbes live within true bugs and these result in a wide range of fitness outcomes for the host. Burkholderia are known to positively affect the fitness of some true bugs, but the Burkholderia genus contains a range of species with known benefits as well species that are pathogens or commensals. Due to the large range of roles within the genus, it is an ideal system to study the effect of different microbiota on host fitness. Squash bugs, Anasa tristis, are true bugs that possess specialized organs, midgut crypts, which house Burkholderia. To understand the effect of different Burkholderia species on squash bug fitness, we first characterized the diversity of Burkholderia within wild squash bug populations. Burkholderia grown on LB plates from the midgut crypts of adult squash bugs were PCR-amplified and sequenced across the commonly used 16S rRNA gene and a Burkholderia-specific multi-locus sequence typing (MLST) scheme that includes the atpD, gltB, gyrB, lepA, and recA genes. The 16S rRNA sequences were aligned and clustered into Operation Taxonomic Units (OTUs), while the MLST sequences were concatenated prior to clustering. We recovered several Burkholderia OTUs with both typing schemes and compare phylogenies constructed with each scheme to fully resolve the Burkholderia diversity in the squash bug crypts. Each adult squash bug harbored a unique community of Burkholderia, and some squash bugs were co-infected with multiple OTUs, suggesting the possibility of a large diversity of Burkholderia within squash bug populations. In addition, preliminary rearing experiments with GFP-labeled Burkholderia indicate squash bugs may acquire species in the Burkholderiaceae family outside of the diversity represented in our assay. These data suggest that the Anasa tristis-Burkholderia endosymbiosis includes several Burkholderia species or strains, and we discuss this diversity in the context of variable fitness benefits to the host.

Diversity and Transmission of Symbiotic Bacterial Communities in Haplosclerid Sponges of the Caribbean Sea.

Michael Dewar, Megan Zappe, Cole Easson, Bob Thacker

Sunday, June 22, 2014 -Poster #32

Sponges and their associated symbiotic bacterial communities represent major primary producers in marine environments, often comprising over half of coral reef biomass. Despite their ecological importance, the interacting factors that regulate the structure, phylogenetic diversity, and transmission of symbiotic microbial communities remain uncertain. As a rapid, high-resolution technique to characterize diverse bacterial populations, we analyzed terminal restriction fragment length polymorphisms (T-RFLPs) of the relatively conserved bacterial 16S ribosomal RNA gene sequence from replicate samples of fifteen haplosclerid sponge species collected over a five year time span in Bocas del Toro, Panama. We examined the effects of spatial, temporal, and host-species variation on bacterial community structure. Preliminary results indicate a statistically significant contribution from all three sources of variation, but with a high degree of community similarity within species across space and time. These data suggest the presence of host-specific bacterial lineages that are transmitted through a combination of vertical and horizontal modes of transmission, congruent with a recently proposed model of “leaky” vertical transmission.

Concept Essay on Why Life Evolves in the Universe

James Thornton

Sunday, June 22, 2014 -Poster #33

Brief Summary of a Concept Essay on Why Life Evolves in the Universe

Theoretical considerations and scientific research on the origin of life are focused on how life evolved. Important advances continue to be made on this front in research facilities around the world.

There remains an intriguing second question one step removed from how life evolved. That question is: Why did life evolve? Exploring the nature of the forces, mechanisms, and laws which impact the creation of animate from inanimate matter is both theoretically interesting and useful to understanding the nature of life. Defining those effectors, whatever they may be, will surely help advance our understanding of the potential for the creation and evolution of life throughout the universe, and will help to answer the perplexing question: What is life?

An attempt to understand what those effectors may be is encapsulated in this brief theoretical essay. Similarities in the the evolution of complex matter throughout the universe, be that animate or inanimate, are explored in an attempt to explain why life evolves in the universe.

Edward O. Wilson's "conversion": a current polemic about group selection.

Lívia Maria Santos Assunção, Mark Borrello, Charbel Niño El-Hani

Sunday, June 22, 2014 -Poster #34

Since the publication of On The Origin of Species, in 1959, the level of biological organization at which natural selection works has been under discussion by evolutionary biologists. The idea that natural selection could work in different biological hierarchies, specifically at the level of individuals and at the level of the groups of individuals was first proposed by Charles Darwin. However, Darwin argued that it could work only in a few cases, such as the evolution of morality in humans and sociality in hymenopterans. After this publication, group selection was intensely discussed by authors as Peter Kropotkin (1902) and Vero Copner Wynne-Edwards (1962) that defended that the group should be understood as the target of selection. However, from the middle of 1960s, the theory of group selection began to be widely rejected. One of the causes of this rejection was the decisive critic from George C. Williams and the advent of alternative explanations to the origin of social behaviours and morality such as kin selection theory. Within this debate, one of the great figures that opposed to group selection theory was the biologist Edward O. Wilson. He began to be directly involved in the debate about the forces of social evolution since the publication Sociobiology, in 1975. For the next 40 years, Wilson opposed to the idea of group selection as a theoretical basis to explain the evolution of social behaviour. However, with the publication of Rethinking the Theoretical Foundations of Sociobiology (2007) with the collaboration of David Sloan Wilson – a well-known supporter of group selection theory – Wilson changed his positioning. This change was maintained in subsequent publications, such as the 2010 paper written with Martin A. Nowak and Corina E. Tarnita where the authors not only defend group selection but also criticized kin selection theory. This project aims at analysing Wilson's conversion toward the theory of group selection from his publication of Sociobiology until his current publications. In order to do so, it has been done a chronological analysis about his work (books, papers and letters published in peer-review magazines) that discusses group selection, the evolution of altruism, evolution of sociality and related topics. Some of the early results from this research (that is currently in progress) are that Wilson did not neglect the discussion about levels of selection. Also, there was a clear change in Wilson's attitude regarding his acceptance of group selection and kin selection theory.

Comparison of Sex-Biased Gene Expression and Behavior in Drosophila melanogaster between Wild and Lab Strains

Clair Han

Sunday, June 22, 2014 -Poster #35

Domestication can alter selective pressures on organisms compared to conditions they face in natural environments. Upon domestication, sexual selection is relaxed and sexual dimorphism is reduced. To compare the differences between wild and lab-domesticated Drosophila melanogaster strains, we collected wild flies from orchard and established isofemale lines in the lab. We survey three time points during this lab domestication: first generation wild flies, and their progeny 6 and 12 months after moving to lab conditions. In addition, common lab strains which have been maintained in lab condition for hundreds of generations were used as control. We characterized the behavioral changes that occur during domestication through behavior tracking and examined gene expression changes using RNA-seq. Simulations were conducted to test biases in edgeR's normalization parameters. We find changes in behavior and sex-biased gene expression associated with domestication, suggesting manifestation of sexual dimorphisms in D. melanogaster do indeed change during the process of domestication. We discuss our findings in the context of the relaxation of specific selective pressures on lab maintained individuals.

Are Maternal Effects Species Specific?

Kyle Benowitz, Katherine Moody, Allen Moore

Sunday, June 22, 2014 -Poster #36

Parental care often plays an important role in determining adult phenotypic characters. The burying beetle species Nicrophorus orbicollis and Nicrophorus vespilloides, which differ significantly in body size, both feed regurgitated carrion to their offspring in early larval development. By switching mothers at the time of larval hatching, we are able to manipulate a burying beetle mother into rearing a brood of a different species. We use this ability to cross-foster between species to estimate the relative strengths of maternal effects and their contributions to size differences between N. vespilloides and N. orbicollis.

Clinal variation of nest-building behavior in house mice (Mus musculus domesticus)

Ting-Ting Lin, Michael Nachman

Sunday, June 22, 2014 -Poster #37

How organims adapt to local environments remains one of the most interesting questions in evolutionary ecology. Although many behavioral stategies are thought to be adaptive, few studies have attempted to link genotypes and with adaptive behavioral phenotypes. My project aims to understand the contribution of genetic mechanisms to behaviors that are likely playing a role in local adaptation. This preliminary study asks a simple question: do house mouse populations from different latitudes show differences in nest-building behaviors? We collected wild mice from upstate New York (NY), Florida (FL) and Brazil (BZ), and established laboratory colonies. I compared nest-building behaviors in wild-derived progeny from these populations reared in a common laboratory environment. I predicted that nest-building behavior might be a component of adaptation to differing temperatures in these populations and, therefore, that mice from higher latitudes would build bigger nests (Lynch 1992). My results supported this prediction: NY mice built the largest nests, BZ mice built the smallest nests, and FL mice built nests of intermediate size. Moreover, variance among individuals in nest-building also increased with latitude. Since these mice were reared in a common environment, these results suggest that genetic differences may underlie clinal variation in nest-building in natural house mouse populations.

Using genomics to detect local adaptations and assess conservation risks in populations of the California Gnatcatcher

Josie Griffin

Sunday, June 22, 2014 -Poster #38

Populations divisions based on phenotypic variation may not be readily detectable using standard methods due to recent evolutionary origins. The coalescent times of both nuclear DNA and mitochondrial DNA could be too long to reflect local adaptions, so understanding population differentiation on a finer time scale is necessary. This can be done by identifying adaptive loci that are under selection and analyzing those separately. Here I plan to take an adaptive genomic approach to understanding clinal phenotypic variation in the California gnatcatcher. If recent local adaptation in subpopulations can be measured, it will help settle the debate about the gnatcatcher's conservation status and could play a huge role in conservation decisions in the future.

Evidence of two distinct evolutionary host lineages in Pseudoperonospora cubensis through comparative genomic analysis

Anna Thomas, Kisurb Choe, Ignazio Carbone, Peter Ojiambo

Sunday, June 22, 2014 -Poster #39

Pseudoperonospora cubensis, the causal agent of cucurbit downy mildew is a destructive pathogen of cucurbits worldwide. Five pathotypes of P. cubensis were identified earlier in the US based on host differential compatibility of the pathogen with Cucumis spp., Citrullus lanatus and Cucurbita spp., which is suggestive of host specialization within this pathosystem. However, it is still not clear how either the host or the pathogen influences the level and extent of host specialization. The goal of this study is to explore genome-wide variation for evidence of host specialization in P. cubensis. Genomic DNA extracted from nine isolates of P. cubensis collected from Cucumis sativus, C. melo var. reticulatus, Cucurbita maxima, C. moschata, C. pepo and Citrullus lanatus, were subjected to whole genome sequencing using the Illumina HiSeq platform. Comparative analysis of a cohort of these nine genomes using GATK, VCFTOOLS and PLINK revealed the presence of two distinct host lineages in P.cubensis. Sliding window FST analysis showed significant divergence and cryptic population structure between one host lineage that included isolates from Cucurbita pepo, C. moschata and Citrullus lanatus and a second host lineage that comprised isolates from Cucumis spp. and Cucurbita maxima. The average linkage disequilibrium decayed slowly across most contigs with a few showing rapid decay and recovery providing evidence of recombination between distinct host lineages. Further studies will explore the genomic signatures of genetic differentiation and cryptic speciation within these evolutionary distinct lineages.

In vitro models of endangered species: transcriptomic characterization of Rana sevosa genes associated with chytrid fungus response

Cynthia Steiner, Marlys Houck, Oliver Ryder

Sunday, June 22, 2014 -Poster #40

A major impediment to the advancement of genomic studies that involve threatened species is the availability of samples. The development of banks that establish and maintain primary cell cultures from biopsies has provided a crucial alternative to access to high-quality DNA and RNA specimens from numerous endangered species. Cell lines represent a promising in vitro model that can facilitate studies of wild species, providing resources for assisting genome annotation, SNP discovery, and identification of functional genes associated with ecologically relevant traits in populations. This approach is particularly significant for amphibians, currently showing more than 32% of species threatened in the wild by habitat loss and the emergence of infectious diseases such as chytrid fungus. We are interested in studying the dusky gopher frog (Rana sevosa), one of the most imperiled amphibians in the United States, listed as critically endangered on the IUCN Red List. We aim to determine the significance of developing in vitro models for assessing adaptive genetic variation associated with response to chytrid fungus infection. For that, we partially characterized the transcriptome of two Rana sevosa cell lines by sequencing cDNA libraries obtained from fibroblast cell lines, developed and banked at the San Diego Zoo's Frozen Zoo®. We identified about 18% of genes expressed involved in GO categories such as immune, cellular and stress response, and 21% of genes implicated in cytoskeleton structure. About 6,000 putative SNPs were identified in genes associated with skin integrity maintenance (keratins, collagens), MHC and interleukin genes, and head shock proteins, among others. These preliminary results highlight the potential use of in vitro models in endangered species as a tool for assessing adaptive genetic variation via genomic studies.

Positive selection drives the evolution of a major histocompatibility complex gene in an endangered Mexican salamander species complex

Karen Tracy, Kelly Zamudio, Karen Kiemnec-Tyburczy, Gabriela Parra Olea, J. Andrew DeWoody

Sunday, June 22, 2014 -Poster #41

Polymorphism in the genes of the major histocompatibility complex (MHC) may help vertebrates combat novel and diverse pathogens by increasing the number of pathogen-derived proteins that can initiate the host's acquired immune response. Theory predicts that balancing selection will act on MHC genes that confer resistance to pathogens; therefore, MHC variation is of particular interest in the management of threatened species which may be experiencing disease-related declines. Emerging infectious diseases pose a major threat to amphibians globally, and many salamander species persist in highly anthropogenically-disturbed habitats where they are likely exposed to both chronic and novel infections. In this study, we used a combination of adaptive and neutral markers to assess MHC variation in populations of five salamander species within the Ambystoma velasci complex, a group that consists of 15 recently diverged species, including several endangered species, endemic to Mexico. These five species exhibit diverse life history types, dispersal, and levels of heterozygosity, all of which influence genetic diversity. We isolated 31 unique MHC class II B1 alleles from 75 individuals (in the five species combined) and inferred a phylogeny representing the evolutionary history of Ambystoma MHC. Using this phylogeny, we found signatures of positive selection on the overall gene, putative peptide-binding regions (PBRs), and several allelic lineages. In contrast, we did not detect signatures of selection on two reference loci from the same individuals, making it unlikely that a genome-wide selective process is causing global signals of positive selection. We therefore have strong evidence that positive selection is a major evolutionary force driving patterns of MHC polymorphism in this recently radiated species complex.

Local adaptation and linkage maps - a first step towards the genomic architecture of fitness-related phenotypes in natural populations

Christopher Friedline, Brandon Lind, Erin Hobson, D. Ethan Harwood, Annette Delfino-Mix, Patricia Maloney

Sunday, June 22, 2014 -Poster #42

Evidence for adaptive evolution among populations of plants is commonly documented at both the phenotypic and molecular levels, so that some of the best examples of adaptive evolution within lineages come from the field of plant genetics. Central to an understanding of local adaptation is the concept of genetic architecture, which includes the genomic organization of the loci affecting fitness-related phenotypes. Ideally, the genomic organization of loci contributing to variation in fitness-related traits would follow naturally from the production of a genome sequence. This is not feasible for many taxa, as finished genome sequences, even with next generation sequencing technologies, are cost-prohibitive. A useful and often neglected alternative is the production of a dense linkage map. Here, we leverage this idea to produce a dense linkage map for foxtail pine (Pinus balfouriana Grev. & Balf.) using a double-digest restriction site associated DNA sequencing approach (ddRADseq) on megagametophyte arrays from four maternal trees. The resulting consensus linkage map is composed of approximately 20,000 contigs (>40,000 single nucleotide polymorphisms) representing almost 2.0 Mbp of the foxtail pine genome grouped into and ordered within 12 linkage groups, which is the haploid chromosome number for this species. Average marker spacing was 1.34 cM, with an average of 23 contigs located at each position on the linkage map. Inspection of marker distributions on each linkage group suggest that, conditional on our samples sizes, the genome of foxtail pine has been saturated with genetic markers. A minimum of one marker at each position on the consensus linkage map had a strong candidate for a homologous sequence in loblolly pine (P. taeda L.), thus allowing us to leverage this model conifer species to obtain further functional information. We subsequently utilize this linkage map to illustrate how non-model conifer species can be used to test fundamental hypotheses about the genetic architecture of local adaptation.

The two-component regulatory system, etk is involved in biofilm morpholog In the symbiotic bacterium, Vibrio Fischeri

Amy Nava, Michele Nishiguchi

Sunday, June 22, 2014 -Poster #43

Bacterial biofilms are considerably more resistant to environmental change, antimicrobials, and eukaryotic predation and thereby, more fit than their planktonic counterparts. As a biofilm associated community, bacteria can regulate genes involved in exopolysaccharide synthesis in a strategic manner at various genetic loci to cope with environmental fluctuations. Biofilms have evolved specific mechanisms to counteract both abiotic and biotic factors such as predatory grazing from protozoans, competition for space from other types of bacteria, and changes in temperature, salinity, and nutrient availability in the environment. These mechanisms include tightly compacted biofilm structures, release of toxic compounds, global communication through quorum sensing between strains within the biofilm, and change in biofilm morphology. To better understand how these mechanisms work in conjunction with one another in response to stress, we compared various strains of V. fischeri with single nucleotide polymorphisms at the etk locus to determine if sequence variants are responsible for changes in morphological and biochemical features of the biofilm, and subsequently, as a concerted, global effort towards increased fitness. The etk locus (exopolysaccharide tyrosine kinase) is highly conserved in many bacteria and has been proposed to be a polysaccharide chain lengthener. Our results indicate that despite no difference among V. fischeri strains ES114 (Hawaii) and ETBB10-1 (Australia) in growth rates, significant differences in motility were observed, where V. fischeri ES114 was greater. Conversely, V. fischeri ETBB10-1 formed denser biofilms and was exponentially more bioluminescent than V. fischeri ES114. Mutational analyses of etk in both strains demonstrate that subtle genetic differences observed may be responsible for differences in biofilm phenotype. By determining whether genetic diversity within the etk locus controls phenotypic variation in V. fischeri biofilms, we can demonstrate the large evolutionary and ecological benefits among different ecotypes.

Factors influencing rates of autogamy among populations

Alison Post, Laura Galloway

Sunday, June 22, 2014 -Poster #44

As the ice sheet over North America started to recede at the end of the Pleistocene, plant species previously restricted to southern refugia were able to expand their ranges northward. As a consequence of migration, within these northern populations, genetic diversity decreased, homozygosity increased and inbreeding depression decreased. Therefore, self-pollination was not as large a fitness cost, so higher rates of autogamy could evolve in northern populations. This pattern is found in the protandrous woodland herb, Campanula americana. It has a primarily outcrossing mating system, however, it is also completely self-compatible. This study looked at possible mechanisms behind the increasing autogamy rates over a geographic gradient observed in C. americana. Specifically, it explored differences in the timing of floral gender phases, as well as in floral morphology, particularly stigmatic lobe curling, among five C. americana populations exhibiting a range of autogamy rates. Differences between populations were found in time to onset of female phase, however, all populations became female while pollen viability was still high. The rate of pollen degradation and stigmatic lobe curl also differed among populations, with some populations having a faster rate of pollen degradation and a faster rate of stigmatic curling, suggesting an overall accelerated floral life cycle. Greater stigma curl was correlated with greater self pollen deposition onto the stigmatic lobes, signifying a possible mechanism for delayed self-pollination. However, these differences between populations did not correspond to the latitudinal variation in autogamy rates, suggesting that a different mechanism contributes to these variations among populations.

Experimental Evolution of Divergence with Gene Flow: Testing for Local Adaptation in Yeast

Tyler Hether, Matthieu Delcourt, Paul Hohenlohe

Sunday, June 22, 2014 -Poster #45

The generation of local adaptation depends on a suite of demographic, genetic, and evolutionary factors. For example, 'Divergence with Gene Flow' (DGF) scenarios are commonly found in nature and are characterized by different populations, each with their own local selection pressures, exchanging migrants with one another. Thus there is a balance that exists where selection promotes local adaptation and linkage disequilibrium while migration and recombination breaks down genome-wide differences. Herein we explicitly test for local adaptation under DGF using experimental evolution of yeast populations. First we created an admixed population by crossing two divergent haploid strains (differing at ~70,000 SNPs & 10,000 structural variants). Next we quantified the extent of standing genetic variation for growth rate under NaCl and SDS stress from F2s in terms of different components of genetic (co)variance (additive, epistatic, and random environmental). In the absence of gene flow, we found strong evidence for trade-offs in adaptation to the two stressors. Using a replicated design, we evolved population pairs where each population experienced a different stressor while experimentally manipulating the level of migration between populations. Lastly, we tested if local adaptation attenuates with increasing migration. Experimental evolution provides a unique context in which to assess the role of standing genetic variation in adaptation under DGF, and also to investigate the effects of DGF on genomic patterns of genetic differentiation.

Larrea populations exhibit multiple solutions to freezing stress with contrasting implications for persistence in a warming world

Juliana Medeiros

Sunday, June 22, 2014 -Poster #46

Fundamental plant ecological theory suggests that stress resistance and growth rate in the absence of stress are diametrically opposed. Thus, prior adaptation to freezing could reduce competitive ability in a warming world, particularly if past selection has reduced within-population variation in freezing resistance. Yet, plants can solve the problem of freezing stress in other ways besides increasing freezing resistance. Other solutions include: responding plastically to growth temperature, avoiding freezing via phenology, or allowing damage to expendable tissues followed by rapid recovery (tolerance). These could allow for faster growth during the warm season while still protecting against intermittent short-lived freezing episodes. The evergreen arid-land genus Larrea spans a range of thermal environments, and previous work demonstrated that xylem resistance to freeze-thaw embolism increases at higher latitudes. Nevertheless, questions remained concerning within-population variation in freezing resistance, the contribution of plasticity to latitudinal variation, and the possibility of differences in freezing resistance between xylem and leaves, which could provide a mechanism for freezing tolerance or avoidance. We measured leaf and xylem traits related to freezing resistance and growth rate for two Larrea species (L. tridentata and L. divaricata) from high and low latitude populations grown in the field and in a common garden.

We found that, regardless of growth environment, high latitude L. divaricata consistently produced leaves and xylem with higher freezing resistance and exhibited sustained photo-protection in response to short periods of cold acclimation, both of which can negatively affect growth rate in the absence of freezing stress.

Compared to other populations, this population was also characterized by lower within-population variation in freezing resistance and slower growth rate in the absence of freezing. Thus, prior selection for freezing resistance may limit the ability of this population to respond positively to climate warming. In contrast, low latitude L. divaricata had lower freezing resistance in leaves and xylem, but exhibited higher within-population variation, greater plasticity of leaf and xylem characters and more rapid re-growth post-freeze, which likely allows them to tolerate infrequent freezing events. Furthermore, we found that high latitude L. tridentata exhibited within-population variation, xylem plasticity and semi ring-porous wood structure, a phenological trait associated with freezing avoidance. Thus, we show that ability of Larrea populations to respond to local freezing regime likely facilitated historical population expansion into diverse thermal environments. Furthermore, our data suggests that some populations could be better poised to respond positively to a variety of future climate scenarios.

Temporal dynamics of neotropical Epidendrum species (Orchidaceae) under climate change

David Draper, Isabel Marques

Sunday, June 22, 2014 -Poster #47

The genus Epidendrum L. is the largest orchid genus in the Neotropics, with about 1,500 species. It is mainly distributed throughout Tropical America from sea level to 3,700 meters elevation. Species can be terrestrial or lithophytic but the greatest number occurs as epiphytes in wet cloud forest on the slopes of the Andes. In a changing world, several species of this genus had proven to be very aggressive colonizers, and many species which were once rare in this genus have become more common as the result of human activities. Our aim was to analyze the temporal dynamics of in the distribution of Epidendrum species between the Last Glacial Maximum (LGM) and the present day. We modeled species distribution with the Maximum Entropy Modeling (MaxEnt) based on GBIF occurrences and Worldclim datasets. These models were also projected considering the future emission scenarios SRES-A1B, SRES-A2 and SRES-B1 proposed by the IPCC. Results point out the importance of the Western Andean Portal, as a meeting point for the future occurrence of lowland species and Andean/Amazonian species. The Western Andean Portal is a corridor between the Northern and Central Andes at the latitude of southern Ecuador/northern Peru (3–5°S). This region also played an important role during the marine incursions between the Eocene and the Middle Miocene from the Pacific Ocean. Our results also support the hypothesis that the upper basin of the Zamora River is as one of the most vulnerable areas of biodiversity in the Andean range.

Genome-wide effects of factorial fire and thinning in fire-suppressed populations of Jeffrey and sugar pine

Brandon Lind, Christopher Friedline, Erin Hobson, Malcolm North, Andrew Eckert

Sunday, June 22, 2014 -Poster #48

The goal of the proposed project is to understand how the interaction of logging and prescribed fire promote adaptivity and gene flow within the native stands of two syntopic mid-elevation pine trees (Jeffrey pine, Pinus jeffreyi; and sugar pine, P. lambertiana) of the fire-suppressed central Sierra mountains of California, USA. Questions driving this study include those such as, How does genotypic autocorrelation differ among treatments, distance and size classes? How does historical estimates of gene flow (variance in allele frequencies) compare to contemporary estimates of gene flow (parentage analysis)? What effect does the landscape have on these patterns and processes? In what ways can we orient these dirigible systems towards an evolutionary trajectory capable of coping with stochastic change?

This study takes advantage of existing replicated factorial treatments of fire and thinning across 180 acres at Teakettle Experimental Forest (N = 19 814 adult conifers) and explores the frontier of the genetic dynamics of anthropogenic disturbance 12 years post-treatment. Through the combined use of census sampling (N = 6 047 pine seedlings through adults) and next generation sequencing, this enterprise endeavors a novel and globally applicative approach, intensive to both intraspecific population and genomic representation. Specifically, all sampled pines will have haploids genotyped by 15 chloroplast SSR markers in addition to genotyping-by-sequencing via the Illumina HiSeq 2000 platform, identifying >10K SNP markers. SNPs mapped to partial genome sequences (assembled de novo per species) allow loci to be annotated through the loblolly (P. taeda) and sugar pine reference genomes. By better understanding the mechanistic response of treated stands, managers can better prepare the world’s forests to respond to future disturbance such as fire, harvest, and climate change, ensuring longevity and persistence of federally managed forest lands.

Proof-of-Concept for the development of environmental DNA tools for Atlantic sturgeon management

Jameson Hinkle, Greg Garman, Rodney Dyer

Sunday, June 22, 2014 -Poster #49

Atlantic Sturgeon (Acipenser oxyrinchus oxyrinchus, Mitchelle), is an anadromous fish that uses all of the major estuaries on the east coast including the James, Potomac, and Hudson Rivers. The species’ lineage diverged approximately 200 million years ago to form the unresolved Atlantic Sturgeon clade (Robles et al., 2004). A large fishery for Atlantic Sturgeon existed in the tidal James River until the mid-20th century for both the fish and its cavier (Atlantic Sturgeon, retrieved 2013). Environmental DNA (eDNA) is a non-invasive means of detecting rare, endangered, or invasive species by isolating discrete pieces of nuclear or mitochondrial DNA (mtDNA) from the water column. (Lodge, et al., 2012). Through the use of eDNA, thus far we have found 93% success in tank control samples, and 83% spiked environmental water samples. Future research will include biomass calibration curves through calibration and validation of real-time PCR (qPCR).

Body size evolution in catfish (Siluriformes)

Dave Campbell, Jacob Schaefer, Wilfredo Matamoros

Sunday, June 22, 2014 -Poster #51
The evolution of body size has long been a topic of interest to biologists due to the close link between size and various aspects of an organism's biology. Adult body size is influenced by the underlying tradeoff in energy allocation between maintenance, somatic growth and reproduction. We studied the evolution of a large group of globally distributed (primarily freshwater with some marine forms) fishes to test some basic hypotheses about the evolution of adult body size. Catifish (Siluriformes) are an excellent group for this type of research as they represent approximately 11% of fishes and species range in size from over three meters (family Pangasiidae) to a few centimeters (family Trichomycteridae). Because they are such a large and diverse group, we worked at the genera level and compiled sequence data for construction of a phylogeny along with body size, body shape, distribution and ecological data. The final dataset included 212 genera representing over 2,300 species. We first tested for the strength of phylogenetic signal in body size. Next, we used phylogenetic least squared methods to test for the effects of distribution (range size and latitude), habitat (freshwater vs. marine), trophic ecology and body shape on body size in catfish. Because we worked at the genera level, we were also able to quantify and analyze patterns of variability in body shape within groups (coefficient of variation in size within a genera).

Impact of dietary adaptation on gastrointestinal biology across trophic levels in Lake Malawi cichlids

Kaitlin Coyle, Natalie Roberts, Reade Roberts

Sunday, June 22, 2014 -Poster #52
Dietary adaptation is a universally important factor in organismal fitness as well as a key driver in the evolution and diversification of species. Response to diet is a complex interaction between nutrient intake, genetic factors impacting physiology and metabolism, and gut bacterial content. Because of the massive impact of diet on development and health, there has been significant effort to characterize the contributions of these elements in traditional models such as mice and zebrafish; however, the genetic underpinnings of dietary adaptation remain poorly understood, as is their contributions to evolution and speciation. East African cichlids are an excellent model system for studying evolution due to a recent adaptive radiation that has resulted in extreme phenotypic divergence in many traits, including those involved in adaptation to diet. I am using multiple cichlid genera with different dietary specializations representing three trophic levels to investigate the effect of diet on two traits involved in dietary adaptation: gut length and gut bacterial microbiome. Individuals from each genus are raised on animal, vegetable, and mixed diets. Fish from each genus by diet cohort are collected at multiple developmental time points for characterization of gut morphology and 16S bacterial profile. Preliminary results show notable differences in the normalized gut lengths of individuals from different trophic levels as well as plasticity in gut length early in development. We also see differences in bacterial profiles across cohorts of different genera just ten days after feeding begins. These preliminary results show genus-specific differences and suggest that future comparative genomics and mapping in interspecific crosses will allow for identification of genetic factors underlying divergence across trophic levels.

Ecology and Evolution of Common Tetras (Teleostei: Characidae) in shallow streams of southwestern Ecuador

Windsor Aguirre, Ronald Navarrete, Virginia Shervette, Paola Calle, Antonio Torres, Enrique Laaz, Marissa Locke, Grecia Valadez, Vinh Vu, Alexandra Confer

Sunday, June 22, 2014 -Poster #53
Little is known about the ecology and evolution of freshwater fishes of western Ecuador despite serious environmental threats. The fauna in this region has been isolated for millions of years by the rise of the Andes Mountains and is known for its high rates of endemism. The Characidae are a hyper-diverse family that has been particularly neglected in the region because of the taxonomic challenges it presents and because most characids are small and not of direct economic importance. We conduct a preliminary examination of ecological, morphological, and genetic variation among common tetras in southwestern Ecuador based on collections conducted throughout the region between 2008 and 2013. The abundance of the species in different regions and habitats is examined and data on stable isotopes of Carbon and Nitrogen are used to provide some insight into their ecology. Geometric morphometric methods are used to examine the major patterns of body shape divergence among species. DNA sequences from a mitochondrial and a nuclear gene are used to infer genetic relationships and species are mapped on a larger evolutionary tree of characids based on available DNA sequences. Although much more work is needed, our study provides a framework for understanding some of the major patterns of ecological differentiation and evolutionary diversification of tetras in the region.

Effects of temperature and water flow on morphology and swimming performance in Astyanax mexicanus (Teleostei: Characidae)

Winer Reyes, Windsor Aguirre

Sunday, June 22, 2014 -Poster #54
As ectotherms, fishes are particularly susceptible to environmental conditions during development, which can impact their phenotypes and survival. Vertebral morphology and body shape variation are particularly susceptible to environmental conditions and these have been shown to significantly impact swimming performance.

This project addresses the impact of ecologically important environmental variables on the surface form of the model species Astyanax mexicanus, and how different temperature treatments and water flow regimes impact their vertebral phenotypes, body shape variation and swimming performance. Temperature and water flow were selected because they are particularly important parameters affecting morphological variation in nature. Geometric morphometric methods are used to examine body shape variation and fast-start reactions are measured to examine swimming performance.

The present study focuses on a member of the diverse Neotropical fish family Characidae.. By providing insight into how common environmental variables impact morphological variation and swimming performance in this model species, I seek to provide a baseline for future studies on the influence of environmental variables on characids in nature and the developmental mechanisms that lead to changes in morphology between species.

Body shape variation in Rhoadsia (Teleostei: Characidae) along a low altitude gradient in Western Ecuador

Grace Malato, Maxine Loh, Webster Vital, Catherine Collins, Vinh Vu, Grecia Valadez, Paola Calle, Ronald Navarrete, Windsor Aguirre

Sunday, June 22, 2014 -Poster #55
Rhoadsia is a highly divergent fish genus in the family Characidae containing only two recognized species, R. altipinna and R. minor. They are indigenous to Western Ecuador and Northern Peru, where they are relatively common and ecologically important. The two species are distinguished based on differences in body size, body shape, and in the altitudes at which they occur. Rhoadsia altipinna is larger, deeper bodied and is common at low altitudes, while R. minor is smaller, has a more elongate body, and has been described from higher altitudes. Little is known about these species despite their abundance in the region. Additionally, the validity of R. minor as a separate species has been questioned due to the plastic nature of fish shape and the lack of information about either species. We collected R. altipinna at altitudes between 31 and 625 m in the Santa Rosa River in southwestern Ecuador. We compared body shape of fish from different elevations and found that there was a significant relationship between elevation and elongation, with higher elevation individuals being more elongate. We then compared average shape of all R. altipinna to that of paratypes of R. minor using geometric morphometrics to put the variation within R. altipinna in context of the differences between species. Allometry and sexual dimorphism were also examined in R. altipinna. Finally, we compared mtDNA sequence data obtained from Santa Rosa River samples of R. altipinna to that of samples from the larger Guayas River drainage to ensure that the Santa Rosa River population is genetically similar to populations from other parts of the range of the species. This research provides insight into the factors associated with phenotypic variation within this divergent characid genus and establishes a baseline to further examine its evolution in future studies.

Differential symmetry in the limbs of emydid and kinosternid turtles: are more important limbs more symmetrical?

Jonas Oppenheimer, Cally Deppen, Ben Welkie, Gabe Rivera

Sunday, June 22, 2014 -Poster #56

Fluctuating asymmetry is defined as small, random deviations from bilateral symmetry, and is thought to have bearing on the evolution and development of an organism, perhaps indicating greater fitness. Understanding how selective forces influence asymmetry remains an active area of research in evolutionary biology. One hypothesis, which has received minimal attention, suggests that morphological characteristics can be ranked in importance based on symmetry. Specifically, it posits that features with greater functional importance should have higher levels of symmetry. The aim of our research was to examine the patterns of fluctuating asymmetry present in the limb bones of turtles (Families: Emydidae and Kinosternidae). Both families primarily employ a hind-limb dominant swimming style, and are therefore excellent groups in which to test the biomechanical hypothesis of symmetry. We hypothesized that the forelimbs would display greater fluctuating asymmetry than hind limbs, given their lower level of functional importance. We measured the left and right hind- and forelimb bone lengths in various members of the two families, and used their measurements to calculate fluctuating asymmetry in each set of bones for each species of turtle. Our data show that both display a significantly greater level of fluctuating asymmetry in their forelimbs than in their hind limbs, which was predicted given their particularly hind-limb dominant style of locomotion. These results begin to generate a clearer picture of the evolutionary pressures exerted by the need for biomechanical efficiency in locomotion. The next step in our research is to integrate data from other families, including from the superfamily Chelonioidea, which exhibits forelimb-dominant swimming, to understand if this pattern is truly a product of biomechanics and is not unique to Emydidae and Kinosternidae.

Polygenic Sex Determination in the Cichlid Fish Astatotilapia burtoni

Natalie Roberts, Scott Juntti, Allyson Ryan, Russell Fernald, Reade Roberts

Sunday, June 22, 2014 -Poster #57
The adaptive radiation of East African cichlid fish serves as a powerful model system for the study of evolution and development, and an astounding diversity of genetic sex determination systems have been revealed from just a handful of studied species. In some of these species the interaction of multiple, independently segregating alleles determines sex, a phenomenon known as polygenic sex determination. The species Astatotilapia burtoni is an important model for sexually dimorphic physiology and behavior, and also serves as an immediate outgroup to the adaptive radiations of cichlids in Lake Malawi and Lake Victoria. A better understanding of the basis of sex determination in this species should provide important context for behavioral studies within A. burtoni, as well as studies of the evolution of genetic sex determination and sexual conflicts in East African cichlids. Here we describe the mapping of sex determination loci in the species A. burtoni, using a combination of bulked segregant mapping and restriction-site associated DNA sequencing (RADseq) strategies. Mapping in a number of

independent families demonstrates the presence of at least three distinct sex determination alleles in A. burtoni, strongly suggesting the existence of polygenic sex determination in this species. Additionally, our genetic data has allowed characterization of local- and karyotype-level structural differences on A. burtoni chromosomes relative to other East African cichlid species.

Population Genetics of the Blackspotted Topminnow using Genomic SNP Analysis

Eric Westhafer, Jacob Schaefer

Sunday, June 22, 2014 -Poster #58

The black spotted topminnow, Fundulus olivaceus, exhibits a broad distribution ranging from southeastern Texas to central Missouri. Within drainages, this species occupies the full range of habitats along the river continuum from intermittent headwater streams to the margins of large rivers. This distribution makes F. olivaceus an excellent model for studying population dynamics across heterogeneous habitats and environmental gradients. We sampled headwater and large river environments in the Gasconade and Meramec Rivers in Missouri to assess genetic structure. Genetic analysis was conducted by sampling single nucleotide polymorphisms (SNPs) using the genotype by sequencing (GBS) method. The data set included 248 individuals sampled from two headwater and two large river habitats in each drainage. A total of 5744 loci with less than 3% missing data were analyzed. An analysis of molecular variance (AMOVA) revealed that 20% of the variation was distributed between drainages, 9% of the variation was distributed among populations within drainages, and 71% of the variation occurring within populations. Genetic structure was more evident in the Gasconade River with 15% of the variation distributed among populations, compared to 6.5% of the variation in the Meramec River. A principle component analysis (PCA) separated drainages along the first axis and each of the four headwater populations along axes 2 through 5. The genetic distinctiveness of the headwater populations was also demonstrated in a STRUCTURE analysis. The distribution of genetic variation is consistent with accelerated genetic drift in the headwater populations relative to the large river populations.

Contrasting Genetic Structure of Two Topminnow Species in Adjacent Contact Zones.

David Duvernell, Jacob Schaefer

Sunday, June 22, 2014 -Poster #59

Topminnows in the Fundulus notatus species complex exhibit broadly overlapping geographic distributions throughout the central and southern United States. In drainages where both species are present, the blackspotted topminnow (F. olivaceus) is usually, distributed in headwaters, while the blackstripe topminnow (F. notatus) is more typically present downstream along the margins of larger rivers. These habitat differences have been associated with several life-history differences between the species. This distribution is notably reversed in a few drainages with F. notatus occurring in headwater habitats. In the Little River drainage system in the southern Ouachita Highlands, the species exhibit both distributions in different parts of the drainage. In the Cossatot River F. olivaceus occupies the headwater habitat and F. notatus is found downstream at the confluence with the Little River. Further upstream in the Little River drainage, F. notatus is found in the headwaters of the Glover River and F. olivaceus is distributed downstream at the confluence with the Little River. We predicted that this unusual upstream-downstream reversal of species distributions within the same drainage system would be associated with genetic divergence among the respective populations in one or both of the species, and that historical introgression between the two species may have facilitated shifts in habitat preferences. We tested these predictions using genome-wide SNP data from non-hybrid individuals outside the contact zones in these respective rivers. We assessed genetic structure and determined if hybridization has led to introgression of alleles in the genomes of either species. Also included in the analysis was SNP data from population samples of F. olivaceus in the Gasconade and Meramec River drianages in the northern Ozark Highlands, and F. notatus in Cahokia Creek, a tributary of the Mississippi River in western Illinois.

Phylogeny and reclassification of the plant-associated species of the family Rhizobiaceae.

Seyed Abdollah MOUSAVI, Kristina Lindström

Sunday, June 22, 2014 -Poster #60

The family Rhizobiaceae belongs to the order Rhizobiales positioned in the class Alphaproteobacteria. There are at least eight genera in the family Rhizobiaceae, from which six genera including Rhizobium, Neorhizobium, Allorhizobium, Agrobacterium, Sinorhizobium (syn. Ensifer) and Shinella harbor plant-associated species. Evolution of four housekeeping genes of the plant-associated species of the family Rhizobiaceae was studied in the current study. Phylogeny of the Rhizobiaceae clade supports the delineation of new genera and combinations in the family Rhizobiaceae. Furthermore, the evolution of forty orthologous housekeeping genes of 120 whole-genome sequenced members of Alphaproteobacteria is being studied. Results of Multilocus Sequence Analysis (MLSA) of plant-associated species of Alphaproteobacteria will be presented.

Hybrid Dysgenesis and Transposable element variation in Drosophila simulans

Tom Hill, Christian Schlötterer, Andrea Betancourt

Sunday, June 22, 2014 -Poster #61

Hybrid dysgenesis is a phenomenon that manifests in Drosophila as sterility and the failed development of ovaries. Dysgenesis is sometimes seen in crosses between Drosophila lines with different transposable element (TE) content, such as with the P-element in Drosophila melanogaster. Specifically, offspring of crosses in which the paternal line contains a dysgenesis-causing TE that the maternal line lacks show DNA damage due to rampant transposition, usually resulting in failed ovary development. Here, we cross D. simulans flies from different geographic regions and examine the offspring for the presence of hybrid dysgenesis. We readily observe apparent dysgenesis in these crosses, suggesting that there may be recent horizontal acquisition of a dysgenesis causing TE or TEs in D. simulans. We further identify potentially causal TEs from these crosses.

Temporal Stability of Molecular Diversity Measures in Natural Populations of Drosophila pseudoobscura and Drosophila persimilis

Jennifer Gredler, Mohamed Noor, Alex Hish

Sunday, June 22, 2014 -Poster #62

Many molecular ecology and evolutionary studies that sample species of wild populations at a specific moment in time fail to consider that the genetic data they collected represents genetic variation from a potentially unrepresentative snapshot in time. Variation across time in genetic parameters is especially likely in species that produce multiple generations of offspring every year. Processes including strong genetic drift and/ or selection (e.g., via seasonal changes in allele frequencies) have been documented in a variety of species and may be responsible for such variation across time. Here, we test for changes in molecular evolutionary measurements from wild caught samples collected 16 years (~100 generations) apart at the same time of year at the same site. We compare the genetic diversity seen in 1997 and 2013 cohorts of Drosophila persimilis and Drosophila pseudoobscura using values of Tajima's D and pi from sequences at four X-linked and two mitochondrial loci to assess genetic stability. We found no major changes in overall nucleotide diversity in either species. Similarly, we found no overall trends in measures of Tajima's D in D. pseudoobscura, but identified a drastic shift in Tajima's D at one locus. Our data also suggest that the D. persimilis population has undergone a recent expansion, as evidenced by consistently more negative Tajima's D values in the 2013 cohort in comparison to the 1997 cohort across all loci. Overall, this study reinforces the importance of considering potential temporal variation in some population genetic parameters even within single populations over short evolutionary timescales.

The Repetitive Landscape of Megachile Rotundata

Aressa Coley

Sunday, June 22, 2014 -Poster #63

The pollination of plants is one of the most important ecological services in natural systems. The hymenopteran Megachile rotundata aids in this vital process by serving as a commercial pollinator for the alfalfa plant. The purpose of this study is to determine if there is a strong transposable element presence in M.rotundata and if so, to identify and classify the repetitive sequences in to their respective classes and families so that they can be used for future analysis. As a result of my initial analyses, we believe M. rotundata is home to several different transposable element families. The first step in the analysis process is to construct a transposable element library. Transposable element families are identified using the de-novo repeat family identification and modeling package RepeatModeler. Using this process alone would suffice when analyzing a small set of genes; however, when searching for transposable elements, RepeatModeler and BLAST can result in millions of hits for each element. In order to combat this, the bioinformatics tool Process_hits is implemented. The output from process hits is then manually aligned to generate a consensus sequence. This consensus sequence is then added to a transposable element library specific to Megachile rotunda. Consensus sequences added to the transposable element library must then be classified as superfamilies according to a classification system proposed by Wicker et al. Classification of transposable elements in to subfamilies involves identification of the genes within the sequence, the target site duplication, and the protein coding domain of each sequence. Names were given to any novel element families and submitted to Repbase.

Chromosomal variation and reproductive isolation in wild house mice (Mus musculus domesticus) in Switzerland

Sofia Grize, Jeremy Searle, Barbara König, Anna Lindholm

Sunday, June 22, 2014 -Poster #64

The Swiss Alps are well-known for closely situated populations of house mice (Mus musculus domesticus) which vary in their karyotype. This variation, due to Robertsonian (Rb) fusions, can lead to impaired development of germ cells in population hybrids heterozygous for Rb fusions, making the house mouse a model in speciation studies. However, Swiss populations are poorly studied. We trapped fifty-nine wild house mice from three locations 10 – 20 km apart in the Rhine valley of Eastern Switzerland. They were shown to belong to three distinct chromosomal populations: 2n=22 (BUC), 2n=28 to 32 (WEI) and 2n=27 to 29 (VIL). Crossings between neighboring populations BUC and WEI, and WEI and VIL were performed, with longer meiotic chain configurations expected in hybrids of the former. Epididymal sperm counts were performed for male offspring. BUCxWEI hybrids had low fertility, some with no sperm found. Backcrossing of female hybrids to parent populations supported this, with few litters born. This suggests that gene flow between the first two populations would be more strongly impeded by chromosomal incompatibilities than between the second and third population. Genetic analyses using mitochondrial DNA, three Y-specific and twenty-five autosomal microsatellites indicated that most of the molecular variation was among populations, rather than among individuals within populations. However, the difference in hybrid fertility was not reflected in these genetic analyses. In order to understand these results, we are planning a detailed SNP analysis for better resolution.

The Contribution of Repetitive Elements to Genome Size in North American Fireflies

Katharine Korunes, Sarah Sander, David Hall

Sunday, June 22, 2014 -Poster #65

Massive genome size variation exists across North American fireflies in the family Lampyridae. We used random 454 sequencing to obtain genome sequence data from 21 species to identify and classify repetitive DNA contributing to genome size variation within this family.

Exploiting the full potential of next-generation DNA sequencing through genotype imputation

Daniel Money, Kyle Gardner, Sean Myles

Sunday, June 22, 2014 -Poster #66

Next-generation DNA sequencing (NGS) is increasingly being used to investigate questions of evolutionary importance across diverse organisms, but bioinformatic tools that exploit the full potential of NGS are lacking. Genotype imputation is a powerful method for exploiting the full potential of NGS by filling in missing genotype data, but most imputation tools have been developed for human whole-genome NGS data and benefit from high quality genotype calls from a panel of reference samples. In studies of non-model organisms, methods such as RADSeq and genotyping-by-sequencing (GBS) are often used to generate genome-wide polymorphism data from NGS data and it remains unclear what the most suitable imputation algorithms are for these data. Here we evaluate several genotype imputation methods on GBS data generated from over 500 varieties of apple (Malus domestica), a highly diverse and heterozygous crop without a reference panel of high quality genotype data. We report metrics of quality, accuracy and utility for each imputation algorithm and provide recommendations for studies using similar methods in non-model organisms.

Does selfing facilitate niche shifts? Evidence from niche modeling

Alannie Grant, Susan Kalisz

Sunday, June 22, 2014 -Poster #67

Across all species, range size varies by approximately twelve orders of magnitude. These stark differences may be the result of variation among species' colonizing ability. Range expansions maybe critically influenced by a species' ability establish in a diverse assortment of uncolonized habitats beyond its current range. Population establishment in these novel habitats is equivalent to a niche shift. Recent studies find that selfing plants tend to have larger ranges than their outcrossing congeners. Since the most common evolutionary trend in flowering plants is the transition from outcrossing to selfing, we hypothesize that this transition may have also been accompanied by a shift from a narrow niche to a wider niche. Thus, implicating selfing as a key trait that aides in colonizing ability. To test this, we conducted extensive multivariate analyses and constructed species distribution models (SDMs) using more than > 4,000 georeferenced species locations from sixteen species (eight sister taxa, each pair consisting of one selfer and one outcrosser) and environmental data layers to estimate each species' niche and niche width. By contrasting SDMs between sister taxa, we find evidence of substantial niche divergence. Niche widths for selfing taxa differed significantly from outcrossers (p

Genotype by social environment interaction for male aggressive behavior in Drosophila melanogaster

Palle Jensen, Bryn Gaertner, Kirsty Ward, Trudy Mackay

Sunday, June 22, 2014 -Poster #68

Aggressive behavior in animals plays an important role in acquisition and defense of resources, and in establishing dominance hierarchies among social animals. In humans, elevated aggressive behavior is associated with some psychiatric- and neurodegenerative disorders, which have large social- and economic costs. Aggressive behavior is a typical quantitative trait, with variation in natural populations due to segregating variation at many interacting loci, environmental variation, and variation in the extent to which different genotypes respond to the same environmental perturbation (genotype by environmental interaction, GEI). Obtaining a better understanding of the relative contribution of these underlying sources for variation in aggressive behavior is therefore of great importance. Several candidate gene studies have been performed to elucidate the genetics of aggression, and have shown that the same genetic mechanisms are conserved across taxa – from invertebrate model systems to humans. Social deprivation is known to increase different aspects of aggression in humans and other mammals, and this pattern is also observed in invertebrates. However, most studies of the genetic basis of aggression utilize preselected candidate genes, and the environmental effects of social deprivation have not been examined across different genetic backgrounds. Here, we use the Drosophila melanogaster Genetic Reference Panel (DGRP), a population of 205 sequenced inbred lines, to evaluate genetic variation in aggressive behavior as well as GEI for aggression under different social environments. We developed an assay to facilitate high-throughput acquisition of aggression data on pairs of individuals (one DGRP fly and a common control (Canton S B) fly). We applied this assay to DGRP male flies that were isolated or reared in social groups from eclosion. We filmed each pair for 2 minutes and subsequently scored aggressive behavior, for a total of 24 pairs / line / social condition. We used a two-way generalized linear Poisson model to assess whether the DGRP lines exhibit different levels of aggression, whether there is difference between socialized or isolated individuals from same line, and whether there is genetic variation in these differences. Our preliminary data on a subset of the DGRP lines shows that there is strong genetic variation in aggressive behavior in both social groups; that on average isolated males have higher level of aggressive behavior than social males; and that there is GEI for aggressive behavior. We will report the results of a genome-wide association study for aggression and the difference in aggressive behavior between social rearing conditions.

Partial behavioral isolation between two divergent populations of Drosophila melanogaster and their mating potential with other wild type populations.

Phillip Barnes, Phoebe Winn, Melanie Argueta, Lucy Drayson

Sunday, June 22, 2014 -Poster #70

Although a DDT-resistant strain of Drosophila melanogaster (91R) and its unselected control (91C) were both derived from the same foundation population obtained from nature in 1952, recent studies have shown significant behavioral isolation between these two populations. Three hypotheses can be proposed for how genetic changes could have occurred to cause the observed behavioral isolation between these two strains: 1) behavioral and genetic changes occurred in both strains simultaneously, 2) behavioral and genetic changes occurred primarily in the 91C strain, or 3) behavioral and genetic changes occurred primarily in the 91R strain. Both the 91C and 91R strains were compared to five laboratory wild type "tester" strains by multiple-choice, simultaneous mass-matings. Random mating was consistently observed between 91C and all of the tester strains. However, 91R showed significant behavioral isolation (within-group preferences) with some of the tester strains. These results tentatively support Hypothesis 3: that behavioral genetic changes have occurred primarily in 91R. These changes may be associated with the intense selection that occurred for resistance to DDT and/or with possible random genetic changes that could have occurred during bottlenecks of the 91R stock that happened during the artificial selection regime.

Maintenance of plasmid-encoded drug resistance in Acinetobacter baumannii in liquid culture and biofilms

Genevieve Metzger, Eva Top, Jack Millstein, Silvia Smith, Thibault Stalder, Matthew Settles

Sunday, June 22, 2014 -Poster #71
Biofilms are increasingly recognized as a medical problem because of their resistance to eradication by antibiotics and the increased appearance of multi-drug resistant (MDR) bacteria. Plasmids encoding drug resistance are common and allow resistance to be transferred between bacterial strains, but the mechanisms by which plasmid-encoded resistance is maintained in the spatially structured environment of a biofilm are poorly understood. In this study, we examined the persistence of plasmid-encoded drug resistance in Acinetobacter baumannii, a well-known wound pathogen. According to a recent CDC report, the number of healthcare-associated infections with Acinetobacter is estimated to be 12,000 annually in the United States alone, with 500 leading to death. We introduced MDR plasmid pB10 into a strain of A. baumannii, and grew the strain in well-mixed liquid cultures and biofilms, with and without antibiotic selection. Clones from each population were then analyzed for retention of antibiotic resistance, and a subset was completely sequenced to examine the corresponding genotypic changes in plasmid sequence. In the absence of selection, the resistance was retained much longer in biofilms than in liquids. Moreover, bacteria that were evolved under antibiotic selection in liquid cultures retained the resistance traits much longer than their ancestral counterparts when selection was removed. Assembly of plasmid DNA sequences showed that large deletions occurred in some of the replicate lineages, and that truncated versions of pB10 had been inserted into the chromosome in others. We are currently comparing the location and frequency of chromosomal insertion between the lineages to determine how the environment and spatial structure may affect the pathways through which MDR plasmids are maintained by bacteria. Our results suggest that in bacterial pathogens like A. baumannii the stability of plasmid-encoded resistance can rapidly arise through multiple genetic mechanisms.

The distribution of major mutational effects: assaying thousands of Arabidopsis thaliana insertion mutants with unPAK

Matt Rutter, Courtney Murren, Hilary Callahan, Allan Strand, Michael Wolyniak

Sunday, June 22, 2014 -Poster #72
unPAK (undergraduates phenotyping Arabidopsis knockouts) is a consortium of institutions involved in large-scale phenotyping of a set of Arabidopsis thaliana T-DNA insertion mutants generated by the SALK Institute. For each line, the locus of insertion has been identified. The project involves screening lines to identify single insertion lines, bulking seed for distribution across participating institutions and phenotyping replicate mutant plants. Subsets of plants are grown in multiple laboratories and/or in multiple ecologically relevant environments. In addition, the mutant plants are used in course-based research experiences and the entire project is being studied to investigate the effect of participating in a research network on the accrual of scientific social capital by undergraduates. Here we report the distribution of mutational effects on fitness-related phenotypes for these large mutations. The results can be used to describe broad trends in the effects of mutation and environment on plant phenotype. In addition, the database can be used to identify particular loci for which mutations have large effects on fitness.

Uncovering mutant and natural variation phenotypes in Arabidopsis roots

Courtney Murren, Clare Kohler, Michelle Jordan, Amber Frazier, Gorka Sancho

Sunday, June 22, 2014 -Poster #73
While root biology in natural systems has been a subject of much recent interest, there have not been similar approaches in model plants such as Arabidopsis. However, genomic tools are available in model plants that are not available for other natural systems. We are synthesizing approaches from both classic plant ecology and plant genomics to describe the ecological genetics of whole plant root and shoot development in natural and mutant strains of Arabidopsis thaliana. We have uncovered substantive effects of both edaphic and genetic factors on several root phenotypes. Our approaches allow identification of potentially important root trait genes, uncover the influence of mutation positions on root phenotypes as well as offer the potential to put mutant effects in the context of natural ecological variation.

How cardiac system developed during metazoan evolution

Hiroshi Shimizu

Sunday, June 22, 2014 -Poster #74
Former research on the evolution of cardiac system or cardiovascular system has dealt with the heart in lower vertebrates or primitive invertebrates, e.g. fishes, chordates (tunicate),

molluscs (Aplysia), arthropods (Drosophila) as model systems. However, extensive discussion was not made about how the cardiac system started in evolution. A breakthrough for this problem came from the identification of a non-hox type homeobox gene Nkx-2.5. This gene originally identified as tinman in Drosophila as the gene expressed in dorsal vessels (flies' heart) mesodermal muscle has now been recognized as a heart progenitor gene, namely the genetic switch for heart formation. It is now known that orthologues of Nkx-2.5 is expressed not only in the cardiac mesoderm but also in tissues that show pumping movement, e.g. pharynx of nematodes, peduncle of hydra. There the pumping is not always involved in cardiac function. The pharynx of nematodes has a function to send bolus into the gut demonstrating that the pumping contributes to digestion. Then again a question arises as to how the situation was in more ancestral examples. Here we propose a possibility that the cardiac function started originally as a tool to provide hydropressure for the locomotory activity of metazoans.

Modularity and integration in the mouse scapula

Madeline Keleher, James Cheverud, Charles Roseman

Sunday, June 22, 2014 -Poster #75

The components of the scapula have different genetic and developmental origins, potentially allowing for morphological modularity. These different origins were used to formulate hypotheses about the degree of modularity and integration in the mouse scapula, ranging from complete modularity to global pleiotropy. Sixteen landmarks on five scapular regions were double-measured in 1,200 individuals from the F10 generation of an advanced intercross of LG/J and SM/J mice. The phenotypic variation was mapped to regions of the genome using interval mapping. The results revealed 73 scapula quantitative trait loci spread across the genome with an average heritability of 0.309 for the morphological traits. The hypotheses of complete modularity and global pleiotropy were rejected. There is pleiotropy across the genome, but it is often clustered into modules, indicating that the mouse scapula is comprised of separate regions that are moderately integrated with each other.

Heteropatric Speciation: picking a mate over space and time

Abigail Kimmitt

Sunday, June 22, 2014 -Poster #76

Sexual selection is thought to play a significant role in population divergence, both in allopatry and in sympatry. Divergence may also be caused by natural selection on reproductive timing, if hybrids between populations with different phenology perform more poorly than either parental type. The dark-eyed junco, a small migratory songbird, is comprised of populations that differ markedly in both morphology/appearance and phenology. The Carolina and Northern subspecies winter in the Appalachian Mountains, but breed separately after the northern juncos migrate to Canada in spring. We will conduct mate preference trials to determine whether female choice is driven more by male morphology/appearance (i.e. plumage and bill coloration, body size) or by seasonal readiness to engage in courtship behavior. If females prefer males of their own subspecies, whether or not they are reproductively ready, this will support a stronger role for sexual selection on appearance than natural selection on phenology in population divergence. If, on the other hand, females prefer males that exhibit seasonal readiness regardless of their appearance, this will support a stronger role for natural selection in population divergence. Results are pending.

Genomic regions under divergent selection as a by-product of character displacement in spadefoot toads

Heidi Seears, Karin Pfennig, David Pfennig, Amber Rice

Sunday, June 22, 2014 -Poster #77

Character displacement takes place when co-occurring species avoid resource competition or reproductive interactions by evolving divergent characters. Selection for character displacement acts only on co-occurring (sympatric) populations of different species, and not where these species occur alone (allopatric). The role of character displacement in finalizing speciation is well known; however, it may also initiate speciation if the divergent selective environments between allopatric and sympatric populations lead to reproductive isolation. We are using double-digest RADseq to identify the genomic regions under divergent selection between allopatric populations of the spadefoot toad, Spea multiplicata, and populations sympatric with the closely related S. bombifrons. In the southwestern U.S., Spea multiplicata has undergone both ecological and reproductive character displacement where it co-occurs with S. bombifrons, but not in nearby allopatric populations. Thus, populations of S. multiplicata in sympatry versus allopatry have diverged in ecological and reproductive traits. Microsatellite data indicate that gene flow between allopatric populations of S. multiplicata and populations sympatric with S. bombifrons is reduced. Using ddRADseq, we are examining thousands of SNPs across the entire genome of hundreds of individuals of S. multiplicata. SNPs that show enhanced divergence across multiple sympatric versus allopatric population comparisons may be linked to genes under divergent selection and involved in reproductive isolation. If character displacement is promoting reproductive isolation between populations of S. multiplicata in these divergent environments, it may be playing a vital role in early speciation.

Reiterative evolution during rapid radiation of Diospyros (Ebanaceae) in New Caledonia uncovers the basis of adaptation

Ovidiu Paun, Barbara Turner, Jérôme Munzinger, Mark W. Chase, Rosabelle Samuel

Sunday, June 22, 2014 -Poster #78

Diospyros (Ebenaceae) is a large genus of woody, tropical and subtropical plants. Among these, a young group of 24 endemic species has rapidly radiated after a single long-distance dispersal event on New Caledonia, an archipelago in the southern Pacific. Due to its special geological history, New Caledonia is a mosaic of soil-types, and in combination with the climatic conditions this results in a heterogeneous environment across a fairly small geographic range. Most of the Diospyros species in the radiating group are morphologically and ecologically clearly differentiated. To resolve the shallow phylogenetic relationships in this group we employed restriction site associated DNA sequencing (RADseq). Over 8,400 SNPs filtered from Illumina HiSeq reads show a low genetic divergence among species, but generally confirm species delimitations and help infer a mostly well-supported phylogeny. Despite the high number of informative loci investigated, the phylogenetic resolution is still partly insufficient, indicating that processes blurring phylogenetic signals, such as interspecific hybridization and/or incomplete lineage sorting, may have been common during some speciation episodes in this group. Because it requires the presence of a rich ancestral genetic pool, unavailable in this group, we consider rather improbable that incomplete lineage sorting has significantly affected, on a genome-wide scale, the phylogenetic patterns here. Indeed, Splitstree and Structure analyses provide evidence for the presence of admixture between species, documenting local gene flow. The observed phylogenetic relationships point to some regional clustering among populations and species, indicating that allopatric speciation may have had a role in the initial differentiation within the group. However, several sister species, some of them sympatric, have distinct preference for different substrates. Our results therefore suggest that both (sympatric) ecological divergence and allopatric diversification shaped successive rounds of speciation in the Diospyros radiation. To further investigate the molecular targets of natural selection during the iterative divergence in substrate preference, we searched for loci that are systematically differentiated between sister taxa occurring on different soil-types. This method pointed to several loci that correspond to genes involved in transporting and binding through/to the cell membrane. As the New Caledonian soil-types are different in heavy-metal content and availability of mineral nutrients, these specific adaptations in binding and transporting substances to/through the cell membrane appear meaningful. It is, however, difficult to argue that this differentiation is responsible for particular speciation events or if it has evolved later.

Population structure reflects patterns of sexual isolation in a case of reinforcement in Drosophila

Emily Bewick, Michael Bray, Kelly Dyer

Sunday, June 22, 2014 -Poster #79

When recently diverged species come into secondary contact, there is a new opportunity for hybridization. Natural selection can act to increase species assortative mating to reduce maladaptive hybridization, a process known as reinforcement. Here, we study Drosophila subquinaria, which shows a pattern of reproductive character displacement consistent with reinforcement in the geographic region where it is in contact with its sister species D. recens. These sympatric D. subquinaria females not only reject D. recens males, but they also reject allopatric conspecifics. In contrast, D. recens shows neither reproductive character displacement nor sexual isolation among conspecific populations. In this study, we examine patterns of genetic differentiation among populations within each species and potential introgression between the two species. Consistent with patterns of sexual isolation within species, we find genetic differentiation to be much stronger between sympatric and allopatric populations of D. subquinaria compared to differentiation among populations of D. recens. We find evidence for asymmetric introgression between species, with more gene flow from D. recens into D. subquinaria than the other way around. In sum, our results suggest that early genetic divergence between sympatric and allopatric populations is occurring and may indicate incipient speciation within D. subquinaria, and despite the evolution of high female choosiness in D. subquinaria, gene flow appears to be ongoing between D. subquinaria and D. recens, keeping divergence incomplete.

Using molecular sequencing to assess the geographic origin of an introduced obligate brood parasitic finch (Vidua macroura)

Noah Burg, Julie Lockwood, Phillip Cassey, Mark E. Hauber

Sunday, June 22, 2014 -Poster #80

Co-invasion, host-parasite coevolution, and contingency are all presumed to play roles in the successful human-facilitated introduction of obligate avian brood parasites (which lay their eggs in nests of other bird species), and their hosts, to novel and disjunct distributions. The Pin-tailed Whydah Vidua macroura is an African endemic, with recently established exotic breeding populations within two of the world’s biodiversity hotspots: on the Caribbean island of Puerto Rico, and in Southern California, where suitable, estrildid finch host species had been previously established. Anecdotal evidence suggests that the introduced populations of V. macroura may have the ability to successfully switch to novel, non-African estrildid hosts in these introduced ranges.

Previous, single-locus mitochondrial molecular evidence, based on limited sampling, points to a split between western and southern African V. macroura populations. We are conducting a multi-locus phylogeographic analysis of native and introduced V. macroura populations, and expand on previous research to sample a wider distribution of museum specimens from across their endemic African distribution, as well as present the first molecular analysis of V. macroura specimens collected from their introduced New World distribution and from captive populations in the USA. Our preliminary analyses provide corroboration for a western African - southern African split and suggest that the California and Puerto Rico populations of V. macroura map to a western African origin.

Characterization of parasite population dynamics across their introduced range serves as a foundation for tests of the relative roles of intrinsic and extrinsic factors in the establishment of these new populations. Our plan of study will provide further insight into the adaptive process resulting from recent human-facilitated vicariant events and will aid in the development of models to test predictions about the host-switching potential and invasion potential of V. macroura in other introduced localities. The ability to make predictions about these birds’ invasive potential and host-switching potential may mitigate the potentially negative environmental and economic impact such invasions can cause and will inform management and conservation decisions regarding these feral populations.

Towards an avian model system for speciation genomics: gene expression divergence in zebra finches (Taeniopygia guttata)

John Davidson, Christopher Balakrishnan

Sunday, June 22, 2014 -Poster #81

Hybrid incompatibility occurs when mating between two diverging populations yields inviable or low fitness offspring. This process potentially results in genetic isolation between the populations and, over time, may result in speciation. Little, however, is known about the genetic contributions to hybrid incompatibility, particularly in birds. Due to the recent sequencing of the zebra finch (Taeniopygia guttata) genome as well as recent advancements in sequencing technology, gene expression data may be efficiently analyzed in this developing model system for genomics. In this study, tissue specific transcriptome data were compared between the two zebra finch subspecies: T. guttata castanotis, from Australia and T. guttata guttata, from the Lesser Sunda islands. These species appear to have diverged in allopatry for around one million years. To test for genetic incompatibilities, we also examined experimentally generated hybrids between the two subspecies. By mapping reads to the zebra finch reference genome, quantifying gene expression, and testing for differential expression, we find evidence both of gene expression divergence among species, and gene dysregulation in hybrids. Brain tissue samples showed genes involved in metabolic processes, protein binding, and oxidation-reduction processes differed between the Australian and hybrid populations when compared to the Lesser Sundas population. Although gene expression was largely conserved among populations, hybrid gene expression profiles more closely resembled T. guttata castanotis, the maternal species, than T. guttata guttata, the paternal species in the cross.

The repeatability of variability: exploring intra- and inter-individual variation in seasonality

Kevin Matson, Maaike Versteegh, Irene Tieleman

Sunday, June 22, 2014 -Poster #82

Animals exhibit seasonal cycles in a variety of physiological and behavioral traits. Studies of these cycles can potentially offer new insights into the evolution of individual differences. For natural selection to act, a trait must be both distinctive within individuals and variable among individuals. The extent to which the amplitude and phase of seasonal cycles fulfill these requirements is not well documented. As a preliminary analysis, we investigated seasonal cycles in the body mass of pigeons, which we weighed quarterly over a period of six years. We employed several of statistical techniques aimed at 1) quantifying the repeatability of seasonality and 2) comparing within- and among-individual variation in seasonality. Our goal is to take what we have learned from our analyses of mass and apply it to other seasonally variable physiological traits, including variables related to immune function.

Visual transcriptomics of seasonal forms of the butterfly Bicyclus anynana

Aide Macias, Adriana Briscoe, Antónia Monteiro, Furong Yuan

Sunday, June 22, 2014 -Poster #83

Vision is physiologically costly and so visual performance is expected to decrease under relaxed selection. Here we test whether there is plasticity in the expression of phototransduction and vision-related genes in a butterfly species with two seasonal forms where visual performance of males and females in one of the seasons is expected to be under relaxed selection. Bicyclus anynana is a sex role-reversed species displaying plasticity in which sex is choosy. We hypothesized that choosy individuals should have enhanced visual function and vary in gene expression from its non-choosy same-sex form. We extracted RNA from the eyes of dry season and wet season males and females and created RNA-sequencing libraries using Illumina technology. We made a de novo assembly and performed read-mapping of the individual libraries back to the assembly to explore the expression of phototransduction genes. Our data identifies several key vision-related genes that decrease in expression from choosy to non-choosy females.

An amino acid polymorphism in the Drosophila insulin receptor demonstrates pleiotropic and adaptive function in life history traits

Annalise Paaby, Paul Schmidt

Sunday, June 22, 2014 -Poster #84

Finding the specific nucleotides that encode adaptive phenotypes is a major goal in evolutionary biology, but polygenic traits pose a challenge because experimental power cannot always resolve the complex genotype-phenotype relationship. However, natural selection working in large wild populations can shift allele frequencies and indicate responsive regions of the genome. Previously, we showed that the two most common alleles of an amino acid insertion-deletion polymorphism in the Drosophila insulin receptor show independent, parallel clines in frequency across the North American and Australian continents. Here, we report that the cline is stable over at least a five-year period and that polymorphisms at InR demonstrate temporal shifts in allele frequency over seasonal time points. The alleles are associated with predictable differences in fecundity, development time, body size, stress tolerance, lifespan and levels of insulin signaling. These phenotypes are consistent with patterns of Drosophila life history variation across geography that very likely reflect adaptation to the climatic environment. Our results implicate insulin signaling as a major mediator of life history adaptation in Drosophila, and suggest that substantial life history tradeoffs can be explained by extensive pleiotropy at a single locus.

Evidence that previous experiences anchor mate choice decisions in male Drosophila

Kimberly Dolphin, Ashley Carter

Sunday, June 22, 2014 -Poster #85

Many sexual selection studies typically assume that males are indiscriminate in their matings and females are the selective and choosey sex. This paradigm is now shifting with more evidence that male mate choice plays a role in sexual selection. In two experiments we provide evidence for a new heuristic in Drosophila mate choice and additional evidence for male mate choice preferences in general.

Male Drosophila presented with two novel female phenotypes took significantly longer to begin courtship than males who were presented with a familiar phenotype female and a novel phenotype female (Kruskal-Wallace, p=0.004). These results are consistent with the process of "anchoring" as described in human psychological studies. Anchoring is a subconscious process in which options are compared to alternatives, or previous experiences, rather than evaluated on their own and can bias decisions in a manner that are not consistent with optimality. Although the male Drosophila previously exposed to one of the phenotypes in the choice experiment took longer to choose and exhibited a significant preference for one phenotype, there was no difference in female fecundities to explain the overall preference. In contrast, in a second experiment, virgin males unexposed to females showed no preference between two distinct phenotypes despite significant differences in fecundity between them.

These two sets of results indicate that while male Drosophila do exhibit mate choice behaviors, rather than being an objective assessment of the optimal female phenotype they may be influenced by anchoring effects that result in less optimal choices.

The T-type calcium channel from basal eumetazoan Trichoplax adhaerens highlights the fundamental features and evolution of the Cav3 channel family

Adriano Senatore, Liana Artinian, Arnaud Monteil, Wendy Guan, Arianna Tamvacakis, Vincent Rehder

Sunday, June 22, 2014 -Poster #86

Four-domain voltage-gated sodium (Nav) and calcium (Cav) channels are fundamental for neuronal and myocyte function, but little is known about what purpose these channels served in the early stages of animal evolution, before the neuromuscular system arose. T-type (Cav3) calcium channels are ubiquitous in animals where they regulate neuronal/myocyte excitability by amplifying sub-threshold depolarization. Key for this are their fast kinetics and low voltages of activation, which delineates them from their high voltage-activated relatives, the L-type calcium channels that underlie excitation-contraction coupling, and the N- and P-/Q-type calcium channels that underlie fast synaptic excitation-secretion coupling. Molecular cloning and expression of a T-type calcium channel homologue from Trichoplax adhaerens, an extant basal animal that diverged before the advent of neurons and muscle, reveals that the hallmark structural and biophysical features of T-type channels, which are optimally suited for regulating cellular excitability, pre-date the neuromuscular system. Furthermore, the Trichoplax T-type channel is moderately permeable to sodium, supporting a model where ancestral T-type channels conducted pronounced mixed Ca2+/Na+ currents, and that enhanced Ca2+ permeability occurred independently and by different mechanisms in both protostome invertebrates and deuterostome vertebrates. Indeed, understanding what T-type and other “neuron-/muscle-specific” genes do in Trichoplax can shed light on the early stages of neuromuscular system evolution, and perhaps clarify pleiotropic functions for these genes outside of their stereotyped roles.

The contribution of mutation and environmental variation to population variation in gene expression

Andrea Hodgins-Davis, Jeffrey Townsend

Sunday, June 22, 2014 -Poster #87

As some of the earliest molecular phenotypes in the genotype-phenotype map, mRNA levels are expressed across a range of dynamically changing environments and developmental contexts. Thus, understanding the mode and tempo of gene expression evolution requires understanding, not only the roles of natural selection and neutral drift in shaping population variation for expression levels in a single environment, but their also impact on expression variation across a range of ecologically relevant environmental contexts. We have previously revealed extensive genetic variation for genome-wide gene expression plasticity in Saccharomyces cerevisiae in response to an ecologically relevant gradient of copper environments. Here, we present the first analysis of genome-wide mutational variance for expression plasticity. To identify the extent to which novel expression variation supplied by mutation varies across environments, we have assayed gene expression via RNA sequencing for nine S. cerevisiae mutation accumulation (MA) lines and their ancestral genotype across a copper gradient. Gene expression reaction norms harbored substantial evolutionary potential for change in both expression values within environments and plastic changes between them. This assay revealed on average a higher proportion of losses of plasticity with mutation accumulation than gains of plasticity. However, the degree of mutational variability revealed for plasticity was unequal across the reaction norm: plasticity was gained more frequently between environments of copper sufficiency and starvation than between environments of copper sufficiency and excess. Because natural environments that are sources of yeast populations may be more likely to be characterized by high copper levels than an absence of copper, this work raises the question of whether this difference arises due to differences in the interaction of new mutations with the breadth of physiological effects of copper starvation and excess on yeast cells or whether the frequency of past selection has biased mutational variability across the reaction norm. If past selection does indeed shape the magnitude of mutational variance for plasticity, populations may experience an increased supply of variability precisely when confronted by novel ecological contexts.

Molecular evolution of 13 mitochondrial OXPHOS genes in Euteleost fishes

Feifei Zhang, Richard Broughton

Sunday, June 22, 2014 -Poster #88

All mitochondrial protein-coding genes encode subunits in the oxidative phosphorylation (OXPHOS) complexes, the major energy producing unit in all eukaryotes under aerobic condition. How the evolution of these genes was affected by environmental factors (temperature and salinity), locomotive ability, and natural selection has not been investigated in fishes in large scales under the appropriate phylogenetic background. We investigated these questions by looking at the rates of evolution (both nonsynonymous substitution rates and synonymous substitution rates) of 13 mitochondrial protein-coding genes in 956 fish species across a broad range of taxonomy.

A Comparison of Molecular Markers for Analyzing Population Structure in Three Species of Shark

Drew Duckett, Gavin Naylor

Sunday, June 22, 2014 -Poster #89

Genetic studies of population structure, gene flow, and effective population size are central to conservation biology and resource management. Such studies have traditionally used PCR technology to collect microsatellite, mitochondrial, or nuclear intronic data. Recent advances in genomic gene capture approaches make it possible to expand the scale of such studies by orders of magnitude. Genomic scale data provide unprecedented opportunities to explore the relative statistical power of different molecular approaches.

This study compares the effectiveness of (1) introns obtained through gene capture, (2) microsatellites and (3) mitochondrial data to asses population structure in three species of shark, each of which has a distinctly different life history: The globally distributed and highly migratory shortfin mako, Isurus oxyrinchus, the highly philopatric and regionally variable blacktip reef, Carcharhinus melanopterus, and the fine tooth, Charcharhinus isodon, whose population structure is less understood but is probably intermediate between the previous two. The present study will use simulation to explore how many individuals and loci are needed to effectively distinguish among populations for each of the marker types under a range of dispersal and migration schemes and contrast these results with empirical data collected from the three shark species.

Investigation of Atlantic white-sided dolphin (Lagenorhynchus acutus) population structure in the western North Atlantic based on mtDNA analysis

Nicole Vollmer

Sunday, June 22, 2014 -Poster #90

The U.S. Marine Mammal Protection Act (1972) aims to manage and conserve all marine mammal populations in the face of both natural and anthropogenic threats. However, information on genetic population structure is often not available to accurately identify the true biological populations that are present. The Atlantic white-sided dolphin (Lagenorhynchus acutus) inhabits waters of the western North Atlantic (wNA), ranging from central West Greenland to North Carolina, and is currently managed as one stock. However, evidence based on sightings, strandings, and incidental fisheries takes suggests the presence of three distinct management stocks in the wNA. Currently, little is understood about the population-level relationships of L. acutus in the wNA, and this species has never been investigated using molecular data to determine if current stock delineations accurately represent existing biological populations. For this study, DNA was extracted from 160 samples of L. acutus collected from the U.S. East Coast. A 349 bp portion of the mitochondrial control region was amplified and analyzed to further investigate population structure. Preliminary analysis revealed 35 distinct mitochondrial haplotypes, a relatively high haplotype diversity (0.9189 +/- 0.0109) and low nucleotide diversity (0.0080 +/- 0.0047). Initial results support the designation of a single stock for this species in U.S. waters; however, additional samples from Canadian waters are required to further examine population structure across the entire natural range of L. acutus in the wNA.

Surprisingly simple evolutionary histories of arctic peat mosses (Sphagnum)

Hans Stenoien, Jonathan Shaw, Blanka Shaw, Karen Golinski, Kristian Hassel, Kjel I. Flatberg

Sunday, June 22, 2014 -Poster #91

Genetic and phylogenetic patterns in arctic angiosperm species are typically very complex, with strong local and regional population differentiation superimposed on extensive allopolyplody. We investigated the genetic/phylogenetic structure of three peatmoss species (Sphagnum inexspectatum, S. miyabeanum, S. orientale) common in Alaska to test a previously published hypothesis that one is a homoploid hybrid of the other two, and to assess population differentiation among disjunct infraspecific population systems.

Evolutionary patterns in these three species are far more simple than in many of the arctic angiosperms that have been studied. Bryophytes are characterized by highly effective dispersal and although allopolyploidy occurs in this group and in some other bryophytes, the frequency and complexity of allopolyploidization does not appear to be especially elevated in arctic taxa. Our results are consistent with Beringia as a Pleistocene refugium.

Species delimitation and morphological evolution in the Heteronotus delineatus complex (Insecta: Hemiptera: Membracidae)

Olivia Evangelista, Marcio Pie, Julie Urban, Jason Cryan

Sunday, June 22, 2014 -Poster #92

Treehoppers in the family Membracidae are renowned due to their extraordinarily developed pronota, a thoracic structure that often shows bizarre shapes thought to play multiple roles in treehopper biology. The subfamily Heteronotinae shows a remarkable diversity of such ornamentations, most notably species in the genus Heteronotus, whose pronotal processes appear to mimic ants, wasps or be cryptic, and in some cases exhibit extreme sexual dimorphism. Currently circumscribed to H. delineatus are several pronotal-related morphological syndromes representing unique camouflage adaptations; deep divergences in multi-locus sequence data between sampled specimens suggest that this consists of a complex of sexually dimorphic species which occur sympatrically. The major goals of this research are to: a) estimate the species-level diversity in the H. delineatus complex by assessing the congruence in different coalescent-based delimitation methods, b) evaluate the correspondence between morphological syndromes and resulting delimitation schemes based on geometric morphometric data from their pronotal ornamentation, and c) understand the tempo and the mode of their morphological diversification.

New species of metaine spiders (Araneae, Tetragnathidae)

Bob Kallal, Gustavo Hormiga

Sunday, June 22, 2014 -Poster #93

The orb-weaving genera Meta Koch, 1836, and Metellina Chamberlin & Ivie, 1941, contain 34 and 7 species respectively, and are found around the world. They have never been revised, and the exact circumscription of the subfamily Metainae is controversial. Support for two separate genera has stemmed from several morphological characters, including the loss of the cymbial ectomedian process (CEMP) in male copulatory organs of Metellina. This study describes four new metaine species (two Meta and two Metellina), with molecular support for a new Meta from Taiwan, the third Meta species to be sequenced. Our data supports the continued use of the CEMP to diagnose the two genera. Furthermore, a major geographic range extension of Metellina is described based on collections from the Usambara Mountains, a region in eastern Africa with high endemicity. More metaines remain to be described, particularly from Africa, Asia, Australia, and the Pacific Islands.

Phylogeny and historical biogeography of the Rhinolophus pusillus species complex

Balaji Chattopadhyay, Kritika Garg, Swamidoss D Paramanantha, Sripathi Kandula, Uma Ramakrishnan

Sunday, June 22, 2014 -Poster #94

Rhinolophus pusillus is widely distributed across East and South East Asia. The phylogeny of this group is not resolved and so the question of its origin and evolution. In the present study we have addressed these questions using multiple nuclear and mitochondrial markers. We have reconstructed phylogeny of this group and used a comparative framework to address its possible origin, rdiation and colonization history.

Redescription and systematics of the sheet web spider genus Lomaita, Bryant 1948 (Linyphiidae).

Thiago da Silva Moreira, Gustavo Hormiga

Sunday, June 22, 2014 -Poster #95

The spider fauna of Central America and the Caribbean remains very poorly studied, known only by punctual faunistic works, and the 19th century monography Biologia Centrali-Americana. However many of those descriptions, quite outdated for modern standards, remain until today as the only source of information for those specimens. Here we present a revisionary work of the monotypic genus Lomaita Bryant 1948. We present an updated description of L. darlingtoni male, the first description of the female with remarks on the genus natural history and distribution. We also present the first phylogenetic hypothesis of Lomaita position among Linyphiidae.

The Cochineal Insect Genome: Dactylopius coccus Genome Assembly

Alex Van Dam, Simon Rasmussen, Bent Petersen, Rubini Maya Kannangara, Paiman Khorsand-Jamal, Bjoern Madsen, Finn Okkels, Mads Bennedsen, Kim Binderup, Thomas Sicheritz Pontén, Ulf Thrane, Birger Lindberg Møller, Uffe Hasbro Mortensen, Rasmus J. N. Fandsen

Sunday, June 22, 2014 -Poster #96

The cochineal insect genome assembly is described. ALLPATHS-LG was used for the initial assembly of Illumina short-read genomic data. Then RNA-seq data was used to merge scaffolds from the ALLPATHS-LG assembly. Trinity was used to reconstruct a de-novo transcriptome used by L_RNA_scaffolder to merge and orient scaffolds from the ALLPATHS-LG assembly. Next BWA was used to align all of the RNA-seq data to the new L_RNA_scaffolder assembly. The BWA alignment was then used to further merge scaffolds using Opera. We then used REAPR to find errors in the Opera genome assembly. Finally a PacBio data set is planned for a hybrid assembly to close the genome.

Population genomics of Dascyllus trimaculatus (Rüppell 1829) in the Indian Ocean

Eva Salas

Sunday, June 22, 2014 -Poster #97

ABSTRACT:

Large scale, comprehensive genetic surveys of marine species in the Indian Ocean are scarce, but neccesary to identify major multi-species genetic breaks and key conservation sites. Here, we contribute with the population genomics of a widespread coral reef fish in the Indian Ocean, Dascyllus trimaculatus. We used double digest Rad sequencing to compare SNPs among 9 populations, including sites within the Red Sea, the Arabian Sea, the African coast, the Mozambique channel, Seychelles and Chagos archipelago. Preliminary data with 2,500 neutral and non-neutral SNPs suggest that there is little genetic structure within the Indian Ocean populations, only Oman was significantly different. Analysis with non-neutral SNPs will be presented, to shed light into the roles of natural selection in these patterns.

Phylogeography of Mesoamerican bumble bees

Michelle Duennes, Sydney Cameron

Sunday, June 22, 2014 -Poster #98
Understanding the historical patterns of biodiversity in complex environments is a principal challenge in evolution. In particular, the geographically complex region of Mesoamerica harbors unusually high levels of biodiversity. Little is known about the genetic diversification of insects in this region, even though they represent a large component of species richness. The bumble bee, Bombus ephippiatus, can serve as a model in which to study insect/pollinator evolution in Mesoamerica. Moreover, bumble bees are important commercial and native pollinators in this region, yet the importation of non-native species for crop pollination has the potential for detrimental ecological consequences throughout the region. Previous phylogenetic research by these authors on Bombus ephippiatus has revealed that this species is a species complex comprising at least four distinct genetic lineages across Mesoamerica, with the Nicaraguan Depression and the Isthmus of Tehuantepec serving as geographic barriers. Using 8 microsatellite loci for over 400 samples from across Southern Mexico, Guatemala, and Honduras, we address how the Isthmus of Tehuantepec and various mountain chains in Mexico have shaped the high amount of genetic diversity present within Nuclear Central America.

To Sprout in Drought: A Genome-Wide Association Study of Drought Resistance in Cultivated Sunflower (H. annuus) Seedlings.

Rishi Masalia, Kody Brindley, John Burke

Sunday, June 22, 2014 -Poster #99
Drought is a significant environmental stress, which limits both vegetative biomass and reproductive output. As global temperatures and global population size continue to rise, water supplies will decrease, forcing agricultural programs to maximize crop productivity under drought conditions to improve food security. Here, we are using a genome wide association analysis of a previously characterized sunflower (Helianthus annuus) mapping population to identify associations underlying agronomically important morphological traits involved in drought resistance at the seedling stage. The population used is comprised of 288 diverse accessions and captures nearly 90% of the allelic diversity present within the cultivated sunflower germplasm. I'm focusing on drought stress during seedling establishment because this is an important limiting factor at a critical developmental stage, particularly in rainfed regions, where cultivated sunflower is traditionally grown. This work is still on going and preliminary results of this study will be presented here.

Evolution of flowering time and disc color across the genus Helianthus

Kaleigh Davis, Chase Mason, Lisa Donovan

Sunday, June 22, 2014 -Poster #100
This research explores the effects of various environmental factors on flowering time evolution across the genus Helianthus, as well as the role flowering time and disc color might play as an evolutionary mechanism for sympatric speciation. A common garden approach was used to assess flowering time and disc color variation across multiple populations each of 28 species of wild sunflower (Helianthus). A phylogenetic comparative approach was used to test relationships between flowering time and temperature seasonality, frost and drought risk, soil fertility, and life history. Species and populations from more seasonal habitats and habitats with high risk of drought and frost are hypothesized to flower earlier, and species and populations from more fertile habitats are hypothesized to flower earlier as well. It is hypothesized that annuals will flower earlier than perennials due to the evolutionary risks involved in monocarpy. Furthermore, it is hypothesized that sympatric sister species will exhibit larger differences in flowering time and more frequent disc color differences than allopatric sister species, due to the process of reinforcement. This research expands our understanding of the ecological and evolutionary responses of flowering time and disc color, which will allow for improved prediction of species persistence and displacement under global climate change.

Understanding floral trait evolution in wild sunflowers (genus Helianthus)

Hiral Patel, Chase Mason, Lisa Donovan

Sunday, June 22, 2014 -Poster #101
In order to predict both crop and wild species' reproductive success and persistence under looming environmental changes, we must understand how floral traits are currently adapted to specific climates and pollinator regimes. This study seeks to investigate the underlying ecological and evolutionary causes of variation in floral traits across the genus Helianthus. Sunflower species vary wildly in habitat use, and also vary strongly in both flower size and floral morphology. Given this variation, an evolutionary trade-off is hypothesized to exist between investment in two classes of floral traits, those governing pollinator attraction and those underlying seed production. The evolutionary strategy adopted by specific species under this trade-off is hypothesized to be affected by differences in life history and pollinator density in native habitats. Annuals are hypothesized to invest more heavily in attraction than perennials, due to the strong dependence on successful pollination during the single reproductive event of annuals, relative to the multiple opportunities for reproduction in perennials. Additionally, species found in habitats known to have higher densities of pollinators (e.g., forests and prairies) were predicted to invest relatively less in attraction and more in seed production than species from habitats known to have lower densities of pollinators (e.g., deserts and rock outcrops). Multiple populations of 28 species of wild sunflower were grown in a common garden

greenhouse experiment and a variety of floral morphological traits were assessed. A phylogenetic comparative approach was used to assess the correlated evolution of floral traits, and the evolution of traits during shifts to different habitats. Understanding trade-offs in floral biomass allocation has broad ecological consequences. For instance, Species adapted to specific pollinator densities via optimization of floral trait strategy may be unable to adapt to changing conditions under the short time scales of current climate change and pollinator declines, resulting in an inability to attract pollinators and failures in seed set that reduce population size and threaten species persistence. Also, this research will help us understand the balance between achieving sunflower pollination in the field for self-incompatible varieties and obtaining maximum seed yield.

Mechanisms maintaining two feeding strategies in the moth Symmestrischema lavernella

Stephanie Cruz Maysonet, *T'ai Roulston*

Sunday, June 22, 2014 -Poster #103

Traditional explanations for specialized host use patterns by herbivores include evolving to use high quality plant hosts, avoid natural enemies and make efficient use of the most common food resource in the environment. While several studies have combined two of these hypotheses, we are still in need of understanding how an increasing number of factors interact to determine herbivores' diets. Symmetrischema lavernella is a phytophagous gelechiid moth whose hosts appear to be limited to the genus Physalis (Solanaceae). Flower buds and fruits serve as larval substrates producing budworms and frugivores, respectively, and both strategies are used in each of the 3+ generations of the moth. However, each larva can adopt only one strategy, leading to the prediction that the most profitable strategy should persist over time. Alternatively, frugivores and budworms would coexist if selective pressures render both strategies similar in costs and benefits or show enough variation to impede fixation on the preferred strategy. This study was aimed at explaining the occurrence of these two feeding strategies in S. lavernaella by assessing the effect of food quality, natural enemies and resource availability through field observations and experiments. Pupal weights of frugivores were found to be 33% greater than in budworms, with females being heavier for both strategies. Frugivores also showed greater survival than budworms in natural patches of their host plant, despite 69% of parasitoid attacks being observed in frugivores. Lab experiments showed that the strategy chosen corresponds to the size of the floral bud entered: caterpillars that enter small floral buds (Additionally, in an experiment exposing uninfected plants to varying densities of moths, budworms occurred mostly when density of adults was high, suggesting this strategy is adopted when preferred bud sizes are unavailable, thus reducing intraspecific competition. Together, these results imply tradeoffs between performance, survival and competition maintain both feeding strategies in S. lavernella.

Plant Trait Variation of Big Bluestem (Andropogon gerardii) Across Great Plains' Reciprocal Gardens

Matthew Galliart

Sunday, June 22, 2014 -Poster #104

Midwest grasslands are dominated by big bluestem, Andropogon gerardii that grows across a strong precipitation gradient (500 to 1200 mm/yr from western KS to IL). Grassland response to drought is critical for informing restoration plantings and predicting response to climate. We used reciprocal gardens to investigate ecotype differences in vegetative and reproductive traits. Three ecotypes (from central KS (CKS), eastern KS (EKS), and southern Illinois (SIL)) were reciprocally planted in Colby, Hays, and Manhattan, KS, and Carbondale, IL. We evaluated ecotypic differences in vegetative (canopy area, height, blade width, and emergence) and reproductive features (seed production and flowering time) across planting sites. We predicted ecotypes would perform best in their home environment. Canopy area and height increased from west to east, with no evidence for any ecotype differences in Colby and Hays. However, in Carbondale, the SIL ecotype showed disproportionate increase indicating local adaptation. Ecotypes varied in blade width (SIL>CKS>EKS), and blade widths of all ecotypes increased eastward. For all ecotypes, leaves emerged earlier in eastern Illinois site. In Carbondale and Manhattan planting sites, the CKS ecotype flowered 20 days earlier than other ecotypes and showed a greater probability of seed production in the western sites relative to other ecotypes, while the SIL ecotype had greatest seed productivity in its home site. The CKS ecotype shows a suite of traits consistent with drought tolerance—reduced canopy, short stature, and early flowering in its home environment. Our results provide insight into plasticity of trait variation and ecotypic adaptability in drier climates.

Selective pressure by pollinators on floral nectar of female Eurya japonica

Kaoru Tsuji, *Takayuki Ohgushi*

Sunday, June 22, 2014 -Poster #105

Divergence of floral traits within species has emerged by trait evolution through flower-pollinator interactions. In dioecious plants, pollinators may contribute to sexual dimorphism of floral traits. Under no pollen limitation, pollinated female flowers do not need pollinators any more, while male flowers still require pollination to increase their fitness. It is accepted that males produce larger flowers with greater rewards to subsequently attract pollinators. If male flowers are attractive to pollinators than female flowers, pollen limitation is more likely to occur in female flowers that are inferior to male flowers in between-sex competition for pollinators. Therefore, under pollen limitation females may evolve attractive floral traits for pollinators. Eurya japonica is a polygamodioecious shrub in East Asia, and male flowers are larger than female flowers. Then, to examine whether pollinators work as a selective agent for greater attractiveness of female flowers, we investigated (1) whether nectar amount of E. japonica differs between sexes, (2) how nectar amount affects attractiveness to pollinators, (3) whether there is a sexually-biased attractiveness of pollinators, and (4) whether females suffer from pollen limitation. We measured volume and sugar contents of floral nectar, and counted the number of pollinators. To reveal how nectar amount affects plant fitness through pollinator attraction, we examined the proportion of fruit set and matured seeds. In addition, we conducted a field experiment to examine pollen limitation by artificial pollination. Smaller female flowers provided greater amount of nectar with higher sugar contents than male flowers. The number of pollinators, and the proportion of fruit set and matured seeds increased with increasing nectar volume and sugar content. The number of pollinators visited to female flowers did not differ from male flowers. Although the proportion of fruit set of female flowers exposed to pollinators did not significantly differ from that of artificially pollinated flowers, the proportion of matured seeds in flowers exposed to pollinators was significantly lower than artificially pollinated flowers. Our results demonstrated that despite small size, female flowers attracted pollinators, as same as male flowers under pollen limitation. This is probably because female flowers provided greater rewards to pollinators, which may compensate for disadvantage of small floral size. The greater rewards of female flowers to pollinators may be adaptive to the pollen limitation. Since pollen limitation would be common in many pollination systems, it is likely that pollinators work as a selective agent for greater amount of high quality nectar of female flowers.

Anchored Phylogenomics: Rapidly Expanding Across the Tree of Life

Michelle Kortyna, Alan Lemmon, Emily Lemmon

Sunday, June 22, 2014 -Poster #106

Hybrid enrichment is quickly becoming the preferred method of phylogenomic data collection, because it allows hundreds or thousands of nuclear loci to be obtained at a lower cost than other approaches. Anchored hybrid enrichment, by utilizing probes representing several diverse lineages within a target clade, is particularly powerful because it allows researchers to target loci with sufficient sequence variation to answer phylogenetic questions at both deep and shallow scales. Here, we summarize over 20 Anchored Phylogenomics projects in Vertebrates, Arthropods, Annelids, Molluscs, and Angiosperms. These studies demonstrate that the Anchored Phylogenomics approach is an effective method of obtaining well-resolved species trees in non-model systems.

Species delimitation of Cattleya coccinea and C. mantiqueirae (Orchidaceae): insights from phylogenetic and population genetics analyses

Jucelene Rodrigues, Cassio van den Berg, Aluana Abreu, Mariana Novello, Elizabeth Veasey, Giancarlo Oliveira

Sunday, June 22, 2014 -Poster #107

The high-altitude Southeastern Brazilian 'Cattleya coccinea' clade includes two taxonomically challenging species, Cattleya coccinea and C. mantiqueirae, the latter considered restricted to the mountain range of Serra da Mantiqueira. In order to hypothesize the existence of evolutionary independent lineages corresponding to these species, we inferred phylogenetic relationships and described patterns of population genetic diversity and structure of populations from six localities based on ISSR and cpDNA sequence data. Results do not support the species C. coccinea and C. mantiqueirae as previously circumscribed. We propose the recognition of two species according to phylogenetic and population genetic patterns recovered: C. coccinea, in this study represented by three northeastern localities in the Serra do Mar and Serra da Mantiqueira and C. mantiqueirae corresponding to other three southwestern populations. Also, specimens from Lima Duarte from Serra da Mantiqueira clearly do not belong to neither of the two groups and demand further investigation concerning a possible hybridization scenario of C. coccinea and C. brevipedunculata. Population genetic patterns of variation are in agreement with pollination observations for this group and with a drift-selection model of speciation. Owing to the high genetic differences among populations, with low levels of variation within populations, conservation priorities should favour protecting most populations as possible.

Assessing the Phylogenetic Utility of the ITS Regions

Kevin Bird

Sunday, June 22, 2014 -Poster #108

The internal transcribed spacers of the nuclear ribosomal RNA gene cluster, termed ITS1 and ITS2, are the most frequently utilized nuclear markers for phylogenetic analyses across many eukaryotic groups including most plant families. The reasons for the popularity of these markers include: 1. Ease of amplification due to high copy number of the gene clusters, 2. Available cost effective methods and highly conserved primers, 3. Rapidly evolving markers (i.e. variable between closely related species), and 4. The assumption (and/or treatment) that these sequences are non-functional, neutrally evolving phylogenetic markers. Here, our analyses of ITS1 and ITS2 for 50 species suggest that both sequences are instead under selective constraints to preserve proper secondary structure, likely to maintain complete self-splicing functions, and thus are not neutrally evolving phylogenetic markers. Our results indicate the majority of sequence sites are co-evolving with other positions to form proper secondary structure, which has implications for phylogenetic inference. We also found that the lowest energy state and total number of possible alternate secondary structures are highly significantly different between ITS regions and random sequences with an identical overall length and Guanine-Cytosine (GC) content variation. Lastly, we review recent evidence highlighting some additional problematic issues with utilizing these regions as phylogenetic markers, and thus strongly recommend alternate markers and

Extreme genetic homogeneity: Phylogeography of the salamander genus, Pseudotriton

LaShonda Caine, David Beamer

Sunday, June 22, 2014 -Poster #109

The salamander genus Pseudotriton (family Plethodontidae) has several races, yet red salamanders (Pseudotriton ruber) and mud salamanders (Pseudotriton montanus) remain the only identified species of the genus. Pseudotriton is widely distributed across the eastern United States, ranging from New York in the north to Florida in the south westward to the Mississippi River. While the distinctiveness of the two species of Pseudotriton has long been recognized, the genetic variation and structure of populations has never been analysed. In general plethodontid salamanders are characterized by a pattern of extreme geographic partitioning and cryptic speciation but to date no studies have addressed these issues in Pseudotriton. We have sampled 150 populations spanning the extent of this genera's distribution. For each population sampled, we extracted DNA, amplified and sequenced a 1686 base pair fragment of the mtDNA genome. Here we present the results of a Bayesian phylogenetic reconstruction for this genus.

Features of diversification in a ubiquitous freshwater crustacean, the Hyalella azteca species complex

Gary Wellborn, *Jonathan Witt*

Sunday, June 22, 2014 -Poster #110

The ubiquitous North American amphipod crustacean, Hyalella azteca, is a diverse species complex characterized by often deep genetic divergence among lineages, but limited phenotypic divergence. Here, we explore phylogenetic and morphological patterns of evolutionary diversification in the species complex. Based on analysis of mitochondrial COI sequence, we posit that more than 80 species may occur in North America, with only a few of these formally described. Most putative species occur in isolated springs within western North America, and several additional species have large geographic distributions. We report phylogenetic structure of the Hyalella azteca radiation, and describe prominent phenotypic patterns in their diversification. One notable feature is the repeated occurrence among lineages of large- and small-bodied ecomorph species that have extensive geographic distributions, with ecomorph types corresponding to ecological conditions of their habitats.

Statistical Analysis of the Factors Affecting the Distribution of Genome size in Angiosperms

Rosana Zenil-Ferguson, *Gordon Burleigh, Jose Miguel Ponciano*

Sunday, June 22, 2014 -Poster #112

In angiosperms, the distribution of genome sizes at different ploidy levels is often explained by a rapid genome downsizing following a whole genome duplication (WGD). Yet, constraints on chromosome number and genome size might influence this distribution. We performed a simulation study to analyze whether genome downsizing alone is responsible for the observed genome size distribution, and alternately, if constraints on the maximum chromosome number or genome size influence this distribution. Using the public the dataset of Kew Royal Botanical Gardens, containing 7542 angiosperm taxa and information about chromosome number (2n), ploidy level (x), and genome size (1C), we explore the empirical chromosome number and genome size distributions. Finally, we performed a series of bootstrap simulations using the observed genome size distribution to evaluate the role of a genome reduction rate, chromosome number constraints, and genome size constraints on the distribution of genome sizes following WGDs. Simulation results show that both the genome downsize hypothesis and the threshold hypothesis can explain some of the variation in the distributions of genome size at different ploidy levels, but it is difficult to distinguish the effects of these hypotheses.

Insect Phylogeny from the 1000 Insect Transcriptome Evolution (1KITE) initiative

Karl Kjer, *Xin Zhou, Bernhard Misof*

Sunday, June 22, 2014 -Poster #113

Despite extensive efforts over the past 50 years, the sequence and timing of many insect relationships remain controversial. We address this problem by inferring the phylogeny of insects, using 1,478 protein-coding genes from 144 taxa as data, and estimating dates of emergence of all major extant insect groups with a rigorously validated set of fossil calibrations. Phylogenetic analyses, using site-specific rate models or domain-specific amino-acid substitution models, produced robust and congruent results. Polyneoptera (e.g., stoneflies, earwigs, grasshoppers, termites, mantis, roaches) was recovered as a natural group together with the enigmatic Zoraptera (ground lice). Lice (Psocodea) were more closely related to Holometabola (e.g., beetles, flies, wasps, bees) than to true bugs (Hemiptera) and thrips (Thysanoptera). We show that the tremendous diversity of extant winged insects (Pterygota) can be traced back to just four lineages, i.e. Palaeoptera, Polyneoptera, Hemiptera+Thysanoptera and Pscodoea+Holometabola. Our phylogenomic analysis provides a uniquely robust temporal and phylogenetic framework for studying the causes and consequences of morphological and physiological innovations in insects and for comparative analyses in the prospering field of insect genomics.

Comparative transcriptomics reveals orthologous loci for spider phylogenetics

Jesus Ballesteros, *Prashant Sharma, Rosa Fernandez-Garcia, Gonzalo Giribet, Gustavo Hormiga*

Sunday, June 22, 2014 -Poster #114

Comparative transcriptomics reveals orthologous loci for spider phylogenetics

Molecular systematics of spiders (Araneae) have lagged behind other animal groups regarding the number of genetic markers available for phylogenetic inference. Current studies rely on a handful of genes (five to six, including both mitochondrial and nuclear genes), and their analyses often result in conflicting relationships and/or lack of statistical power to test evolutionary hypotheses. In addition, often there are problems of base compositional biases and paralogy that have been previously detected for these markers . All these issues are particularly challenging when deep nodes are involved (family level and above). For example, conflicting phylogenetic hypotheses of the relationships between the families in Araneoidea obscure our understanding of the evolution of complex behavioral characters such as those leading to the diversity in web architecture .

In this study we present the results from a pilot survey for novel informative loci based on the comparison of three spider transcriptomes (representing the araneoid families Araneidae, Linyphiidae and Tetragnathidae). Additionally we include the transcriptomes of two outgroup species, assembled from raw reads accessed from public databases.

The main goal of this study is to test our pipeline to recognize sets of orthologous loci of potential use for araneoid systematics.

Solving and contrasting tokogenic relations in nuclear gene ITS-2 and mitochondrial msh-1 of Caribbean Octocorals.

Lina Gutierrez, *Juan Sanchez*

Sunday, June 22, 2014 -Poster #115

Incongruence between mitochondrial and nuclear genes is a common issue when trying to integrate both sources of information in phylogenetic and species delimitation studies. The main problem is related to multiple loci copies, allelic variation and heterozygosity in the nuclear genome compared to mitochondrial genes. In the present study we use the: species as fields for recombination (s-FFF) approach to understand species delimitation in two species of Caribbean octocorals: Briareum asbestinum, Gorgonia mariae, G. ventalina and G. flabellum which present multiple copies of the gene ITS-2. This is a non-topological methodology in which species and populations are not defined a priori but are established according to allelic pools among taxonomic units, so individuals holding alleles of a given allelic pool in a specific locus will belong to the same group known as: Field For Recombination. On the other hand we will sequence mitochondrila msh-1 for contrasting and comparing puroposes. Results are shown in the form of haplotype networks with additional connections between shared allelic pools. G. mariae will share higher proportions of allelic pools with G. ventalina given its possible reticulate evolutionary process. Likewise individuals of different morphotypes in B. asbestinum will show different allelic pools than individuals of similar morphotypes given its incipient divergence process.

A phylogenetic approach for estimating amounts of nonhomologous gene conversion in duplications

Xiang Ji, *Jeffrey Thorne*

Sunday, June 22, 2014 -Poster #116

Widely used probabilistic models of nucleotide substitution assume independent change at corresponding sequence positions in duplicated genes. This assumption is violated when nonhomologous gene conversion occurs between the duplicated regions. We are developing an approach that allows a nucleotide substitution at one position in a duplicated region to increase the probability of the same substitution at corresponding paralogous positions within the genome. We will outline our approach as well as its strengths and weaknesses.

Understanding the Benefit of Soma during the Origin of Cellular Differentiation

Erik Hanschen, *Richard Michod*

Sunday, June 22, 2014 -Poster #117

To understand the hierarchy of life in evolutionary terms we must explain why groups of one kind of individual evolve into a new higher-level individual as observed in the evolution of eukaryotes, multicellular organisms, and eusocial societies. During these transitions in individuality, division of labor facilitates functional integration of the lower level units for the benefit of the group. In the evolution of multicellularity, this division of labor occurs through reproductive germ and non-reproductive soma. Previous life history theory predicts that somatic cells specialize on colony viability but is agnostic to the mechanism through which this benefit occurs. While empirical work has identified several potential mechanisms, this research has focused on species with thousands of somatic cells such as Volvox carteri. We have utilized a closely related species, Eudorina illinoisensis, which has facultative somatic cells to test if these mechanism apply to the origin of somatic differentiation. We have demonstrated variation in presence and number of somatic cells and propose several experiments to test previous adaptive mechanisms for the benefit of somatic cells, including the source-sink hypothesis, the flagellation constraint hypothesis, and the environmental mixing hypothesis. Understanding the mechanisms through which somatic cells initially provide benefit would inform the likelihood of evolving cellular differentiation as well as any additional benefits of soma once high numbers of soma have evolved. If so, there are additional benefits of increased soma number and somatic differentiation may be more likely to persist evolutionarily.

Nutrient effects on energy allocation among body parts within an individual.

Goggy Davidowitz, *Autumn Moore, Andrew Daws, R. Craig Stillwell*

Sunday, June 22, 2014 -Poster #118

We use a common currency, calories, to examine relative investment among body parts (head, thorax, legs, wings, abdomen) within individuals as a function of body size, diet quality, and sex, in the hawkmoth Manduca sexta. 50-90 moths per sex, per diet (478 total), were disarticulated and each body part dry weighed. Separate calibration curves for the caloric content of each body part, diet, and sex were generated using a bomb calorimeter. These calibration curves were used to calculate the predicted caloric content of each of the 5 body parts in the 478 moths. As expected, moths invested more into individual body parts as diet quality increased. Contrary to our prediction, however, males and females allocated resources very differently when diet quality varied. For example, mass-specific (cal/g) allocation to the thorax in females increased with thorax size on high quality diet but decreased on low quality diets. This trend was opposite in males: as thoraces increased in size, cal/g decreased on high quality diet but increased on low. Similar inverse relationships for males and females were found in other body parts. Tradeoffs in caloric investment were seen only between the abdomen and other body parts. The head, thorax, wings and legs did not trade off with each other in caloric content. These patterns of tradeoffs held for both sexes and all diets. This pattern of tradeoffs disappeared, however, when examined on a mass specific level. Together these results show that males and females have different rules of mass-specific caloric investment into individual body parts when diet quality varies. These results help explain differences in flight performance between males and females, but further implications of these different allocation rules require further study.

Predator induced aggregation of Chlamydomonas reinhardtii by a diffusible signal

Sarah Cossey, Chris Berger, Nicole Richardson, Bradley Olson

Sunday, June 22, 2014 -Poster #119

The evolution of multicellularity is a major evolutionary transition, occurring at least twenty five independent times across eukaryotic lineages. However, the ecological pressures that stimulate this transition are poorly understood. Chlamydomonas and its multicellular relatives show a linear progression of morphological complexity, from unicellular Chlamydomonas reinhardtii to colonial multicellular Gonium pectorale to Volvox carterii which is multicellular with differentiated tissues. It has been hypothesized that multicellularity evolved to increase organismal size thus, allowing it to evade predation. In the presence of predators such as Daphnia, we found that C. reinhardtii will rapidly form aggregates. However, in nutrient limited media we did not see aggregation. We hypothesize that the aggregation response seen in the predated C. reinhardtii has become genetically permanent in multicellular volvocine algae species. To test this hypothesis, we are characterizing the predator response in C. reinhardtii and exploring how it evolved in its multicellular relatives. First, bacteria can induce aggregation of C. reinhardtii cells, so we developed a method to prepare axenic Daphnia (removal of bacterial and fugal contaminants) such that their sole food source is C. reinhardtii cells. The axenic Daphnia then feed on the C. reinhardtii cells and a rapid aggregation response is observed. When media from the predator treated C. reinhardtii cells is added to untreated C. reinhardtii an aggregation response is also observed, suggesting that there is a mobile signal released into the media, causing this response. Interestingly, G. pectorale, a colonial multicellular relative of C. reinhardtii does not respond to predation by aggregation, suggesting that the aggregation response may be genetically permanent in this species. Here we will report the characterization of the signal that is responsible for this aggregation response. In summary, our data indicates that predation may have driven the evolution of multicellularity in the volvocine algae.

Evolution of sex-biased gene expression in human and non-human primates

Nichole Rigby, Rob Kulathinal

Sunday, June 22, 2014 -Poster #120

Sex-biased genes –those that are sexually dimorphic in expression –tend to evolve rapidly in protein sequences, possibly due to the effects of positive selection. Sex-specific patterns of expression across the genome are prevalent in birds, insects, and worms and demonstrate the ubiquitousness of sexual dimorphism at the molecular level across an array of taxa. However, relatively little work has been done to examine sex-biased gene expression across multiple closely related primates. Here, we use transcriptome data from a number of different tissues to characterize sex-biased genes in both human and non-human primates. This analysis will provide insight into the dynamics of sex-biased gene expression evolution across primate lineages including humans.

Unsorted homology within locus and species trees

Diego Mallo, Leonardo de Oliveira Martins, David Posada

Sunday, June 22, 2014 -Poster #121

To properly understand genome evolution we need to rethink how sequence homology relationships articulate at the species, locus and gene tree levels. At the molecular level, the concepts of orthology, paralogy and xenology are fundamental to understand the evolution of gene families and whole genomes, and as such they have remained invariable for decades. However, we are witnessing a conceptual and methodological shift in phylogenetics prompted by the availability of genome-wide data sets collected from multiple individuals. This transformation entails the explicit consideration of different phylogenetic layers involving species, loci and gene copies, within and between species. In particular, we will show how incomplete lineage sorting can create a set of homology scenarios that, as far as we know, have not been explicitly discussed before. We also demonstrate how these situations can easily mislead commonly used parsimony reconciliation approaches, pointing out the need of quickly adopting the newest methodologies. All in all, we propose a reexamination of sequence homology at the boundary between population genetics and phylogenetics.

Network Structure of Gene Expression Anticorrelation in Saccharomyces cerevisiae

Christopher Morales, Joshua Rest

Sunday, June 22, 2014 -Poster #122

The expression level of any gene, measured across a set of environments, forms an expression profile that may be shaped by both the gene’s function and by specific or non-specific interactions with other cellular proteins. Genes that perform similar functions belong to modules of correlated expression profiles. Genes involved in opposing biological processes typically have anti-correlated profiles, and genes that do not interact have, on average, noncorrelated profiles. Here, we investigate whether anti-correlated gene expression patterns can be explained by these functional considerations, or whether other mechanisms must be invoked. We hypothesized that proteins that would physically interfere with one another through off-target interactions may also be strongly anti-correlated. We predict that these represent a set of strong anti-correlations that can't be described by functional patterns. In order to test this hypothesis, we used publically available gene expression data for Saccharomyces cerevisiae across hundreds of environments to determine the global distribution of expression correlations. We find as many pairs of genes with negatively correlated expression profiles as with positively correlated expression profiles. We show that these anticorrelated expression profiles are not simply a byproduct of the existence of positively correlated expression profiles, but that they are likely driven by multiple selective and neutral forces.

Witnessing Adaption in Action via Synthetic Phage Genomics

Alex Kula, Catherine Putonti, Katherine Bruder

Sunday, June 22, 2014 -Poster #123

Viral pathogens often require their host's biosynthesis machinery in order to optimize the viral pathogen's translational efficiency. The interaction between a virus and host relies heavily upon the virus' ability to adapt to the host's genetic preferences. One of the ways to examine this viral-host genetic compatibility is to examine the use of certain codons found in a bacterial host. Extensive computational analysis has demonstrated that viral genomes frequently reflect these host-preferred codon biases. In order to explore how this correspondence arose, we examined the viral-host interaction between the bacteriophage ΦX174 and Escherichia coli. More specifically, we have engineered a synthetic H gene within ΦX174, which substitutes host-preferred codons for codons that are less preferred by the host. We hypothesize that once the synthetic phage genome has a reduced fitness which will subsequently be under selection for genomic composition reflective of the E. coli preferred codons. Thus, we can observe the evolution of virus-host codon correspondence.

Community detection on networks of topologies and bipartitions identifies conflicting phylogenetic signal

Jeremy Ash, Guifang Zhou, Wen Huang, Melissa Marchand, Kyle Gallivan, James Wilgenbusch

Sunday, June 22, 2014 -Poster #124

In the phylogenomic era, there exists an ever greater need to fully characterize the phylogenetic information contained in sets of phylogenies. One potentially rich and unexploited avenue for accomplishing this goal is to characterize this information as networks, either of phylogenies themselves or their component bipartitions. Once formed, community detection methods allow researchers to explore relationships between competing phylogenetic signals in these networks. We have implemented tools for network construction and community detection in the software TreeScaper. Here, we perform an initial simulation-based benchmarking of these community detection approaches. Specifically, we focus on the detection of strongly conflicting signals in a single set of trees caused by the movement of a small number of taxa – the so-called 'rogue taxon problem'. Multiple sequence alignments (MSAs) were simulated such that bootstrap and/or Bayesian analyses of these data produced tree sets with support divided across multiple topologies. These tree sets were then analyzed in TreeScaper using both networks of topologies and bipartitions to test if the known conflict could be detected. Across a broad range of simulation scenarios, we find that when there is little phylogenetic signal in the MSA, TreeScaper recovers little evidence for conflicting signal. However, when the MSA contains strong support for a few distinct phylogenies, TreeScaper recovers clear evidence for conflicting signal. Since conflicting signal was caused by differences between the models used for simulation and analysis, we performed parametric bootstrapping and posterior prediction to see if network structure could be used to detect model violations. Finally, we analyzed some of the simulated data with alternative rogue taxon identification approaches and compared their performance to our network-based approach. Network-based approaches provide a new, quantitative approach for exploring conflicting phylogenetic signal in sets of trees.

Identification of downstream targets of the Pax gene in the sponge Ephydatia muelleri

Ajna Rivera, Nathan Haberkern, Arvind Arul Nambi Rajan, Dora Posfai, April Hill

Sunday, June 22, 2014 -Poster #125

Previous investigations have implicated Pax genes in eye/neural development in phylogenetically diverse organisms as part of the Pax/Six/Eya/Dac network (Kozmik, 2005). To understand the evolutionary origins of this conserved network, we are investigating the downstream effects of Pax in sponges, the most basally branching group to express Pax as part of a simple PSED network (consisting of Pax/Six only) (Rivera et al, 2013) We employed the use of bioinformatic analysis to identify likely sponge cis-regulatory elements upon which the paired domain of Ephydatia muelleri Pax (Em-Pax) might act. We then evaluated the proposed downstream cis-regulatory sites through a dual-reporter assay to confirm that the proposed cis-regulatory elements were actual downstream targets of Em-Pax. The Pax gene family is known to control the development of sensory organs, such as eyes, in many species. A recent study (Ludeman et.al, 2014) suggests the cilia found in sponge oscula are sensory, and communicate in a manner, such that the osculum may be considered a sensory organ. We plan to conduct RNAi gene knockdown of Em-Pax and its downstream target genes to evaluate potential behavioral changes in sponge oscula. This will allow us to elucidate the potential control Em-Pax exerts on sensory organs in the sponge E. muelleri.

Variability of rRNA operon number and its effect in the growth parameters of Bacillus isolates from an oligotrophic ecosystem

Pedro Márquez-Zacarías, Jorge Valdivia-Anistro, Gabriela Delgado-Sapien, Luis Eguiarte, Valeria Souza

Sunday, June 22, 2014 -Poster #126

Cell growth is determined by diverse factors, as the nutrient availability and the rate in which biomolecules and subcellular components are synthetized. In bacteria, has been suggested that the number of rRNA operons (rRNAop) is an important factor influencing directly the growth parameters. Previous works have focused on deletions in the rRNAop at the same strain to see the effects on growth and other parameters. However, it is not known how variable is the rRNAop number and what is the effect in cell growth of this factor in strains from natural communities.

With the objective of understand how variable is the rRNAop number, and how this affects the growth parameters in natural communities of bacteria, we isolate strains of Bacillus from the Cuatro Ciénegas Basin, an aquatic oligotrophic ecosystem, and we determine the rRNAop number and the growth parameters.

71 strains were isolated, and from the analysis of the hipervariable region in the 5' of the 16S ribosomal gene, 19 phylogenetic groups were identified. The quantification of the rRNAop number was made by pulsed field gel electrophoresis, and confirmed by Southern hibridation.

We found that bacilli in Cuatro Ciénegas have between 6 and 14 copies rRNAop copies. Compared to the bacteria or the bacilli in the rrNDB (a global database of rRNAop numbers in eubacteria and archaea) our dataset has a different distribution of the frequencies of rRNAop numbers, showing a gaussian distribution of the frequencies in contrast with the exponencial distribution of the mentioned datasets. We did not found any relation between rRNAop number and the distribution of the phylogenetic groups.

15 strains with different rRNAop number were selected to make Colony Forming Units (CFU) assays to determine: maximum growth rate, lag-phase duration, and maximum population density. Results from the CFU assays were adjusted to a logistic curve to obtain the parameters. We did not found any statistically significant linear relation between this three parameters and the rRNAop number.

We conclude that the rRNAop number do not explain the growth dynamics of bacilli in Cuatro Ciénegas. Other important factors could be involved in the regulation of cell growth of bacteria in natural environments, as interspecific interactions and nutrient availability. Research on this factors could give us better understanding of the ecological and adaptive significance of the rRNA operon in natural communities.

Testing host-defense functions of the giant panda RNase A genes

Sara Budney

Sunday, June 22, 2014 -Poster #127

The ribonuclease (RNase) A superfamily is a vertebrate-specific gene family which has been known to have functions in digestion, male reproduction, and host defense. It is believed that host defense is the reason for the diversification of the RNase superfamily. There are two lineages of host defense which are characterized by the function of the RNases in them. The first relates to antiviral activity and the second relates to antibacterial activity. Typically, only one copy of RNase 6 is present in a given species; however, the Giant Panda has seven known copies of RNase 6. Furthermore, sequence analysis indicates that positive, Darwinian selection is operating on these panda RNase 6 genes, suggesting their adaptive roles during the giant panda evolution. In this study, we investigate the function of each of the new copies in the context of host defense by cloning and expressing the RNase 6 genes in yeast and bacterial host. Purified proteins are tested for their ability to kill bacterial cells and to degrade RNA substrates.

Macroevolutionary Patterns of Plant Phenolic Metabolites in the Onagraceae

Jeffrey Ahern, Daniel Anstett, Marc Johnson, Juha-Pekka Salminen

Sunday, June 22, 2014 -Poster #128

Plant species vary greatly in their allocation to different plant defenses, but existing theory has struggled to explain this variation. To examine the macroevolution of plant defenses, we have employed comparative analyses of the phenolic chemistry of different species in the evening primrose family (Onagraceae). Using 26 Oenothera (Onagraceae) species, we have found evidence that secondary chemistry has evolved rapidly during the diversification of Oenothera. This evolution has been marked by allocation tradeoffs between traits, some of which are related to herbivore performance. Finally, the repeated loss of sex via permanent translocation heterozygosity (PTH) appears also to have constrained the evolution of plant secondary chemistry, which may help to explain variation in defense among plants. Ongoing work has expanded sampling to over 80 species in the Onagraceae; examining multiple tissue types, their phenolic chemical profiles, and functional assays of phenolic bioactivity.

The role of the environment in specialized plant-insect interactions

Anahi Espindola, Scott Nuismer

Sunday, June 22, 2014 -Poster #129

The role that the environment plays in plant-pollinator trait matching and mismatching at spatial scales is poorly understood. To investigate this, we use a set of specialized oil-rewarding Calceolaria plants and their interacting oil-collecting bees as study-systems. Our dataset consists of plant and insect traits measured on specimens collected across the species ranges, as well as ecological data associated to each sampled location. Using this, we first identify plant traits under selection and then quantify their local and spatial correlation with insect traits. Finally, we combine these results with ecological data and explicitly evaluate the explanatory value of environmental variables in the observed patterns of plant and insect trait correlation.

The microscopic battle of David and Goliath: competing large and small viruses

Alexandria Cooper, Catherine Putonti, Monica Janeczek

Sunday, June 22, 2014 -Poster #130

While many of the viral species causing disease in humans have compact, small genomes just a few thousand nucleotides long, larger viruses – including the giant viruses recently discovered -- appear to be ubiquitous. These larger genomes, which can range from hundreds of thousands of nucleotides to millions, often correspond to generation times on the order of hours, relative to minutes. How these larger viruses persist and proliferate amidst more expedient, adaptable competitors is unknown. The bacteriophages PhiKZ and PP7 both infect the same host, Pseudomonas aeruginosa, providing the unique opportunity to compete the large (280Kbp) dsDNA PhikZ against the smaller (3.5Kbp) ssRNA PP7. PP7 has a generation time of about 12 minutes contrary to PhiKZ's 2.5 hours. We infected P. aeruginosa with PP7 and PhiKZ simultaneously and observed their population changes over time. We focused on two separate time frames, recording observations throughout each. For the short term competition we examined growth between inoculation and 24 hours. The long term competition spanned a twelve day time frame. Intermittently, samples were taken in order to to test the bacteria for bacterial resistance as well as characterizing the phage species' prevalence in the population. Due to a smaller physical size, rapid life cycles, and the increased likelihood of mutation and adaptation of RNA, we initially hypothesized that PP7 would be more successful than PhiKZ. Our data thus far, suggests a cyclical pattern of PhiKZ out competing PP7. Through direct competition of these two very different viruses, we can watch the evolutionary arms race in action. Furthermore, we can begin to unravel the fitness advantages which have arisen as a consequence of different lifestyles, size, chemical composition and structure of the genome.

Sources, sinks, SNPs, and snappers: population structure of deepwater snappers in protected and non-protected areas of Puerto Rico

Stuart Willis

Sunday, June 22, 2014 -Poster #131

Snapper Unit 1, comprised of deepwater snappers, represents the majority of the landings off the west coast of Puerto Rico. However, catches have declined in recent years, presumably from overfishing. We evaluated levels of genetic variability, genetic relatedness, and population structure among three species of deep-water snappers (silk snapper, Lutjanus vivanus; blackfin snapper, Lutjanus buccanella; and vermilion snapper, Rhomboplites aurorubens) from four marine protected areas (MPAs) and six non-protected sites in the region. The objective was to test the hypothesis that source-sink meta-population dynamics prevailed among these sites. Our dataset consisted of several thousand single nucleotide polymorphisms (SNPs) developed from double-digest, restriction site-associated DNA sequences (RADseq). Genetic divergence among sites, based on allele frequencies, was small (FST

The orchid thief and friends: A look into the evolution of the loss of photosynthesis in plants

Kathryn Massana

Sunday, June 22, 2014 -Poster #132

Photosynthesis is perhaps one of the most important chemical processes on which life depends. Photosynthetic plants arguably have an advantage over non-photosynthetic plants because they do not rely on a host for energy. Therefore, it is interesting that photosynthesis has been lost multiple times in plant evolutionary history. Does losing the ability to phosynthesize increase their diversification? Using a large phylogeny and discrete character data, we use a multiple state speciation and extinction model to assess diversification. Results support decreased diversification in plants that are completely parasitic, and generally a similar diversification rate in semi-parasitic and non-parasitic plants.

Annual Arabidopsis thaliana has faster substitution rates than perennial A. lyrata at numerous loci consistent with plant generation time hypothesis

John Braverman, Matthew Hamilton, Brent Johnson

Sunday, June 22, 2014 -Poster #133

The generation time hypothesis, which states that species with shorter generation time accumulate substitutions at the DNA sequence level faster than species with longer generation times, has been well-studied and supported in animal systems. Only a few studies have addressed this explanation for rate heterogeneity in plants (e.g., Soria-Hernanz et al. 2008). In part, the challenge has been to find the appropriate plant species with the relevant life history strategies corresponding to longer and shorter generation times. The present research project aims to test this hypothesis using the extensive genomic data available. The first species tested, A. thaliana is an annual plant, normally reproducing every year, should incurr larger mutational input and thus substitutions than its perennial relative, A. lyrata. As tests for heterogeneity in substitution rate also require an outgroup, this study relied on a prior study to provide two appropriate outgroups and public genomic sequencing data to provide a third (B. rapa). The main result is that more comparisons (annual vs. perennial) show that the annual more often exhibit faster evolution than the perennial, according to a sign test (n=256; e.g., p=3.4E-05). A number of particular tests were applied, including Tajima's 1D and 2D (Tajima 1993). The results are discussed in light of the life history characteristics and the analysis of large data sets with multiple comparisons. In conclusion, the generation time hypothesis is supported in plants.

Darwin's peaches: grape-phylloxera galls interrogated by RNA-Seq

Wade Dismukes, J. Chris Pires

Sunday, June 22, 2014 -Poster #134

Insect galls are plant structures whose development is controlled by an insect, which Charles Darwin thought resembled peaches. Our current hypothesis is that galling insects have coopted the reproductive development genes of the plant in forming galls (a feeding structure for developing insects). This study compared the differences between grape leaves that were under attack by an insect, known as phylloxera, creating galls, and grape leaves that had no galls on them. To do this, the transcriptomes of galled leaves and leaves were compared. We found differences in 18 floral whorl development genes in galled leaves as compared to ungalled leaves. This suggests that the insect is inducing the expression of floral development genes within the leaf to develop galls.

A Monogamous Mind: Modeling the Co-evolution of Intelligence and Monogamy in Early Humans

Kelly Rooker, Aaron Mishtal, Sergey Gavrilets

Sunday, June 22, 2014 -Poster #135

Two key attributes making humans a uniquely unique species are their incredible capacity for intelligence and their social structure of being a monogamous group-living species. This first quality clearly sets humans apart from all other life on Earth, while the second, although more subtle, similarly places humans in a unique position within the animal kingdom. We posit that human mating strategies are a balancing result of the competing interests of group selection (faithful monogamy) and individual fitness (promiscuity). To this end, we have developed an evolving artificial neural network model in order to investigate the possible co-evolution of these two factors: intelligence and monogamy. In particular, we use the N-person stag hunt game from game theory with our evolving neural networks. In these games, individual cooperation is viewed as remaining faithful to one's pair-bond while defection is the more promiscuous mating strategy (i.e. mating with one or more others in the group outside the pair-bond). We expect that as intelligence increases, monogamy will become the primary mating strategy within groups, although never fully taking over as the exclusive mating strategy.

Modeling all or nothing behavior in social animals

Masoud Mirmomeni, Arend Hintze, Eli Strauss, Christoph Adami

Sunday, June 22, 2014 -Poster #136

The evolution of cooperation has been a conundrum in evolutionary biology because cooperation is vulnerable to selfish cheaters. One example of this dilemma is the “tragedy of the commons”, where individuals can either contribute to a public good or abstain. Since the public good is distributed to everyone regardless of an investment or not, those individuals who abstain will always fare better, unless the public goods multiplier (the synergy) is unrealistically high. While it is possible in principle to enforce cooperation via costly punishment, we found that even though punishment shifts the cooperation regime to emerge at lower synergy thresholds, individuals evolve to become pure cooperators who do not need to punish. This means that the threat of punishment alone is sufficient to drive cooperation, while actual punishment is rare. On the contrary, in natural systems we often observe vigorous punishment. Another difference between the public goods game and (some) natural systems and is that in the public goods game the payoff is a linear function of the amount paid in, while in natural systems often a threshold determines how much individuals need to contribute in order to obtain a fixed payoff that does not depend on the number of contributors who ultimately trigger it (more wolves hunting in a pack does not increase the size of the moose: you either get the moose or you don’t).

To remedy these discrepancies between the public goods game and the game-theoretic dilemma observed for example in collective hunting strategies, we introduce the “public thresh- old game” as an extension to public good game where a fixed payoff is distributed equally once enough individuals cooperate (number of contributors ≥ threshold). This alteration changes the game dramatically. Here, if the investment in the public good exceeds a given threshold, everyone (contributors as well as cheaters) receives an equal share (R/n), where R and n is the fixed payoff and the number players in the game respectively, while if the investment does not reach the threshold, the investment is lost. We find that effective punishment emerges as a stable strategy in this game, which in return facilitates cooperation. This suggests that the “public threshold game” is a better model for natural gambles that are “all-or-nothing”, and in which the triggered payoff does not depend in a linear fashion on the number of investors.

Inter- or Intra-genomic gene conversions between peptide-chain release factor paralogs in Bacteroidetes

Sota Ishikawa, Ryoma Kamikawa, Yuji Inagaki

Sunday, June 22, 2014 -Poster #137

Peptide-chain release factor paralogs in bacteria, RF1 and RF2, recognize stop codons, and promote the release of nascent polypeptides from the ribosome. RF1 and RF2, which are slightly different from each other in codon specificity, share apparent sequence similarity, suggesting that they were separated from each other through a single gene-duplication event. The duplication of RF genes likely occurred in the ancestral bacterial genome, as all bacteria primarily possess the two RFs. Therefore, the two RF families are generally expected to take independent evolutionary paths after the ancestral gene duplication. However, in the present study, our tests based on the phylogenetic and the statistical frameworks revealed inter- or intra-genomic conversions of the 71-aa gene fragment between RF1 and RF2 in 58 species of the phylum Bacteroidetes. Intriguingly, The putative region for gene conversions appears to cover the almost entire portion of “domain 3” in RF1 and RF2, which plays important role in the interaction with the peptydyl-transferase center in 50S subunit of the ribosome, followed by the catalysis of peptidyl-tRNA ester-bond hydrolysis and the release of polypeptides from the ribosome. Most significantly, function and structure of the domain 3 were highly conserved among RF paralogs, that implies that the inter- and intra-genomic gene conversions of between these informational genes can be “acceptable”. On the other hand, we also identified the acquisition and the loss of characteristic 12-aa motif between the domains 3 of two RF families through gene conversions. From these results, in this presentation, we discuss about the driving force behind the conversions of genetic materials between RF1 and RF2, which would help in depth understanding the complicated evolution of paptide-chain release factors in Bacteroidetes.

Synthesizing range biology and the eco-evolutionary dynamics of dispersal

Alexander Kubisch, Robert D. Holt, Hans Joachim Poethke, Emanuel Fronhofer

Sunday, June 22, 2014 -Poster #138

The distribution of species in space and time is one of the oldest puzzles in ecology. Already Charles Darwin pointed this out over 150 years ago, when he asked: “Who can explain why one species ranges widely and is very numerous, and why another allied species has a narrow range and is rare?” (Darwin 1859). And still, although much research has been invested into that topic since the times of Darwin, we still do not comprehensively understand the formation of any given species' range.

We provide an overview of the manifold eco-evolutionary forces, which - in a metapopulation context - determine the formation of species' ranges. Based on the idea that colonizations and local extinctions are the crucial determinants of an emerging range limit, we highlight the importance of dispersal evolution in this context. It is well known that dispersal of species is highly plastic and subject to strong evolutionary changes. However, this fact is still often ignored when distributions of species are investigated. To clarify the influences of dispersal on range formation, we organize relevant forces acting on all hierarchical levels, ranging from the landscape via genes, individuals and populations to communities, in a framework. In combination with novel simulation results this synthesis brings together the multiple interactions between these factors and forces, which may lead to high levels of complexity and non-linearity. Synthesizing the factors and forces affecting range formation and highlighting the importance of dispersal evolution will surely prove to be helpful in advancing our knowledge and mechanistic understanding of species' geographic ranges.

Quorum sensing inhibits the breakdown of cooperative behavior by social cheaters in Vibrio bacteria

Eric Bruger, Christopher Waters

Sunday, June 22, 2014 -Poster #139

Quorum Sensing (QS) is a widespread form of chemical communication used by bacteria that affects

gene regulation in a density-dependent manner. Large suites of genes are regulated by QS, and many

of the positively regulated genes are linked to the production of exo-products, which are subject to the

evolutionary problem of exploitation by cheaters common to public goods. For instance, QS regulation at high density induces production of extracellular proteases in the marine bacterium Vibrio campbellii. In a minimal media environment that contains casein as the sole carbon and energy source, mutant strains that lack the master regulator (LuxR) needed to activate the QS regulon (QS defectors) are growth deficient in monoculture. The growth defect is compensated by supplementing casamino acids, the breakdown products of casein or by supplementing proteases produced by strains that still produce LuxR, which removes the need for protease production. Alternatively, QS prototrophs ("CQS") and locked high-cell density mutants (i.e. Unconditional cooperators - “CU”) grow robustly in casein media. QS defectors (D) invade and ultimately dominate CU strains during competition experiments, exhibiting social cheating. Overexploitation of the protease public good by the QS defector strain ultimately results in a tragedy of the commons, causing a drop in population density. However, regulation of public goods production by a functional QS system allows cooperation to persist in the presence of these defectors at all starting defector frequencies we examined. Additionally, CQS is also competitively superior against CU and is able to invade when rare, despite comparable growth by CU in monoculture. A similar pattern emerges in experimentally evolved populations, wherein CQS persists and resists being swept by de novo defectors, while populations founded from the CU strain rapidly succumb to these defectors. Together, these results suggest that communication via QS can serve as a stabilizing mechanism for protease production in and other cooperative behaviors by enabling resistance to cheating.

Spatially correlated extinctions select for less emigration but larger dispersal distances in the spider mite Tetranychus urticae

Emanuel Fronhofer, Jonas Stelz, Eva Lutz, Hans Joachim Poethke, Dries Bonte

Sunday, June 22, 2014 -Poster #140

Dispersal is a central process to almost all species on earth, as it connects spatially structured populations and thereby increases population persistence. Dispersal is subject to (rapid) evolution and local patch extinctions are an important selective force in this context. In contrast to the randomly distributed local extinctions considered in most theoretical studies, habitat fragmentation or other anthropogenic interventions will lead to spatially correlated extinction patterns. Under such conditions natural selection is thought to lead to more long-distance dispersal, but this theoretical prediction has not yet been verified empirically. We test this hypothesis in experimental spatially structured populations of the spider mite Tetranychus urticae and supplement these empirical results with insights from an individual-based evolutionary model. We demonstrate that the spatial correlation of local extinctions changes the entire distribution of dispersal distances (dispersal kernel) and selects for overall less emigration but more long-distance dispersal.

Genetic and environmental drivers of geographic variation in dispersal traits in Cakile edentula: implications for the evolution of species' ranges

Elizabeth LaRue, *Nancy Emery*

Sunday, June 22, 2014 -Poster #141

Dispersal is key to long-term species persistence and a driver of the extent of species' ranges. Theory predicts that geographic variation in habitat quality, quantity, and stability across species' ranges will lead to differentiation in dispersal traits among populations. However, few studies have explored range-wide variation in dispersal ability and the underlying genetic and environmental mechanisms. Here, we tested for differences in dispersal ability among 30 populations of Cakile edentula var. lacustris (American searocket, Brassicaceae), a wind- and water-dispersed annual plant native to coastal beaches of the Great Lakes, and environmental correlates with variation in dispersal traits. We found that aspects of maternal plant architecture that increase seed dispersal potential are enhanced at the northern and southern range edges compared to the rest of the geographic range. Additionally seed wing-loading, a morphological trait that facilitates wind dispersal, increased linearly with latitude. In ongoing work, we are measuring seed traits that influence water dispersal ability. We are currently testing for correlations between dispersal traits and population density, climatic variables, habitat quantity, and other site characteristics to test the hypothesis that range-wide environmental variation has generated differences in dispersal ability among populations that occupy different positions within the species' geographic range. Variation in dispersal across a species' range is likely to impact the speed of range shifts, total range size, and the propensity for populations to be locally adapted to fine-scale climatic variation. Thus, understanding geographic variation in dispersal propensity will enhance our ability to predict species' responses to climate change, habitat loss and land use change.

Phylogenomic evaluation of parasitic wasps in the genus Aphelinus
(Hymenoptera, Chalcidoidea)

Kristen Kuhn, *Keith Hopper*

Sunday, June 22, 2014 -Poster #142

Aphelinus wasp species are natural enemies of aphids, and they have a long history of use in the biological control of these important agricultural pests. The genus Aphelinus contains 87 species currently treated as valid, but many new species are being discovered, including both cryptic species and morphologically different species. In fact, one impediment to taxonomic progress in this genus has been the prevalence of cryptic species. These species differ slightly in morphological characters, but are phylogenetically distinct lineages that differ in their biology and are reproductively isolated from one another. Next-generation sequencing provides far more data than standard Sanger sequencing, and we have discovered and genotype large numbers of single nucleotide polymorphisms (SNPs) distributed across parasitoid genomes. To get sequence data for the de novo assembly of reference genomes, we are using a combination of both Illumina whole genome paired-end libraries reduced representation libraries. We are mapping the sequences from reduced representation libraries (RRLs) to the appropriate reference genomes to determine identity and homology of SNPs. We have made and sequenced RRLs for 10 species of Aphelinus, with each library generating 1-16 million reads (100-1600 Mb). These reads were then mapped on the A. atriplicis reference genome assembly, giving consensus lengths of 2-9 Mb or 1-2 % of the reference genome with 10-65x average coverage. Using these mappings, we have detected 287k SNPs (with a minimum of 20x coverage) that differ among these species and populations, 55k of which were phylogenetically informative. For comparison, in previous research using Sanger sequencing of known genes, we detected 303 phylogenetically informative SNPs in 2868 bp of sequence from 6 genes among 12 species and populations from these same complexes. Thus, Illumina sequencing of RRLs provided over 180x more phylogenetically informative SNPs than we found using Sanger sequencing of known genes.

Genome Evolution in Orchids and Fungi

Sarah Unruh, *Michael McKain, Patrick Edger, Larry Zettler, J. Chris Pires*

Sunday, June 22, 2014 -Poster #143

Orchids are a unique and charismatic family of flowering plants that contain an estimated 25,000 species. They are characterized by many novel traits, their species richness and their reliance on fungi for germination. I am using next generation sequencing techniques to study the genome evolution of orchids and their mycorrhizal fungi.

To investigate evolutionary phenomena, it is necessary to produce a robust phylogenetic tree. The majority of orchid phylogenetic publications rely on plastid genes to infer evolutionary relationships, but preliminary data from nuclear genes show conflicting topologies with those inferred from organellar sequences. I will build the first multi-locus nuclear gene phylogeny across the orchid family to better determine evolutionary relationships. I will use the sequences generated from this project to investigate incidences of whole genome duplication (WGD), which we have preliminary evidence for a shared event across the family. I will also use these phylogenomic techniques to investigate the functional and evolutionary relationships between orchids and their mycorrhizal fungi.

This work will provide a robust phylogenetic tree across the orchid family that will serve as a foundation for future evolutionary studies. Investigating the fungal relationships will provide new genomic resources as well as new insight into how the genomes have evolved in both groups of organisms.

Refining phylogenetic hypotheses: increasing the resolution of cryptic nodes in the genus Lasthenia

Joseph Walker, Alan Clinton, Michael Zanis, Nancy Emery

Sunday, June 22, 2014 -Poster #144

Highly resolved phylogenies provide critical tools for examining the ecological and genetic drivers of speciation and adaptive diversification in a comparative context. The rise of next-generation sequencing technologies has substantially accelerated the rate at which novel phylogenies can be constructed and existing phylogenies can be refined. Here, we used NGS technology to develop new markers to resolve ambiguous nodes in the phylogeny of Lasthenia (Madieae, Asteraceae), a genus of predominantly annual plant species that are largely endemic to the California Floristic Province of western North America. Previous work had used two nuclear markers (ITS and ETS) and one chloroplast marker (matK) that are nearly universal markers in the Asteraceae to construct a phylogenetic hypothesis for the clade, but several nodes remained unresolved, purportedly because of a burst of rapid diversification deep within the genus. We obtained new sequence data for two of the most distantly related Lasthenia species, L. platycarpha and L. fremontii, by sequencing genomic DNA using the HiSeq Illumina platform. After these sequences were aligned, we designed primers for one nuclear and two chloroplast sequences that exhibited particularly high levels of variation between the two species. Next, we sequenced 24 individuals from 14 species that were subtended by relatively unresolved nodes. Finally, we generated a Lasthenia phylogenetic tree with RAxML that used the ITS, ETS and MatK sequence data for all species and the new sequence data from the 14 targeted taxa. This approach improved the phylogenetic resolution of the deeper nodes in the Lasthenia clade, increasing bootstrap values by as much as 40% (70). This highly-resolved phylogeny will dramatically enhance our ability to efficiently evaluate patterns of ecological and morphological diversification in Lasthenia.

Genetic and morphometric comparison between two lineages of Peromyscus leucopus in northern Michigan

Joseph Baumgartner, Susan Hoffman

Sunday, June 22, 2014 -Poster #145

Populations of the white-footed mouse (Peromyscus leucopus) have been established in northern Michigan since the region became habitable after the last glacial maximum. As these populations were founded, the white-footed mouse separated into geographically defined mitochondrial lineages—one exclusive to the Lower Peninsula (LP) and one exclusive to the southern tip of the Upper Peninsula and Wisconsin (UP). Today these two lineages are responding differently to the climatic changes in Michigan's environment that have taken place over the past forty years. The LP lineage mice increased in abundance while the UP lineage expanded its range across the entire peninsula. It is expected that this difference in history affect the structure and phenotypes of populations today. In the current study, the genetic diversity and phenotypic variation of skull shape are compared between the two lineages of P. leucopus. Two populations, matched for ecological factors, are used in this comparison: Cheboygan (LP) and Menominee (UP). Mice were collected from each population and alleles determined across eight microsatellite loci. The structure of the skull was analyzed for three different datasets (dorsal, ventral and lateral) using Procrustes ANOVA, Principal Component Analysis (PCA), and a discriminate function. The comparison of these two populations will allow further studies of regional responses of a small mammal to climate change.

Identifying hyper-variable regions within the chloroplast genome of Anthurium (Araceae)

Monica Carlsen

Sunday, June 22, 2014 -Poster #146

Anthurium is an extremely diverse and strictly neotropical genus of Araceae that includes ca. 1,000 species. The most recent molecular phylogeny of the genus included 102 Anthurium species and eight outgroups, and was able to distinguished 18 highly supported clades within the genus. However, that dataset also revealed a molecular signature of very low DNA sequence differentiation among Anthurium species. Not surprisingly, relationships among the major clades were not supported, and the backbone of the phylogeny was still unresolved, therefore precluding further assessments of character evolution within the genus. In this study, Next Generation sequencing was used to generate nearly complete chloroplast genomes for 18 Anthurium species representing most major clades in the previous phylogeny of the genus, in order to characterize areas of high variability within the plastome that could be targeted for future phylogenetic studies, as well as to investigate the amount of data necessary to improve the phylogenetic resolution within the genus. Total genomic DNA was used to prepare libraries that were sequenced in an Illumina HiSeq2000 platform with single-end reads. Sequences were assembled to a reference using the software Yasra, and de novo assemblies were performed using Velvet and Spades. As expected, some areas of the chloroplast genome were identified as providing a higher number of variable and informative characters (i.e. "hotspots"). These regions are largely comparable to those previously postulated highly variable regions recommended for phylogenetic analyses in plants. Generally, the most variable regions in the genome were associated with the "trn-" family of genes, and with regions flanking large sections of mono- or di-nucleotide repeats. Overall, the use of full chloroplast genome alignments greatly increased the number of informative sites and phylogenetic support in deeper nodes of the phylogeny.

Chloroplast genome sequence of Amphilophium aschersonii, a liana from Western Amazon

Verônica Thode, Alison G. Nazareno, Monica Carlsen, Lucia Lohmann

Sunday, June 22, 2014 -Poster #147

Next-generation sequencing (NGS) technologies are revolutionizing evolutionary studies by enabling the rapid acquisition of whole chloroplast (cp) genomes in non-model organisms. Plastid genomes have been widely explored as sources of information to reconstruct phylogenetic relationships and as basis to population level studies in plants. Yet, few plastid genomes have been sequenced and assembled to date. In this study we present the cp genome sequence of Amphilophium aschersonii Ule (Bignoniaceae, Lamiales), a species that belongs to a diverse genus of Neotropical lianas. Total DNA was extracted from herbarium material and used as basis to construct a sequencing library using the NEBNext DNA Library Prep kit (Illumina), with an Illumina HiSeq2000 platform and paired-end reads. Sequences were assembled with reference to Olea europaea L. (Oleaceae, Lamiales) using the software Yasra, and a de novo assembly was performed using the software Velvet. Gene annotation was performed using BLAST, DOGMA, and Geneious, with a manual adjustment of start and stop codons and intron/exon boundaries based on comparisons to homologous genes in other cp genomes. Tandem repeats were identified through the Tandem Repeats Database, while Simple Sequence Repeats (SSR) were identified using Gramene and WebSat. Overall, the chloroplast organization and gene order of the A. askersonii cp genome exhibits the general structure of flowering plants. We assembled a partial genome (99%) that included 148,840 bp with a pair of inverted repeats (IR; 23,935 bp each), separated by a small single copy (SSC; 18,124 bp) and a large single copy region (LSC: 82,846 bp). The cp genome presented a 38% GC content and 114 genes of which 80 are protein-coding, 30 are transfer RNA, and four are ribosomal RNA. Those genes cover 72% of the cp genome, with 13% representing introns. The A. askersonii plastid genome presents a total of 36 tandem repeats and 86 SSRs, with mono- and dinucleotide repeats being the most common, while tri-, tetra-, and pentanucleotide repeats occur less frequently. Other Bignoniaceae genomes are currently being assembled and will, together with the plastid genome of A. askersonii, be used as basis to develop new markers for population genetics and phylogenetic studies.

Founder events and morph loss in populations of a tristylous species.

Christopher Balogh, Spencer Barrett

Sunday, June 22, 2014 -Poster #148

In tristylous plant populations, frequency-dependent selection should maintain equal style morph ratios unless there are fitness differences between the morphs. However, genetic drift and founder events may cause the stochastic loss of floral morphs from populations. During 2013 we conducted a large-scale survey of style morph frequencies in 114 populations of invasive Lythrum salicaria (Lythraceae) in Ontario, Canada to investigate the influence of finite population size on morph loss. An earlier survey in the same region by Eckert and Barrett (Evolution, 1992) reported that that 23% of populations (n=102) were missing style morphs with morph loss associated with small population size. One of the objectives of our study was to investigate the extent to which over the intervening 21 years the increased prevalence of L. salicaria in Ontario may be associated with higher levels of trimorphism as a result of increased gene flow among populations. The results of our survey provided no support for this hypothesis; there was no significant difference in the frequency of non-trimorphic populations between the two surveys (2013 survey: 25%;G=0.246, 1 d.f., P=0.62). In both surveys the short-styled morph (S-morph) was most commonly absent from populations. This pattern is predicted by stochastic processes operating in finite populations because the S-allele occurs at a lower frequency than the remaining three alleles at the two loci governing tristyly. However, this pattern may also occur through founder events involving pseudo self-compatible plants of the mid-styled morph (M-morph) of genotype ssMm because on selfing this genotype can only segregate offspring of the L and M-morph. Our survey also revealed 8 populations that were monomorphic for the L-morph. These populations seem likely to have arisen by a similar process, because self-pollination of the L-morph (ssmm) can only produce L-morph progeny owing to homozygosity at the two tristyly loci. Our results suggest that repeated founder events by individuals with weak self-incompatibility may be important in affecting population morph structure in invasive populations. Our current research is evaluating the extent to which pseudo self-compatibility increases colonizing ability by providing reproductive assurance to population founders.

A Directed Mutation-centric Network Model of Protein Adaptation

Violeta Beleva Guthrie, Melissa Standley, Manel Camps, Rachel Karchin

Sunday, June 22, 2014 -Poster #149

A central problem of evolutionary biology is the genetic basis of protein adaptation, i.e. the evolution of new functions. In a widely accepted paradigm, each protein mutation represents a discrete step sequence space along adaptive trajectories toward new functions. Predicting the functional effect of multiple mutations is, however, a very challenging problem, as most adaptive phenotypes of interest are caused by complex interactions between multiple mutations.

We designed a weighted directed mutation-centric network to model how the functional effects of individual mutations combine in adaptation. We used evolution of extended spectrum antibiotic resistance by the bacterial enzyme TEM β–lactamase as our model system. Advantages of this model system are: (1) there is direct correspondence between the enzyme's evolution of new activity, i.e. resistance to extended spectrum antibiotics, and bacterial survival in the presence of such antibiotics; (2) extended spectrum resistance can arise with as few as one or two point mutations.

Our network model is based on phylogenetic reconstruction of evolution of TEM β–lactamase sequences: Network nodes are mutated positions under positive selection for increased antibiotic resistance. Weighted directed links between a position pair i and j represent the frequency with which mutations in position i preceded mutations in position j in the phylogeny. This frequency is averaged over an ensemble of phylogenetic trees from Bayesian MCMC phylogeny runs, with ancestral sequence reconstruction on internal nodes. Links are benchmarked through published results from directed evolution experiments and through measuring relative antibiotic susceptibility of single and double mutants in the lab. The resulting directed mutation-centric network allows us to analyze higher-order evolutionary interactions. Specifically, successful adaptive mutational trajectories, ordered in time, can be predicted from central network paths. To test these adaptive path predictions experimentally, we will measure the extended-spectrum susceptibility of the resulting complex mutants.

Our sequence-based computational method allows us to analyze higher-order evolutionary interactions and can contribute to a better understanding of protein adaptation. It can be particularly relevant to the relationship of protein mutations and acquired drug resistance in pathogens and to optimization of library design for protein engineering experiments.

Combining NGS and Sanger sequencing data to obtain a robust phylogeny of Bignonia L. (Bignonieae, Bignoniaceae)

Alexandre Zuntini, Lucia Lohmann

Sunday, June 22, 2014 -Poster #150

The genus Bignonia (Bignonieae, Bignoniaceae) includes 28 species that are distributed from Southern USA and Mexico to Argentina. Species of Bignonia are lianas, characterized by simple tendrils, dorsally flattened corollas and opaque seed wings. In this study we combine data from Sanger and Next Generation Sequencing (NGS) to reconstruct a robust phylogeny for the genus. We then use this tree as basis to evaluate putative morphological synapomorphies for the genus and its clades. An initial matrix included sequences of two plastid genes, (ndhF and rpl32-trnL), and one nuclear marker (pepC) generated by Sanger sequencing for 79 individuals representing 11 outgroups (belonging to Amphiliphium, Anemopaegma, Mansoa and Pyrostegia) and multiple individuals for all 28 taxa of Bignonia, except from Bignonia neouliginosa, for which we were unable to obtain reliable sequences. This matrix included 3911 characters, 40% of which were variable, and was analyzed under parsimony and Bayesian criteria, using respectively Paup4.10b and MrBayes3.2.2. These analyses consistently recovered eight strongly supported clades that were highly resolved internally. Unfortunately, relationships among the eight clades remained unsolved. To reconstruct the backbone of the Bignonia tree, we sequenced one species per clade using an illumina HiSeq Platform. Pair-end reads were cleaned using SeqyClean and re-assembled “de-novo” in Velvet. The scaffolds produced in Velvet were then analyzed in Geneious 7.1 using the genome of Olea europaea L. as reference. Plastomes were partially assembled (90-99% completion) and annotated using DOGMA, while fragments were aligned using MAFFT and un-assembled regions excluded for all terminals. Overall, 100% of the inverted region and the Small Single-copy Region (SSR), and ~80% of Large Single-copy Region (LSR) were conserved, accounting for 120kb. This new matrix was used to reconstruct the backbone of the Bignonia phylogeny using Paup and MrBayes, leading to a highly supported tree. The initial matrix was then re-analyzed using this backbone as a topological constraint. Selected morphological characters were mapped over the final topology in Mesquite2.75, leading to the identification of key morphological synapomorphies for various clades such as: (1) Bignonia, simple tendrils and lepidote corolla; (2) “Cydista-clade,” flattened corolla, synchronous flowering and lack of nectariferous disk; and, (3) “Clytostoma-clade,” verrucose ovary and single-winged seed. The combined Sanger-NGS approach proposed here led to a strongly supported phylogeny of Bignonia, providing a solid framework for future evolutionary and biogeographical studies in this group. This approach should also be useful for phylogeny reconstruction in other clades of angiosperms.

Multilocus phylogeography of a widespread rodent reveals influence of Pleistocene geomorphology and climate change in the Zambezi Region of Africa

Molly McDonough, Radim Sumbera, Vladimir Mazoch, Caleb Phillips, Josef Bryja

Monday, June 23, 2014 -Poster #1

The role of Pleistocene climate oscillations in shaping mammalian diversity is well characterized for many northern hemisphere taxa. However, understanding of climate versus physiographic barriers in shaping patterns of biodiversity remains limited for many regions of the world. For mammals of continental Africa, a multitude of phylogeographic studies of West and East African lineages have illuminated the roles of both geographic barriers and climate oscillations in shaping small mammal diversity. In contrast, studies in southern Africa, often biased by limited geographic sampling, have revealed conflicting patterns of how mammalian lineages respond to both Pleistocene climate change and geologic events such as river formation. Using mitochondrial and nuclear datasets from 91 individuals from 31 localities across southern Africa, we examined phylogeographic patterns in a widespread savanna adapted African rodent, Gerbilliscus leucogaster, in order to compare signatures of climatic and vicariant biogeographic events across the region. Results indicate that the most recent common ancestor for all G. leucogaster lineages occurred during the Pleistocene and that origins for each of the mitochondrial clades occurred within the last 200,000 years. We documented six divergent mitochondrial lineages, each of which was geographically isolated during periods characterized by alterations to the course of the Zambezi River and its tributaries as well as regional ‘megadroughts’. Results include a widespread lineage exhibiting demographic expansion at a time that coincides with woodland savanna expansion across Southern Africa. Nuclear amplified fragment length polymorphism data revealed a similar pattern but also helped to identify regions of secondary contact. Our results indicate that both climatic fluctuations and physiographic vicariance helped shape the evolutionary history of small mammals in Southern Africa.

The Relationship Between Allometry and Integration: Combining Geometric and Traditional Approaches to Morphological Variarion

Guilherme Garcia, Gabriel Marroig

Monday, June 23, 2014 -Poster #2

A fundamental feature of morphological systems is their tendency to exhibit correlations due to commom developmental processes and functional interactions, a phenomenon called morphological integration. Integration is characterized both by magnitude of correlation between morphological traits and pattern described by inter-trait correlation structure. In mammal systems, traditional morphometrics analysis of integration emphasize the role of size variation in determining magnitude of integration and, through allometric relationships, size can also affect integration patterns. Here, we combine traditional and geometric morphometrics to investigate the relationship between allometry and integration in a broad phylogenetic context. Our sample comprises 5113 anthropoid primate skulls, representing 109 species distributed in 38 genera. We describe morphological integration as phenotypic covariance matrices among 38 euclidean distances for each species. We estimated magnitude of integration as the coefficient of variation of the eigenvalues of each matrix (ICV); pattern is estimated as modularity index for facial and neurocranial traits. Allometric relationships for each species were estimated as the correlation between log centroid size and shape variables; in this case, log-determinant of jacobians calculated over the TPS function for all specimens in reference to the mean shape of each species. We estimate average allometric correlation for facial and neurocranial shape variables; we also estimate the coefficient of variation for centroid size. We observe a strong correlation between centroid size variation and ICV (0.84); therefore, magnitude of integration is strongly affected by the variation in size. For facial traits, average allometric coefficients are positively associated with modularity index (0.64), indicating that allometry has a role in shaping correlation structure among facial traits. We also observe that, as size variation increases, the difference between allometric coefficients for facial and neurocranial shape variables also increases (with a correlation of 0.53), showing that size variation influences magnitude and pattern of morphological integration. Our results agree with the classical traditional distinction between early- and late-developmental factors shaping skull correlations in mammals, and the observation of strong facial correlation structure associated with post-natal growth. Geometric approaches to study morphological integration often eschew the role of size variation, focusing on shape alone, and conclusions regarding pattern and magnitude of integration considering shape alone usually disagree with traditional morphometric approaches. Our results demonstrate that, when size variation is incorporated, results from both approaches agree on the causes of morphological integration.

Evolution of Snout Shape in the Toothless Knifefishes (Teleostei, Gymnotiformes): Morphological Disparity and Habitat Transitions

Tiago Carvalho, James Albert

Monday, June 23, 2014 -Poster #3

To assess how habitat and morphological disparity are interrelated in the evolutionary radiation of the toothless knifefishes (Rhamphichthyoidea), we studied patterns of snout-shape diversification and habitat utilization in a historical context. A total of 37 rhamphichthyoid species was investigated using a geometric morphometric analysis of the oral jaws and lower-jaw suspensorium, time-calibrated phylogenies, and information on habitat occurrence. The results show a strongly disjunct occupancy of the morphospace early in the history of Rhamphichthyoidea, with rapid and phenotypically large shifts in snout shape along three branches at the base of tree, and relative phenotypic stasis in most other branches of the tree. The largest shift occurred in the ancestor of Rhamphichthyidae, with the origin of an elongate and slender snout and small oral jaws, accompanied by a habitat transition to inhabiting deep channels of large lowland rivers. A second large shift occurred in the ancestor of Steatogeninae with the origin of a short and deep snout, and this phenotypic change was not immediately associated with a habitat shift. At least two additional shifts to shorter snout occurred within Hypopomidae, with some Brachyhypopomus species overlapping Steatogeninae in the morphospace. In these Brachyhypopomus species, the presence of a derived short snout is associated with a transition to living on river floodplains. Quantitative analysis of morphological disparity in the snout shape of Rhamphichthyoidea provides a better fit to the Early Burst than to the Ornstein-Uhlenbeck or Brownian-Motion models of phenotypic evolution. However, the accumulation of lineages through time is relatively constant or linear, and no substantial changes in lineage diversification rates were observed, suggesting that the rates of phenotypic divergence and net diversification were decoupled. These findings add to the understanding of general patterns of diversification within the Neotropical ichthyofauna, in which historical bursts of morphological diversification occurred within different periods of the Cenozoic.

Genomic and Fossil Evidence for Lockstep Evolution of Tooth Loss and the Acquisition of a Horny Beak in the Common Ancestor of Modern Birds

Robert Meredith, Guojie Zhang, M Thomas P Gilbert, Erich Jarvis, Mark Springer

Monday, June 23, 2014 -Poster #4

Edentulism, or the absence of teeth, has evolved convergently among vertebrates including birds, turtles, and multiple lineages of mammals. Within Avialae, edentulism has evolved at least four times. Instead of teeth, modern birds (Neornithes) use a horny beak and a muscular gizzard to acquire and process food. The fossil record of early neornithines is fragmentary and it remains unclear if teeth were lost in the common ancestor of modern birds or independently among different members of this clade. In this study, comparative genomic analyses representing nearly all extant bird orders recovered inactivated remnants of enamel and dentin tooth-specific genes. All modern birds share some of the same inactivating mutations within the protein-coding exons of both enamel- and dentin-specific tooth genes. These shared mutations indicate that the common ancestor of modern birds lacked mineralized teeth. Estimates of gene inactivation based on frameshift mutation rates suggest the common ancestor of modern birds lost mineralized teeth, or as least the enamel caps that provide the outer layer of mineralized teeth, ~120 mya. Together, molecular and fossil evidence suggest a two-step evolutionary history for edentulism and the acquisition of a rhamphotheca on the stem neornithine branch. First, tooth loss occurred on the premaxilla and a partial rhamphotheca developed on the premaxilla and anterior mandible. Later, rostrocaudal progression of tooth loss and rhamphotheca development resulted in a complete rhamphotheca that effectively replaced the teeth. Subsequent to these changes, the rhamphotheca was modified in a myriad of ways in crown Neornithes to produce the diversity of beaks that are found in modern birds.

A molecular phylogeny provides new insight into the evolutionary history of African galagids (Primates: Galagidae)

Luca Pozzi

Monday, June 23, 2014 -Poster #5

Galagids are probably the least known of all primates and their systematics is one of the most long-standing problems in primatology. Species diversity has likely been underestimated due to the lack of morphological variation, and most species have been described using bioacoustic data, leading to a large, but quite controversial, increase in species number. Our knowledge of galagid evolutionary history has been limited by a lack of appropriate molecular data and a paucity of fossils. The fossil record suggests early origins for the divergence between galagids and lorisids. However, while the oldest occurrence of stem galagids date back to the Late Eocene, no crown members are known earlier than the Late Miocene/Early Pliocene.

In the present study, I revisit the contentious relationships within African Galagidae by integrating the largest molecular dataset for galagos to date with the known fossil record. Traditional phylogenetic methods (maximum likelihood and Bayesian inference) as well as a species-tree/gene-tree approach were used to analyze the dataset.

Based on the age estimates obtained in this study, Euoticus represents one of the oldest lineages within Primates and its divergence during the Early Oligocene appears to be independent of the radiation that gave rise to all the other main galagid lineages later in the Miocene. Galagoides is paraphyletic, suggesting the presence of two separate genera for the dwarf galagos: the Eastern forms (e.g., zanzibaricus complex) actually cluster closer to greater and lesser galagos than to the Western species (thomasi/demidoff). Morphological and ecological similarities within dwarf galagos are thus likely a consequence of either convergence or plesiomorphic retentions. Despite the amount of genetic data collected in this study, the monophyly of the family Lorisidae remained poorly supported, probably due to the short internode between the Lorisidae/Galagidae split and the origin of the African and Asian lorisid clades. The results of this study suggest an early origin for the crown Galagidae, soon after the Eocene-Oligocene boundary, and a possible biogeographic origin of the extant radiation in central-western Africa. This also implies that one – or possibly more – stem radiations diverged in the Late Eocene and persisted for several million years alongside members of the crown group.

Macroevolutionary trends in the gliriform dental pattern of extant and fossil mammals

Emily Woodruff, _Jonathan Bloch, Kathryn Broecker_

Monday, June 23, 2014 -Poster #6

Mammals exhibit high dental diversity that reflects adaptations to different diets and ecological niches. The number, arrangement, and shape of teeth in the dentition differ among mammal species. One dental pattern in particular has evolved independently in different clades throughout mammalian evolution, including the most species-rich order of extant mammals, the rodents. The gliriform, or “rodent-like”, dental pattern (GDP) is defined here to include three components: 1) high-crowned and ever-growing (hypselodont) incisors, 2) a diastema (a gap) between the anterior and posterior teeth, and 3) a reduced number of teeth. Characteristics of the GDP are not always present together however, and in this study we investigate the patterns of acquisition of these features throughout mammalian evolution. A phylogenetic supertree of fossil (N=255) and extant mammals (N=681) was created and used to analyze the distribution of these three traits individually and as a complex. Ancestral states were reconstructed for discrete and continuous morphological traits that characterize the GDP using maximum parsimony and maximum likelihood methods. Individually, the GDP traits arose multiple times throughout mammal evolution. The diastema has been acquired at least eight times (Glires, Primates, Chiroptera, Carnivora, Perissodactyla, Artiodactyla, Afrotheria, Diprotodontia) and hypselodont incisors have arisen at least three times (Glires, Primates, Diprotodontia). Tooth number has been reduced at least eight times within the same clades in which the diastema was acquired. Variation in the acquisition of the three individual components of this dental pattern across a large sample of mammals implies that these features may have different evolutionary histories and that they did not necessarily evolve together as a complex in all clades. All GDP traits are present, however, in distantly related extant mammals including the rodents and lagomorphs, the wombat, and one primate species, the Aye-aye. Furthermore, fossil rodents and primates from the late Paleocene (~58 Myr) are the earliest known Eutherian mammals that exhibit this dental pattern. Overall, these patterns suggest that the traits that comprise the GDP were acquired early in mammalian evolutionary history and that once acquired, this dental pattern persisted in multiple lineages into the present day.

Endemism and morphological diversification on California's Channel Islands: A study of the Island Night Lizard, Xantusia riversiana

Nicole Adams, Matt Dean, Gregory Pauly

Monday, June 23, 2014 -Poster #7

The Channel Islands are a group of eight islands off the coast of southern California that harbor a plethora of endemic organisms. The Island Night Lizard, Xantusia riversiana (Cope, 1883), is endemic to the southern Channel Islands of San Clemente, Santa Barbara, and San Nicolas. Xantusia riversiana is an "island giant" thought to have diverged from its mainland progenitor ca. 13.7-16 mya and since then evolved a larger body size. Although two subspecies are recognized (X. r. riversiana and X. r. reticulata), a previous morphological analysis suggested that all three island populations were morphologically distinct. We conducted a detailed morphometric study on 75 Island Night Lizards from the three islands to more fully examine morphological variability among island populations. We found statistically significant differences in both body measurements and scale characters among the three different island populations. Thus, current subspecies boundaries do not recognize the morphological distinctiveness of all three island populations. Although we await the results of ongoing molecular analyses before making taxonomic recommendations, these results indicate that recognizing three subspecies would more appropriately represent the underlying morphological diversity. Thus, the number of taxa endemic to the biogeographically unique Channel Islands is likely even greater than currently recognized.

Morphological Homoplasy within Mountain Dusky Lineages (Desmognathus)

Jessica Avila, David Beamer

Monday, June 23, 2014 -Poster #8

Mountain duskies are medium sized lungless salamanders (Desmognathus) distributed across the Appalachian Mountains. Historically, there has been debate about how many species of mountain duskies should be recognized; currently there are six named species: ochrophaeus, orestes, carolinensis, apalachicolae, ocoee, and abditus. These six species were delineated in large part, based on molecular data and the morphological variation within each species remains obscure. In the 1960's Martof and Rose collected over 4,000 Desmognathus from twenty one localities and made fourteen measurements for their specimens. To leverage their large morphological data set, we collected a series of thirty salamanders from the same localities. To place each of these populations in a phylogenetic context we sequenced both mitochondrial and nuclear genes. To understand the morphological variation within each of the lineages, we have photographed and made the same fourteen measurements as Martof and Rose. Here, we present a range wide molecular phylogeny that reveals the relationships of the six currently named mountain duskies, as well as several, apparently unnamed, lineages. Our phylogenetic reconstruction demonstrates both extensive morphological homoplasy and homology with respect to several morphological characters.

Incremental lines in therizinosaurian tooth enamel suggest slowed amelogenesis: Implications for evolution of herbivory in theropods

Khai Button, Lindsay Zanno, Hailu You

Monday, June 23, 2014 -Poster #9

BUTTON, Khai 1,2

Zanno, Lindsay E 1,2

You, Hailu 3

1. Department of Biological Sciences, North Carolina State University, Raleigh, NC, USA

2. Paleontology & Geology Research Laboratory, North Carolina Museum of Natural Sciences, Raleigh, NC, USA

3. Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences, Beijing, China

Therizinosaurians are a clade of large-bodied, theropod dinosaurs that lived in the northern hemisphere during the Cretaceous. Recent work has linked several macroevolutionary trends present in the clade to a dietary shift from carnivory to the omnivory/herbivory spectrum. Such trends include reduced reliance on dentition for food acquisition and processing, concomitant development of a rostral rhamphotheca, and alterations in tooth gross morphology. However, to date, no studies have investigated evolutionary trends in the microstructure of Therizinosauria dentition. Here we characterize the evolution of enamel microstructure in Therizinosauria, and bracket functional and phylogenetic trends by examining the teeth of Falcarius utahensis, the most primitive therizinosaurian described to date, and Suzhousaurus megatherioides, a large-bodied, derived therizinosaurid.

Therizinosaur teeth are generally diminutive. Those in our sample measured no more than 3 cm in basal-coronal length and 0.4 cm mesiodistally. Using a slow-speed saw, we cut longitudinal thin sections through the entire tooth length. We polished these to a thickness of 0.1 mm then etched sections using 1 M hydrochloric acid for 10-60 seconds. We coated samples with approximately 5 nm of Au-Pd and then examined them via scanning electron microscopy.

The schmelzmuster of both taxa is comprised of parallel enamel crystallites, marked with distinct incremental lines. Parallel enamel is the simplest and most basal enamel type and is commonly seen in theropod dinosaurs, including hypercarnivorous dromaeosaurs. These results support previous proposals of strong phylogenetic constraint in enamel microstructure in theropod dinosaurs, despite dietary differences. However, two major trends are evident in our sample. Incremental lines (striae of Retzius), which represent long period amelogenesis, are more numerous and distinct in the enamel of the derived Suzhousaurus and parallel crystallites become more organized when compared to Falcarius. Increasing organization and incremental lines reveal an ecological signal in the data. The higher density and prevalence of these features in derived therizinosaurs suggest slowed tooth growth and decreased replacement rate, in contrast with trends seen in other herbivorous dinosaurian clades. These data support prior hypotheses that the evolution of a rostral rhamphotheca corresponds with reduced role of dentition in therizinosaurs.

Geographically uneven expansion of mammalian diversity

Antonin MACHAC

Monday, June 23, 2014 -Poster #10
Mammalian diversity emerged through the process of evolutionary diversification (= net outcome of speciation and extinction). Similar to other groups, mammalian diversification tends to decelerate over time. These slowdowns have motivated a hypothesis that diversity suppresses diversification. Yet, there is little geographic evidence for slower diversification in diverse regions. In fact, diversity is often thought to promote diversification through its effects on ecological divergence and speciation. Here, we test the two opposing hypotheses using mammals (≈ 5,000 species) as a model system. Specifically, we analyze whether diversity expands or remains saturated across mammalian clades and then project our results on the world map. Based on two independent lines of evidence, we find that most diverse regions have higher proportion of expanding clades. These clades are also far from their enormous carrying capacities. Regions of lower diversity host smaller clades with high degrees of saturation. The core results remain supported even when controlling for clade area, latitudinal extent, or phylogenetic dependence. Together, our findings reject the hypothesis that high concentration of mammals suppresses their diversification. Instead, highly diverse regions (especially the tropics) apparently act as the engine of mammalian richness.

The evolution of phylogeographic sequence data sets: A meta-analysis.

Bryan Carstens, Ryan Garrick

Monday, June 23, 2014 -Poster #11
The data of phylogeographic research over the last 20+ years are investigated. Using a meta-analysis, we collect information on the number of samples, loci and SNPs in phylogeographic data from 1992 to the present in order to discern historical trends and understand the potential impact of new sequencing approaches.

Multilocus species delimitation and phylogeography of the freshwater sleepers,Odontobutis, in the Yangtze River drainage

Zhizhi Liu, Qiang Li, Chenhong Li

Monday, June 23, 2014 -Poster #12
The Yangtze River is the longest river in Asia and the third-longest in the world. It has the highest biodiversity of ichthyofauna in China. The forces shaping the modern biodiversity of aquatic life in the YangtzeRiver has been extensively studied, however, few studies have been done on the small benthic freshwater sleepers, Odontobutis, which are distributed in the Yangtze River and other river systems in Eastern China. Here, we employ a multilocus approach to validate the species status and to examine the genetic variation of Odontobutis found in the Yangtze River. We used the mitochondrial DNA control region and three nuclear introns to analyze over more than 160 fish collected from 17 different sampling sites. The results provide a clear picture about the genetic structure of Odontobutis at different level, which may help us to understand the origin of Odontobutis and the origin of diverse ichthyofauna in the Yangtze River in general.

Demographic history of Indian Cynopterine bats

Kritika Garg, Balaji Chattopadhyay, Sripathi Kandula, Uma Ramakrishnan

Monday, June 23, 2014 -Poster #13
Demographic history of the fruit bats of the Cynopterus genus is well understood, with both species experiencing population contraction. Although, population contraction is expected for the specialist species C. brachyotis, similar contraction for the generalist species C. sphinx was surprising. In this study we are investigating the possible cause and the timing of contraction for the generalist species especially for the high elevation isolated populations.

Reproductive strategy and the efficiency of selection in small populations

Evin Carter, Ben Fitzpatrick

Monday, June 23, 2014 -Poster #14
Small populations can evolve rapidly under some scenarios, but these mostly drift and mutation-driven changes are rarely expected to result in an increase in fitness. Nonetheless, there exist several remarkable examples of rapid adaptation by small populations that do not readily conform to theoretical expectations—most notably among amphibians. The majority of amphibian species exhibit complex life cycles and exceedingly large reproductive outputs, which increases both the number of recombination events per individual and the expected number of mutations per generation relative to standard population genetics models. Using individual-based simulations, we show that high reproductive output and low recruitment rate can act in concert to dramatically increase adaptive capacity and the efficiency of selection in finite populations but that these benefits depend on the number of loci affecting fitness and recombination rates among them. Our results may explain previous observations of rapid adaptation in small populations and might provide meaningful predictions regarding hybrid invasions.

Range-wide assessment of genetic variation and structure in subalpine larch (Larix lyallii)

Marie Vance, Patrick von Aderkas

Monday, June 23, 2014 -Poster #15

Subalpine larch (Larix lyallii) is restricted to a relatively small geographical and altitudinal range, growing only at treeline in the Cascade and Rocky Mountains of the Pacific Northwest. Climate change could further reduce available habitat by increasing levels of late-summer desiccation or by encouraging the upward migration of more competitive timberline species. Recent studies have suggested that subalpine larch is poorly equipped to cope with relatively rapid environmental change; microsatellite data have suggested that it is genetically depauperate in the northern part of its range, most likely as a result of recent bottleneck events and reproductive isolation among spatially discontinuous populations. To examine levels and patterns of genetic variation in this species, we have collected tissue from 61 populations distributed throughout the species' natural range. Restriction site associated DNA sequencing (RAD-Seq) will be used to obtain SNP marker data for population genetics analyses.

Evolutionary history across the range of the black-striped pipefish, Syngnthus abaster

Florentine Riquet, Lital Fleyshmaker, Nuno Monteiro, Tony Wilson

Monday, June 23, 2014 -Poster #16

Glacial cycles have played an important role in modifying species distributions, serving to prime post-glacial evolutionary divergence via genetic drift and/or selection. The black-striped pipefish Syngnathus abaster is a broadly distributed coastal inhabitant found throughout the eastern Atlantic, Mediterranean, Black and Caspian Seas, but recent work suggests that S. abaster may rather represent a species complex of geographically restricted and evolutionary divergent lineages. We tested this hypothesis by comprehensive sampling across the putative range of S. abaster, using a suite of highly polymorphic DNA markers and mtDNA and nDNA sequence data to investigate the role of glacial cycles in structuring marine population genetic diversity in the region.

Influence of land use on Drosophila species and genetic diversity

Andrey Bombin

Monday, June 23, 2014 -Poster #17

Influence of land use on Drosophila species and genetic diversity

Andrey Bombin and Laura Reed

Abstract

The main goal of this project is to identify the influence of a land use on genetic and species diversity of Drosophila. In addition, we will identify native and endemic Drosophila species, the range of their habitat and possible hybrid zones, in the state of Alabama. This study will establish the basis for asking questions about ecological speciation and variations in biological and genetic diversities due to the anthropogenic factors. The University of Alabama is nearly a perfect base for this study. According to historic records, 20 Drosophila species, including at least nine endemic species should be found in the state of Alabama. Here we will resent the initial findings on Drosophila biodiversity data focusing on identified species from our recent collections.

The effect of the dispersal distribution on isolation by distance in a continuous population

Tara Furstenau, Reed Cartwright

Monday, June 23, 2014 -Poster #18

Genetic structure under models of isolation by distance is determined by the probability of genetic identity between pairs of genes according to the distance between them. Wright's neighborhood size represents a standardized measure of dispersal which partially quantifies the relationship between identity by descent and isolation by distance in continuous populations. Here we model dispersal of haploid individuals on a two-dimensional torus using various dispersal distributions. The distributions are parameterized to produce the same second moment of dispersal and therefore neighborhood size. The populations are evaluated to determine if similar patterns of isolation by distance are observed when neighborhood size is held constant. One particularly interesting distribution examined here is the triangular distribution which, in two-dimensions, produces a uniform distribution over a circle which captures 100% of possible parents of central individuals, thus a panmictic unit.

Family matters: multi-scale analyses of relatedness in the pink volcano barnacle, Tetraclita rubescens

Stephanie Kamel

Monday, June 23, 2014 -Poster #19

Small mammal comparative phylogeography in the Arctic: evolutionary, ecological and human land-use implications

Andrew Hope, Eric Waltari, Jason Malaney, David Payer, Joseph Cook, Sandra Talbot

Monday, June 23, 2014 -Poster #20

Culminating from 15 years of phylogeographic studies on small mammals distributed across the northern continents through Beringia, we present a comparative methodological approach to understand the evolutionary processes associated with environmental change across the Arctic landscape, and how these perspectives may be applied for land management, conservation, and the dynamics of suture zones. This integrated multi-disciplinary research relies on extensive specimen-based archives of georeferenced specimens across time, including both genomic resources and fossils. Phylogeographic assessments revealed lineages from each species for which taxon-specific molecular substitution rates were scaled to assess the relative timing of demographic trends across the community. Population size changes were tested using coalescent simulations and distributional shifts of lineages through time were assessed with species distribution models. Predictions of potential future distributions suggest a northward shift in Arctic mammal diversity resulting in novel species assemblages, although our models also predict key regions where ecological community components remain relatively non-overlapping. These key areas are also coincident with an increasing human footprint in the Arctic, suggesting a need for careful land-use planning to accommodate multiple management priorities. A shifting Arctic ecotone between boreal and tundra biomes has multiple implications for evolutionary processes associated with hybridization, adaptation, and exposure to novel pathogens, investigations of which are increasingly feasible considering emerging and integrated genomic and GIS-based methods.

Introducing the Distinction between Static and Dynamic Mutational Robustness in Finite, Asexual Populations

Yinghong Lan, Aaron Trout, Christopher Scott Wylie, Daniel Weinreich

Monday, June 23, 2014 -Poster #21

Traditionally, the more robust organism is defined as the one in which deleterious mutations have more modest effects. In the language of the fitness landscape then, the more robust organism is thought to reside in a region of comparatively shallow gradients. While it's true that the first mutation in such an organism will reduce fitness only modestly, this conception overlooks what happens next. Using simple, individual-based simulations of finite, asexual populations, we show that on the contrary, equilibrium fitness deteriorates more quickly with mutation rate in populations on shallow fitness landscapes than it does when the gradient is steeper. This is because finite populations are more effective at purging deleterious mutations of large effect. We therefore propose distinguishing between an organism's static robustness, defined in terms of the mean effect of the first mutation, and its dynamic robustness, defined in terms of the effect on mutation/selection/drift equilibrium fitness. We discuss connections to previous work on the mutational meltdown and the evolution of the flattest.

Evolution of body mass in the Pan-Alcidae (Aves, Charadriiformes): the effects of combining neontological and paleontological data

Adam Smith

Monday, June 23, 2014 -Poster #22

Hypotheses regarding the evolution of many clades are often generated in the absence of data from the fossil record and potential biases introduced by exclusion of paleontological data are frequently ignored. With regard to body size evolution, extinct taxa are frequently excluded because of the lack of body mass estimates—making identification of reliable clade-specific body mass estimators crucial to evaluating trends on paleontological timescales. Optimal osteological dimensions for estimating body mass in were identified and utilized to generate estimates of body mass for extinct species of Pan-Alcidae (Aves, Charadriiformes). Ancestral state reconstructoins demonstrate that the combination of neontological and paleontological data produces results that conflict with hypotheses generated when extant species data are analyzed in isolation. The wing-propelled diving Pan-Alcidae are an ideal candidate for investigation of body mass evolution because extinct species diversity (≥ 31 spp.) exceeds extant diversity, and because phylogenetic hypotheses of pan-alcid relationships are not restricted to the 23 extant species. Phylogenetically contextualized estimation of body mass values for extinct pan-alcids facilitated evaluation of broad-scale trends in the evolution of pan-alcid body mass and generated new data bearing on the maximum body mass threshold for aerial flight in wing-propelled divers. The range of body mass in Pan-Alcidae is found to exceed that of all other clades of Charadriiformes (shorebirds and allies) and intra-clade body mass variability is proposed as a defining characteristic of the clade. Finally, comparisons of pan-alcid body mass range with penguins and the extinct †Plotopteridae elucidate potentially shared constraints among phylogenetically disparate yet ecologically similar clades of wing-propelled divers.

Fossil Insights to Drivers of Geographic Co-occurrence and Ecological Differentiation Between Marine Bivalves

Stewart Edie

Monday, June 23, 2014 -Poster #23

Character displacement and species sorting are two processes thought to promote the geographic co-occurrence of closely related species. Determining the timing, magnitude, and then mechanism of ecological change that enables the geographic range overlap of closely related, and therefore presumably ecologically similar species, requires spatially explicit data on past trait distributions. Many studies use phylogeny to create this historical context. This study uses the detailed modern and fossil record for one set of closely-related marine bivalves to empirically determine the present and past distribution of burrowing ability–an ecological trait that promotes habitat partitioning. I compared shell outlines–a known proxy for burrowing ability–for two species of Venerid bivalves from the Eastern Pacific: Chione californiensis and C. subimbricata. The present-day allopatric populations of Chione californiensis and C. subimbricata differ in burrowing ability, where C. californiensis burrows more slowly and to a shallower depth than C. subimbricata. Where the two species are sympatric, C. californiensis burrows the same as in allopatry, but C. subimbricata burrows more slowly and shallowly than in allopatry–equivalent to the burrowing ability of C. californiensis. This remarkable convergence in burrowing ability counters the expectation that ecological traits promoting competition should differ in areas of co-occurrence, and instead suggests a filtering for similar traits imposed by the shared environment. A very preliminary examination of the fossil populations (Pliocene and Pleistocene) suggests stability in the spatial distribution of these burrowing traits has existed over the past 5 My. Further measurement of shell shape in fossil populations and the consideration of additional species pairs within the Chione clade will help test the generality of this convergent, rather than divergent trait displacement in sympatry across the genus.

Evaluating drivers of genomic diversification in a tropical moth radiation

Josh Jahner, Thomas Parchman, Lee Dyer, Andrea Glassmire, Christopher Jeffrey, Lora Richards

Monday, June 23, 2014 -Poster #24

A long-standing goal in evolutionary biology has been to identify and understand drivers of diversification. Herbivorous insects have been particularly useful study organisms in this endeavor because of their impressive diversity and predicted patterns of diversification in response to close associations with host plants. Few studies have been able to examine the relative importance of geography, host plant evolutionary history, and host plant chemistry for diversification within important herbivore taxa. We examine these potential promoters of diversification in a hyper-diverse, tropical genus of geometrid moths (Eois) by utilizing genotype by sequencing data to assemble a moth phylogeny made of individuals that specialize on one genus of phytochemically-diverse host plants (Piper) located across the Neotropics.

The Vitória-Trindade Chain (SE Brazil) as a natural laboratory for reef fish evolutionary studies

Hudson Pinheiro, João Gasparini, Jean-Christophe Joyeux, Giacomo Bernardi, Luiz Rocha

Monday, June 23, 2014 -Poster #25

The evolutionary processes of reef fish populations over oceanic seamounts and islands of the Vitória-Trindade Chain, off Brazil, are related to the species´ distribution and colonization strategies, as well as adaptations and distinct speciation patterns. Contemporary colonization events of seamounts and islands are supposed to occur along a gradient from strong and regular to weak and rare, depending on species ecological traits and oceanic currents and stochastic events. However, dispersal could have been more intense in the past when the shallowest seamounts were exposed with higher amounts of suitable habitat for shallow-water species. Thus, present disjunct distributions might result either from past colonization followed by vicariant events or dispersal by stochastic phenomena. Isolated populations on seamounts are likely to be under natural selection to live in deep reefs and self-recruit. Allopatric speciation could have affected small-sized species that depend on shallow habitats that are not found on seamounts today. Parapatric ecological speciation and isolation by distance could have occurred in the endemic species widely distributed in the deep habitats of the seamounts and islands. Paleo-endemics are evidence of the importance of seamount habitats to the maintenance of relict fauna. Genetic drift and extinction can be strong processes acting in some seamount populations and impacts caused by fishing activities, mining and climate change can cause negative evolutionary responses. The goal of this work is not elucidate all evolutionary processes occuring in VTC environments, but instead it intends to show how VTC can be used as a scenario for evolutionary studies.

Evolution of Parental Behavior in Peromyscus

Young Kwon

Monday, June 23, 2014 -Poster #26

Parental behavior is highly variable across species. Paternal care, where the father significantly invests in the care of the offspring, occurs in ~8% of mammalian species while maternal care, though universal, varies between species in both quantity and quality. Paternal care occurs predominantly in monogamous species and very rarely in promiscuous species. While species differences in parental behavior have been heavily documented, the genetic basis of its evolution remains unknown. To study this question we examined two species of Peromyscus, the deer mice genus, that differ in their mating system: P. polionotus, which is highly monogamous, and P. maniculatus, which is highly promiscuous. The parental behavior of these two species, however, has not been directly compared. Here, we studied the parental behavior of these two sister species as a basis to understand its underlying genetic architecture. First, we characterized and quantified the parental behavior of the two species through behavioral assays. Behaviors measured included the latencies to approach, lick, handle (move pup with its paws), huddle (cover pup with its body), and retrieve a pup. Total licking and huddling time, the frequency of retrieval, as well as nest quality (ranked from 0-3) were also included. Apart from retrieving, P. polionotus fathers were as parental as P. polionotus mothers. In contrast, P. maniculatus fathers behaved significantly less parentally than P. maniculatus mothers and both P. polionotus fathers and mothers. To determine the heritability of parental behavior, we conducted interspecies cross-fostering experiments. A newborn litter from one species was exchanged with a litter from the other species and later, these pups’ parental behaviors were analyzed. Minimal differences between cross-fostered and non-cross-fostered individuals suggest a strong genetic component to parental behavior. To further investigate the genetic basis of parental behavior, we performed an F2 intercross between the two species, measuring the parental behaviors of the hybrid offspring and then, the F2 generation. Parental data from more than 700 F2 individuals showed that several behaviors like licking, huddling time, and retrieval frequency, did not have bimodal distributions, suggesting that multiple loci may be involved in the regulation of these behaviors. Moreover, strong correlations between several behaviors excluding retrieval latency indicate possible sharing of loci. Together, these findings elucidate the parental behaviors of these two different sister species and are a preliminary step towards understanding the genetic underpinnings of parental behavior.

The effect of ecological context and relatedness on larval cannibalism in a fungus-associated beetle

Hannah Marti, Corlett Wood, Edmund Brodie

Monday, June 23, 2014 -Poster #27

The fitness consequences of extreme competitive interactions such as cannibalism are often governed by the environment, because the costs and benefits of such behaviors depend on the ecological and social context of the participants. However, most studies of context-dependent cannibalism are conducted under extreme circumstances or examine only a single environmental context, conditions that are unlikely to exist in natural populations. In this study we tested the effect of multiple environmental contexts on the frequency of cannibalism in forked fungus beetle larvae (Bolitotherus cornutus), which develop in three different fungus species. We paired larvae in laboratory trials and measured the effect of (1) ecological context (the three fungi) and (2) the relatedness of the paired larvae on the frequency of cannibalism. We found a strong effect of ecological context on cannibalism: larvae in one fungus cannibalized nearly twice as often as larvae in the other two. We did not detect an effect of relatedness on cannibalism in the one species of fungus in which trials were conducted. Cannibalism conferred benefits in the form of accelerated growth rates in all measured traits relative to non-cannibals. However, contrary to most studies, cannibalism was most common in the highest-quality fungus, contradicting the hypothesis that cannibalism occurs in poor environments to compensate for resource deficiencies. We discuss alternative mechanisms that may drive the ecological context-dependence of cannibalism in B. cornutus, and emphasize the importance of studying context-dependent behavior in naturally occurring environments.

The Evolution of Nitrogen Resorption across Helianthus

Chinyere Uzoigwe, Chase Mason, Lisa Donovan

Monday, June 23, 2014 -Poster #28

Nutrient resorption describes a plant’s ability to re-absorb nutrients from senescing leaves. This ability is beneficial because such recycling increases available nutrient for growth and reproduction. Nitrogen is typically the nutrient most limiting to plant growth, and nitrogen resorption can be measured by the nitrogen content difference between green and senesced leaves. Nitrogen resorption efficiency and proficiency were measured in 2-4 populations each of 28 species of wild Helianthus grown in a common garden. The levels of resorbed nitrogen across populations and species were compared with respect to growth form and life history, home habitat environmental factors, and relative placement along the leaf economics spectrum. First, it is hypothesized that annuals and erect deciduous perennials would have lower resorption ability than basal rosette perennials, which use rosettes of leaves as storage organs for overwintering. Second, it is hypothesized that species from more fertile habitats would have lower resorption ability than species from less fertile habitats, as resorption is costly and would not be favored where soil nitrogen is abundant. Third, it is hypothesized that higher nitrogen resorption would be favored in species with a more “conservative” leaf economics spectrum, as these species are typically found in infertile environments, often use leaves as storage organs, and have a longer leaf lifespan that allows more time for nutrients to be re-absorbed prior to leaf senescence.

The Evolution of Physical and Chemical Leaf Defenses in Helianthus

Breanna Crowell, Chase Mason, Lisa Donovan

Monday, June 23, 2014 -Poster #29

Plant defenses are a result of both evolutionary history and more recent adaptations to the biotic and abiotic factors that define the environment in which a population resides. Plant defenses can be either physical or chemical in nature and act in a number of ways to prevent herbivory. A great number of ecological and evolutionary theories have been proposed to explain variation in plant defense, focusing on trade-offs among defenses, environmental resource availability, latitudinal gradients, and growth rate. Many such theories have been recently tested at global scales through large global datasets and through meta-analysis, with mixed results and the suggestion that testing such questions within closely-related groups might yield clearer answers. This study uses the diverse genus Helianthus (the sunflowers) as a model system to evaluate hypotheses derived from these theories. A greenhouse common garden approach combined with phylogenetic comparative methods was used to examine the evolution of specific defenses during speciation into diverse habitats and the evolution of differential growth form, life history, and leaf economic strategies. It is hypothesized that trade-offs among defenses will exist due to finite resource allocation, that levels of defense will increase with decreasing resource availability, that defense levels will increase with decreasing latitude, and that defense levels will decrease with leaf economic strategies that promote faster growth. Specific defenses under study include a variety of physical and chemical defenses, including tannins, trichomes, lipid content, ash content, leaf thickness, leaf toughness, and leaf dry matter content.

Evidence for widespread positive and negative selection in coding and conserved noncoding regions of Capsella grandiflora

Robert Williamson, Emily Josephs, Stephen Wright

Monday, June 23, 2014 -Poster #30

We sequenced the genomes of 13 Capsella grandiflora individuals and used the allele frequency, divergence, and diversity data to quantify levels of both positive and negative selection across the whole genome. We show that while both positive and negative selection are strong in protein coding and conserved noncoding sequences, consistent with the large effective population size of the species, selection is weak across the vast majority of noncoding sequence. These data seem to support the idea that plant genomes are organized differently from animal genomes, with much less noncoding constraint in plants.

Natural genetic variation in molecular structure-function relationships of PGI of Colias (Lepidoptera, Pieridae)

Jason Hill, Ward Watt

Monday, June 23, 2014 -Poster #31

The glycolytic enzyme phosphoglucose isomerase, PGI, is extensively polymorphic in Colias populations. Its polymorphs' genotypic functional differences successfully predict performance and fitness differences in the wild. The structural basis for this functional diversity has not been studied directly until now. We present a high resolution Xray-crystallographic reconstruction of the native dimer structure of Colias PGI, which supports a range of structure-function studies of PGI's polymorphic variants, both directly and by computer simulation. We explore the structural differences leading to functional differences among representative allelic PGI homozygotes, including further confirmation of the previously found tradeoff in homozygotes between catalytic function and thermal stability. Molecular dynamics simulations based on our structural model provide evidence for variants' action in altering catalytic site geometry, the balance of hydrogen bonding within PGI structure and between PGI and surrounding water (solvent), and measures of internal protein chain packing and overall conformation of the PGI dimer. This study lays the groundwork for exploration of the ways in which identifiable selection pressures have shaped and are shaping the molecular evolution of protein structure in the wild.

Changes in adipocyte cell structure and gene expression during human origins

Sasha Makohon-Moore, Lisa Pfefferle, Greg Wray

Monday, June 23, 2014 -Poster #32

Understanding how molecular functions evolved during human origins allows us to gain insight into both adaptations as well as maladaptive disease risk unique to our species. A notable example is the expansion of the brain during human evolution, which came at a high energetic cost and was likely fueled by changes in both diet and lipid metabolism. While these changes were surely advantageous to our ancestors, a major shift in human diet following the agricultural revolution may have led to an environmental mismatch and subsequently predisposed modern humans to inflammatory diseases that are rare in our closest relative, the chimpanzee. To better understand how metabolic differences evolved during human origins, we are comparing the transcriptome and cell structure of adipocytes (a hub of metabolic activity) between humans and chimpanzees. Using adipose stromal cells we have been able to differentiate adipocytes ex vivo, which allows us to control the differentiation environment and expose genetically based trait differences between species. Here, we report on several interesting differences in both cell structure and gene expression between human and chimpanzee adipocytes. While these differences may have initially been adaptive during human evolution, shifts in the diet of modern humans have resulted in an increased inflammatory state of human adipocytes compared to chimpanzees.

Detecting distributive conjugal transfer in mycobacteria from whole genome sequences

Tatum Mortimer, Caitlin Pepperell

Monday, June 23, 2014 -Poster #33

Distributive conjugal transfer (DCT) is a unique, chromosomally encoded mechanism of lateral gene transfer in Mycobacterium smegmatis which transfers multiple, non-contiguous DNA segments from a donor cell to a recipient via conjugation. The amount of sequence transferred and mosaicism of transconjugants is distinctive in DCT compared to other mechanisms of bacterial lateral gene transfer. Next generation sequencing technologies of bacterial genomes have made it feasible to study DCT and other mechanisms of LGT in natural populations of bacteria at a high resolution. However, recombination detection methods were not designed with DCT in mind. We have tested popular recombination detection methods, including PHI, LDhat, cBrother, ClonalFrame, ClonalOrigin, and BRATNextGen, on whole genome sequence data from experimental M. smegmatis transconjugants in which recombinant tracts are defined. After calculating positive and negative predictive values for each method, we determined that BRATNextGen is the best performing method for identifying DCT transferred tracts. We additionally evaluated the origins and size distribution of tracts output by BRATNextGen. The origins of tracts identified by BRATNextGen were accurate in only 60% of cases. BRATNextGen also divides some larger DCT-transferred fragments into smaller pieces. With this in mind, we recommend BRATNextGen for further study of DCT among mycobacteria with a possible size correction and supplementary method for identifying origins of these recombinant fragments.

Diversification of the deep-sea octocoral Tokoprymno maia across the Antarctic Circumpolar Current

Luisa Duenas, Andrew J. Crawford, Juan Sanchez

Monday, June 23, 2014 -Poster #34

Despite the unquestionable importance of Antarctica to various global processes, the distribution of deep-sea populations across the Southern Ocean remains poorly known. Antarctica is surrounded by the Antarctic Circumpolar Current (ACC), which is the largest and strongest in the world. Even though the ACC appears to be a strong barrier against dispersal, it may be permeable allowing for widespread distributional patterns. The deep-sea primnoid octocoral Tokoprymno maia is widely distributed on the sub-Antarctic regions around New Zealand and Tasmania, and Thouarella sp. is distributed on the Antarctic regions. The polyp structure is extremely similar between these genera suggesting a very close systematic relationship. In this study we wanted to determine the role of the ACC as a barrier for dispersal of these octocorals, assuming they belong to the same taxonomic entity, therefore treating T. maia and Thouarella sp. as the same species and calling them T. maia through out the study. We used sequences from two nuclear regions, ITS2 and 28S, and one mitochondrial region, msh1, to evaluate gene flux between populations from Tasmania, New Zealand and Antarctica. With its2 we found high population structure between Tasmania and New

Zealand, and Tasmania and Antarctica, but no structure between New Zealand and Antarctica. Or results show that the populations from Tasmania and New Zealand may be different species, while the populations from New Zealand and Antarctica still share some alleles, suggesting them as different but early-diverged species. Moreover, with the current data we could discard the hypothesis of the ACC acting as a barrier against genetic flux between northern and southern populations.

The decline and rescue of pupfish inhabiting a small isolated spring

Andrew Martin, Kyle Keepers, Nolan Kane

Monday, June 23, 2014 -Poster #35

In the Mojave Desert near the borders of California and Nevada, we have followed several populations of pupfish that inhabit small springs for nearly two decades. For some populations, population size has steadily declined probably as a consequence of direct and indirect effects of human activities. Genetic rescue was studied in two populatons. In one, as a consequence of a natural immigration event, and in the other as part of a study designed to follow the fate of immigrant alleles. There was clear evidence for differences in survivorship of immigrant, resident and admixed individuals, and rapid shifts in diagnostic genetic markers in the direction predicted if resident individuals suffered from a segregating and fixed load of deleterious alleles. Moreover, the steady decline of population size was reversed. To elucidate the genomic basis of genetic rescue, we initiated study of the fate of introduced and resident alleles during the decline and recovery of one of the isolated populations.

Genomic signals of local adaptation across the range of the allotetraploid weed C. bursa-pastoris

Adriana Salcedo, Stephen Wright

Monday, June 23, 2014 -Poster #36

Polyploids are exceptionally evolutionarily successful and increased adaptive potential may contribute to their prevalence. In addition to the genetic variation generated through gene duplication, polyploidization increases genetic variation through genomic rearrangements, hybridization, and regulatory changes. Whole genome duplication may also relax pleiotropic constraints and increase the speed that beneficial dominant mutations fix. If rapid adaption is important for species success, these processes may then facilitate spread and persistence. However, the extent that these processes contribute to adaptation and polyploid success is currently unclear. Here we investigate the genomic basis of local adaptation in one of the world's most successful weeds. Capsella bursa-pastoris is a recent allotetraploid that spread throughout the world, while its diploid progenitors remain in limited European ranges. We sequenced 261 C. bursa-pastoris accessions spanning Eurasia and looked for climate associations with the GBS SNP data while controlling for population structure. We explore the genetic architecture of adaptive loci and inquire whether adaptive SNPs primarily represent new variation generated through polyploidization or are pre-adapted parental alleles. We assess how strongly adaptation contributes to C. bursa-pastoris' spread and which features of its polyploid genome are involved.

Comparative analysis of active transposable elements in the transcriptomes of three species of heteromyid rodents

Yanzhu Ji, Nicholas Marra, J. Andrew DeWoody

Monday, June 23, 2014 -Poster #37

Virtually every eukaryotic genome is replete with transposable elements (TEs). TE activity (or lack thereof) is of considerable evolutionary interest, as TE insertions may disrupt gene function, create new regulatory elements, etc. Thus TEs are active drivers of genome evolution. Herein, we take a comparative approach to characterize TE activity in three non-model rodent species from the Heteromyidae, a family of new world rodents: Dipodomys spectabilis, Chaetodipus baileyi, and Heteromys desmarestianus. We used these species (a) because rodents have long been productive models for the study of TEs; (b) because the known (and robustly dated) relationships among these species permit strong phylogenetic inference (e.g., ancestral character states); and (c) because their habitats differ (the D. spectabilis and C. baileyi inhabit xeric environments and H. desmarestianus inhabits mesic environments). In previous studies, we characterized key genes that underlie adaptations to these environments and used RNA-seq to characterize the transcriptomes of two different tissues—kidney and spleen—in each of these three species. Most TEs are epigenetically silenced in somatic cells by DNA methylation, histone acetylation, and/or PIWI-interacting RNA (piRNA) pathway. As a result, our null hypothesis was that TEs are transcriptionally silenced in both kidney and spleen tissues. We expected TE derived transcripts to represent a low proportion of total transcript abundance across tissue types and species that experience different environmental conditions. Our data revealed (1) a diversity of TEs are actively expressed in these rodents; (2) there were tissue-specific differences in TE-activity; and (3) there were lineage-specific differences in TE-activity. We interpret these differences in TE activity in light of overall gene expression. Our results contributed to a growing appreciation for the interplay between TEs and their hosts.

Causes and consequences of APOBEC3A rapid evolution in primates

Jacob Gable, Rick McLaughlin, Harmit Malik

Monday, June 23, 2014 -Poster #38

The repertoire of pathogens a host cell must fend off constantly changes over time. This creates conflict, where host and pathogen evolve in response to each other. This recurrent selection of functional novelty creates a pattern of sequence evolution characterized by an excess of non-synonymous relative to synonymous changes – positive selection. The APOBEC3 proteins are a family of cytidine deaminase restriction factors that restrict a large selection of viruses and transposons. In primates, many APOBEC3 proteins have evolved under strong positive selection, including APOBEC3A (A3A). We hypothesize that the restriction targets of A3A have driven its positive selection; if correct, we expect A3A orthologs from diverse primate species will differ in their ability to restrict these pathogens. We also expect changes at positively selected amino acid positions of A3A to underlie any differential restriction function. To test these hypotheses, we measured restriction of the endogenous retroelement LINE-1 by several primate A3A orthologs and found that, surprisingly, several Old World monkey A3As have lost the ability to restrict LINE-1. Intriguingly, previous experiments from another group suggest that these Old World monkey A3As have gained the ability to restrict retroviruses. This suggests that A3A in the ancestor of Old World monkeys gained the ability to restrict retroviruses, but in a tradeoff event, this evolution resulted in a loss of LINE-1 restriction activity. However, when we tested more primate A3A's we found that other Old World monkey A3As could restrict LINE-1, including some species that apparently restrict both retroviruses and LINE-1. Species of Old World monkey that lack LINE-1 restriction by A3A all have the same amino acid identities at four positively selected sites in A3A and all the species of Old World monkey that successfully restrict LINE-1 by A3A have different amino acid identities from those that could not restrict at those sites. This correlates positive selection in A3A to differential restriction of retroelements. We suggest that after the tradeoff event in Old World monkeys, fitness effects of LINE-1 replication mounted and a distinct solution (non-tradeoff) evolved in A3A to restrict both LINE-1 and retroviruses. Our data demonstrates the degree to which pathogens can drive novelty and shape gene evolution in hosts, including changing pathogen targets of a host restriction factor and evolving a mechanism to restrict multiple pathogens.

Genetically complex growth defects in a yeast cross revealed by simultaneously perturbing two components of the environment

Takeshi Matsui, *Ian Ehrenreich*

Monday, June 23, 2014 -Poster #39

Characterizing how genetic background and the environment together specify phenotype is a central aim of ecological and evolutionary quantitative genetics. Controlled growth experiments of cross populations can be used to study this problem. Most such experiments analyze how different genotypes respond to a single aspect of the environment. Here, focusing on recombinant progeny from a yeast cross, we studied qualitative patterns of growth under perturbation of individual environmental factors—temperature and carbon source, as well as perturbation of both of these factors. We found that even though cross parents and all of their progeny were capable of growing fine under standard lab conditions and single factor environmental changes, ~4% of individuals were compromised when both aspects of the environment were altered. By implementing multiple crossing designs and screening tens of thousands of recombinants, we show that the genetic basis of these conditional growth defects is highly complex. Using recurrent backcrossing with phenotypic selection, we identified three loci that seem to play a major role in one segregant's growth defect and have begun to clone the specific causal genes underlying the three major effect loci. Our overall goal is to shed light on the mechanisms that sensitize certain individuals to complex environmental change. Given that multifactorial environmental perturbation is a regular occurrence in natural habitats, our work may represent an important step in increasing the ecological and evolutionary relevance of quantitative genetic studies in the yeast system.

Piwi vs. DNA Transposons: Identifying Piwi homologs in vespertilionid bats.

Sarah Mangum, *Federico Hoffmann, David Ray*

Monday, June 23, 2014 -Poster #40

Of the two classes of transposable elements, DNA transposons and retrotransposons, DNA transposons have been found to have low activity in all studied mammals so far except for one family of bats, the vespertilionid bats including Myotis lucifugus. M. lucifigus and other vesper bats exhibit a recent increase in DNA transposon activity. P-element induced wimpy testis (PIWI) is a vital protein component of the pathway that acts to silence transposable elements via their interaction with a class of small RNAs (piRNAs). We propose that the increase in DNA transposon activity in vesper bats may be related to changes in PIWI expression. In this study, PIWI genes are examined bioinformatically in ten different bat genomes, including Myotis lucifigus. By analyzing the PIWI gene family, expression data and possible deactivations of these genes may be detected. Such pseudogenizations may play a role in allowing DNA transposon activity. Thus far in the study, full PIWI exon sequences have been difficult to obtain. However, some species do possess the full exon repertoire and partial sequences in other species indicate the PIWIs are present and they may or may not be functional. This could possibly be due to changes in the PIWI makeup of the gene family framework which could account for the increase in DNA transposon activity or because techniques used so far have not been successful in finding the full sequences. Deeper and more intense extraction methods will be used in this study to further examine these important elements.

Analysis of Conserved Gene sequences in forty-eight model Organismin reference of rice and development of a phylogenetic tree of life

Pawan Jayaswal, *Vivek Dogra, Asheesh Shanker, Tilak Sharma, Nagendra Singh*

Monday, June 23, 2014 -Poster #41

Analysis of Conserved Gene Sequences in forty-eight Model Organism in Reference of rice and Development of a Phylogenetic Tree of Life

Jayaswal PK1, Dogra V1, Shanker A2, Sharma TR1, Singh NK1*

1National Research Centre on Plant Biotechnology, IARI, Pusa, New Delhi, India-110012

2Banasthali Vidyapeeth, Rajsthan-304022

(*Corresponding Author: nksingh@nrcpb.org)

Large scale genome sequencing has provided new dimensions to our understanding of evolution of different species. In plants, high quality reference genomes of Arabidopsis (Arabidopsis Genome Initiative 2000) and rice (International Rice Genome Sequencing Project 2005) have been used extensively for comparative analysis of plant genomes that could be extended to animal and microorganisms. For this study we have selected unigene sequences of 48 different organism (eukaryote and prokaryote). The aim of our study was to identify the homologous gene sequences expressed in rice and 47 other organism and also to understand the evolution of genomes on the basis of conservation of genes. We found 53,492 rice gene sequence including splicing site variants after BLAST search of EST 44,235 unigenes and with 66,338 CDS sequences of Oryza sativa. Out of this 11,500 gene sequences were unique to rice and the remaining sequences showed varying levels of homology with other species. After comparing with 47 different organism we found Zea mays showed the highest similarity of 60.67 %, followed by Hordeum vulgare 58.89% and wheat 57.94%. On the basis of comparative gene sequence analysis among 48 different organism we found 98 gene sequences conserved in all the 48 species. After annotation of 98 conserved gene sequence into six different group we found that genes for physiological functions were dominated (49 gene sequence) whereas only eight genes were related to stress response. We constructed a tree of life on the basis of these 98 conserved gene sequences using Bayesian analysis approach and found eight independent groups of organisms closely associated with each other that largely corresponds with the accepted evolutionary relationship among these organisms. Study of 98 conserved gene sequence based phylogenetic tree helps to establish evolutionary relationship among the diverse species across the eukaryotes.

A next-generation transcriptomics approach to testing homologies in hoofed mammal cranial appendages

Zachary Calamari

Monday, June 23, 2014 -Poster #42

New hypotheses of the interrelationships of even-toed, hoofed mammals (artiodactyls) challenge previously held views on single versus multiple origins of cranial appendages (horns, antlers, ossicones, and pronghorns), and even suggest that some widely dissimilar cranial appendages may have shared origins. Gene expression homology in artiodactyl cranial appendages is currently untested, and studies of gene expression in cranial appendages are mainly limited to investigating the rapid bone growth of antlers as a cancer analog for human health. Horns and antlers grow from different tissues, thus gene transcription is expected to differ between horns and antlers. To test the hypotheses that transcription changes throughout the development of horns, and that differences between horn and antler growth transcription correlate to differences in development of these structures, horn bud tissues were collected from domestic cattle (Bos taurus) calves at eight and 16 weeks. Genes transcribed in the tissues at the time of sampling were sequenced using Next-Generation methods, then compared to gene ontologies for bone and keratin development. Further comparisons were made between the horn transcriptome and published antler transcriptomes. The genes responsible for horn bud development at these ages, as well as differences between horn and antler transcription, were identified. This work is an important step toward describing the transcriptome of growing bovid horns in Bos taurus, and testing homology of cranial appendage types across Artiodactyla.

Elucidating the evolutionary history of the primate alpha-amylase multi-gene family

Tiare Takaesu

Monday, June 23, 2014 -Poster #43

During the primate evolution, four insertion and duplication events in the amylase multi-gene family resulted in a number of distinct genes that have pancreatic or salivary expression. To elucidate what genetic changes caused such expression divergence, I aim to test three hypotheses of the timing of the duplication of AMY1 and AMY2A, two primate-specific alpha-amylase genes with specific expression patterns, in order to identify the true salivary amylase ancestral promoter sequence that caused the AMY1 gene to switch its expression pattern from the pancreas to the salivary glands.

To this end, I will use MEGA, an evolutionary analysis software, to build phylogenetic trees of all primate alpha-amylase genes and reveal the gene genealogy of this multi-gene family, using their intron, exon, promoter, and protein sequences. Comparing these gene genealogies with the previously-established primate species tree, I will determine the precise time of the divergence of AMY1 and AMY2A, expressed exclusively in the salivary gland and the pancreas, respectively. In addition, by making statistical inferences and manual adjustments using MEGA, I will determine the promoter sequence of the common ancestor of all current-time salivary amylase genes, which will aid my hypothesis testing.

The results of this project will either confirm previously made assumptions with a better resolution of time estimation, or reveal a new evolutionary scenario of how the tissue-specific expression of salivary amylase arose by changes in the promoter sequence.

Transcriptomics of an endemic species flock: Lake Baikal amphipods

Lev Yampolsky, Sergey Naumenko, Maria Logacheva, Georgii Bazykin, Nina Popova, Anna Klepikova

Monday, June 23, 2014 -Poster #44

The endemic species flock of Lake Baikal amphipods is a striking example of endemic adaptive radiation. This species flocks contains over 250 species and demonstrates a high level of morphological and ecological diversity, including miniature and giant species, both conservative amphipod morphology and highly armored forms, a unique plankton species as well as highly specialized active predators, abyssal scavengers and parasites. We have sequenced whole body RNAs from >50 species, resulting in over 26,000 orthologous groups, and identified 5000 – 30000 genes per species. We discuss the use of this dataset, one of the first species flock transcriptomic dataset ever, for the analysis of phylogenetic history, heterogeneity of speciation rate over time and across clades, gene gains and losses and patterns of protein evolution.

Phylogenetic analysis of fatty acid biosynthetic genes in the Asteraceae

Jonathan Corbi, John Burke

Monday, June 23, 2014 -Poster #45

Fatty acids (FA) show a remarkable diversity in terms of structure and composition within species and these features are also conserved between species. Interestingly, orthologous FA biosynthetic genes are often associated with several essential functions, such as defense against herbivores, attracting pollinators, or serving as a source of energy during early seed development. Genes involved in FA synthesis are thus expected to exhibit a complex pattern of evolution. Interestingly, some FA genes have been shown to be under selection during domestication of sunflower. We aim to better understand the selective pressures acting on genes involved in fatty acid biosynthesis across plant species and especially in the Asteraceae, the largest family of flowering plants, which also include the sunflower. Performing phylogenetic analysis to detect specific instances of selection and amino acid coevolution, we focused on key FA genes encoding for: i) the different subunits of the acetyl-CoA carboxylase (ACCase) catalyzing the first committed step to fatty acids synthesis, ii) the stearoyl-ACP-desaturase that introduces the first double bond during FA synthesis, and iii) the oleate desaturase (FAD2) that catalyzes the last step leading to linoleic acid. Overall, the proteins exhibited remarkably low sequence diversity across species, except the biotin carboxyl carrier protein (a subunit of the ACCase). Taking into account all monocot and dicot sequences available in the databases, we found that only the oleate desaturase and the stearoyl-ACP-desaturase showed evidence of accelerated evolution in branches leading to the Asteraceae and to sunflowers, respectively. This suggests an important role of unsaturated fatty acids in these clades. We also detected several coevolving amino acids within each of the proteins that occurred recently in angiosperm evolution, which is consistent with a high level of evolutionary constraint. Deeper examination of the detected residues and their role in a specific structure/function would provide a better understanding of the evolution of this complex pathway.

Introduced guppies induce divergent trajectories of morphological change in an intraguild predator

Bradley Lamphere, Diane Biederman, James Gilliam

Monday, June 23, 2014 -Poster #46

Swimming morphology has proved to be a sensitive and consistent response to predation threat in a number of stream fish. Here we investigate the impact of an introduced species (guppies) on the swimming morphology of a resident (killifish) in Trinidadian streams. Guppies and killifish are mutual intraguild predators, with adults of each species capable of consuming the others' juveniles. Consistent differences in morphology between killifish naturally co-ocurring with guppies (KG) and those with no other fish (KO) indicate that guppies represent an important factor shaping killifish phenotypes. Moreover, those differences offer long-term predictions for four killifish populations exposed to experimental introductions of guppies. Five years post-introduction, none of the four populations had shifted in the direction of the long-term prediction, and at least one has exhibited a signficant response in the opposite direction. Thus, the phenotypic response of the killifish suggests either a circuitous path toward the predicted state or a trajectory leading toward an unpredicted long-term endpoint.

Exposure to vinclozolin, an androgen antagonist, slows social learning in guppies (Poecilia reticulata)

Allyssa Wong, Bronwyn Bleakley

Monday, June 23, 2014 -Poster #47

Guppies, Poecilia reticulata, are an important model system for studying behavioral evolution. Endocrine disrupting compounds (EDCs) are common contaminates that alter physiology and behavior. Some EDCs, such as bisphenol-A, may impair individual learning ability, especially when animals are exposed during development. However, little is known about the effects of EDCs on individuals exposed as adults. Vinclozolin is an EDC that acts as an androgen receptor antagonist and has been demonstrated to affect the sexual behavior of adult guppies but has not be assayed for effects on learning. Inbred lines of guppies are known to vary in cooperative, anti-predator behavior, and social learning. Among the inbred lines of guppies maintained in the Bleakley lab at Stonehill College, RF fish have the highest foraging success rate and fastest rates of social learning. We exposed RF fish to two weeks or four weeks of vinclozolin, or no vinclozolin control conditions, at the environmentally relevant concentration of 2μg/day and then assayed their ability to socially learn. All male or all female groups of four fish were trained in a simple maze task for five days and individually tested on day seven. Learning was measured by recording the number of correct entries, latency to enter the correct chamber, and overall trial score. Time spent shoaling in groups was also recorded. Vinclozolin decreased the overall social learning rates in both high and low treatments. Irrespective of vinclozolin exposure, females learned faster than the males, potentially because they spent more time shoaling. The results show that exposure to vinclozolin effects the guppy's ability to socially learn a novel foraging task and adds to a growing body of literature that EDCs influence complex behavior.

Evolution of tetrodotoxin resistance in avian voltage-gated sodium channels

Joel McGlothlin

Monday, June 23, 2014 -Poster #48

Voltage-gated sodium channels (Nav), which mediate action potentials in excitable tissue, are targets for a variety of naturally occurring neurotoxins such as tetrodotoxin . For this reason, these proteins have become a model system for studying the evolution of toxin resistance in both toxic prey and the predators that consume them. Vertebrates possess between 4 and 10 Nav proteins, which vary in their tissue specificity and physiological properties. Previous work in Thamnophis garter snakes, which consume highly tetrodotoxic Taricha newts, has shown that the evolution of resistance to TTX involves independent evolution in at least 3 Nav paralogs. Although snakes are the most common predators of newts, other species, particularly a number of birds, are also known to consume newts without lethal effects, suggesting that avian Nav paralogs may have evolved TTX resistance in parallel. Here, I present preliminary results from a comparative study of Nav in birds, which indicate that at least two lineages of birds have evolved resistance to TTX in at least two key Nav paralogs. My results suggest that certain lineages of birds may be predisposed to enter coevolutionary arms races with tetrodotoxic prey.

Do inbred lines of guppies, Poecilia reticulata, vary in their lateral line morphology?

Alexander Tavares, Brendan Hughes, James Goodrich, Bronwyn Bleakley

Monday, June 23, 2014 -Poster #49

The fish lateral line is a neural sensory organ that detects the strength and direction of vibrations in water. The lateral line contributes to the coordination of shoaling and other social behavior by providing mechanosensory information about the location and movement of social partners. Effective coordination of shoaling plays a critical role in cooperative antipredator behavior, social learning, and other social behaviors in small schooling fish, such as guppies (Poecilia reticulata). Inbred lines of guppies are known to vary in many aspects of their behavior, including the degree to which they will shoal with, learn from, or cooperate with social partners. The outcomes of these behaviors have important fitness consequences for fish in the wild, but little is known about the proximate mechanisms that might generate individual differences in responsiveness to social partners. Such differences may result in part from micro-anatomical differences in the lateral line. To investigate the possibility that differences in lateral line morphology could structure interactions between social partners, we first investigated whether inbred lines of guppies vary in lateral line morphology. We measured the number and density of neuromast bundles present in the lateral line of adult male guppies from several strains using live-staining florescent DASPEI dye. In addition, we measured differences in the relative intensity of florescence to estimate the average number of hair cells present in neuromast bundles, which will affect the sensitivity of the organ.

Influence of physical barriers to gene flow in a widespread passerine

Theresa Burg, Rachael Adams

Monday, June 23, 2014 -Poster #51

Geological and ecological barriers restrict dispersal and gene flow, leading to isolated populations. Barriers can be obvious physical structures in the landscape; however microgeographic differences can also lead to genetic isolation. Our study examined dispersal barriers at both macro- and micro-geographical scales in the black-capped chickadee, a resident North American songbird. Although birds have high dispersal potential, evidence suggests dispersal is restricted by barriers. The chickadee's range encompasses a number of physiological features which may impede movement and lead to divergence. Analyses of 913 individuals from 34 sampling sites across the entire range using 11 microsatellite loci revealed as many as 13 genetic clusters. Populations in the east were largely panmictic whereas populations in the western portion of the range showed significant structure which often coincided with large mountain ranges, such as the Cascade and Rocky Mountains as well as areas of unsuitable habitat. Unlike populations in the central and southern Rockies, populations on either side of the northern Rockies were not genetically distinct. Furthermore, Northeast Oregon represents a forested island within the Great Basin; genetically isolated from all other populations. Substructuring at the microgeographical scale was also evident within the Fraser Plateau of central British Columbia, and in the southeast Rockies (CO and NM) where no obvious physical barriers are present, suggesting additional factors may be impeding dispersal and gene flow. Dispersal barriers are therefore not restricted to large physical structures, though mountain ranges and large water bodies do play a large role in structuring populations in this study.

Molecular evolution of lynx1, a gene involved in learning

Joanna Warren, Michael McQuillan, Kristin Anderson, Thomas Fox, Jacquelin Botello, Julie Miwa

Monday, June 23, 2014 -Poster #52

Song learning is important for fitness in birds. Birds able to learn their songs better may be more effective in attracting mates, communicating, and identifying species. There are various types of song learners. Closed-ended learners learn their song late in year 1, year 2 or even year 3, while open-ended song learners memorize and rehearse new songs throughout their life. Little is known about the genetic basis for this variation. One candidate gene associated with memory and learning is lynx1. It is expressed in the hippocampus and forms stable complexes with the nicotinic receptors of the cholinergic system. When lynx1 binds to the receptors, it modifies their response properties, which alters learning plasticity. Removal of lynx1 in laboratory mice extends the window of plasticity beyond its normal frame, suggesting that lynx1 puts a molecular brake on learning. The sensitive period of song learning varies in length among birds; thus, interspecific variation in lynx1 may be related to song learning capabilities in different species. Here, we investigated the lynx1 gene across various bird species to test whether positive selection on lynx1 is restricted to specific lineages, and related to song learning type. We also investigated intraspecific variation in the lynx1 gene in Black Capped Chickadees. Patterns of nucleotide polymorphism and amino acid sequence variation suggest lynx1 has been the target of selection during avian evolution. Future research will investigate additional functional consequences of variation in lynx1.

Individual variation in responsiveness to indirect genetic effects on cooperative antipredator behavior in guppies, Poecilia reticulata.

Kyle Ryan, Bronwyn Bleakley

Monday, June 23, 2014 -Poster #53

Social behaviors may change in response to interactions with social partners. Traits subject to variation due to the expression of a social partner's phenotypes are termed "interacting phenotypes." Interacting phenotypes often result from indirect genetic effects (IGEs), or the effect of one individual's genotype on the phenotype of a social partner. Inbred individuals respond strongly and with little variation to IGEs of the social environment. However, it is difficult to extrapolate from inbred individuals to more genetically diverse wild populations whose constituents might vary in their responsiveness to particular IGEs. We investigated whether relative genetic variation present in a strain of guppies influences variation in responsiveness to IGEs, focal guppies (Poecilia reticulata). We compared two different strains (semi-inbred and wild type). Two inbred strains were used to provide the genetic component of the social environment (IGEs) and individuals were tested for cooperative antipredator behavior in the presence of a predator model. We found that wild type individuals (with a higher level of genetic diversity among them) responded less consistently to a standard social environment than did the semi-inbred individuals, which are characterized by a lower level of genetic diversity. In addition, individual response to IGEs varies, regardless of strain, providing ample substrate on which natural selection could act to shape interacting phenotypes. Despite variation in responsiveness, we were still able to detect specific effects of social environment, suggesting that IGEs may be important in wild populations of guppies.

Molecular phylogeny of some Sarcophaginae (Diptera:Sarcophagidae)

Ronald DeBry, Evan Wong, Gregory Dahlem, Eliana Buenaventura

Monday, June 23, 2014 -Poster #54

Sarcophagidae is a family of Diptera comprising ~2500 species worldwide. The family's common name – flesh flies – derives from the fact that a small minority of species have larvae that feed on carrion. The largest of 3 subfamilies, the Sarcophaginae, have recently been the subject of phylogenetic analyses using both morphological and molecular (mtDNA) data sets. These analyses produced results that differ in some important respects. For example, the morphological data support inclusion of the genus Helicobia within the largest genus in the subfamily, Sarcophaga, while the mtDNA data support a monophyletic Sarcophaga, but do not clearly distinguish between Helicobia and Peckia as sister to Sarcophaga. Here we present new nuclear data to explore whether or not the current molecular-based understanding of the phylogeny of Sarcphaginae is biased by reliance on only mitochondrial data, or if the nuclear data reinforce the distinctions between the molecular and morphological phylogenies.

Differential ecomorphological diversification in Paleozoic lobe-finned fishes (Sarcopterygii)

Bryan Juarez, Lauren Sallan

Monday, June 23, 2014 -Poster #55

More than 100 studies over the past decade have examined adaptive radiations of extant lobe-finned fishes (Sarcopterygii), yet we know remarkably little about the mode and tempo of the first 100 million years of sarcopterygian evolution despite the relative abundance of fossil data. It is within the Paleozoic (~540 to ~252 mya) that sarcopterygian fish might have undergone ecological release: increased trait variation associated with broader habitat or resource use or predator/competitor extinction. Living sarcopterygians include ~7,000 amphibian, ~5,000 mammal, ~20,000 reptile, a few lungfish and 2 coelacanth species. The fossil record of aquatic sarcopterygian fishes and terrestrial tetrapodomorphs from the Paleozoic offers a unique opportunity to study patterns of ecomorphological evolution which might be general for vertebrates. Due to the long sarcopterygian fossil record, we are able to model both disparity and diversity at discrete and continuous time intervals during which global biotic and abiotic catastrophes impacted life. Previous research has shown that the Hangenberg mass extinction reshaped ecosystems such that terrestrial sarcopterygians became dominant while aquatic sarcopterygians declined; it remains unclear how this event fully impacted ecological diversity and diversification within the clade. To study these patterns of diversity and disparity, I have thus far created a database of ~400 sarcopterygian species in which I am compiling information on every known fossil and extant lungfish, coelacanth, and tetrapodomorph sarcopterygian fish (excluding tetrapods). In this database I will also be collecting GPS coordinates, geological age and locality, abundance, depositional environment, ecological environment, and morphometric data including but not limited to lateral reconstructions and body sizes. Here I present preliminary results on my use of statistical model-fitting approaches and geometric morphometrics to test for the following: 1) the validity of modeling the initial Silurian evolution and Late Devonian diversification of sarcopterygians as an adaptive radiation, and 2) the differential timing of evolution in cranial and post-cranial traits.

Body-size evolution and diversification in birds: do smaller taxa exhibit higher diversification rates?

Simón Quintero Corzo, Laura Natalia Céspedes Arias, Angela Perilla, Anny Pan, Elkin Tenorio

Monday, June 23, 2014 -Poster #56

One of the most striking macro-evolutionary patterns is the extreme variation in species richness among phylogenetic lineages. One of the hypotheses posed to explain such pattern is that species with smaller body size exhibit higher diversification rates than species of larger size. To test for the relation between body size and diversification rates, we first mapped mean body masses on a nearly complete phylogeny of extant birds. Then, we analyzed the relation between body size and speciation and extinction rates, using the quantitative state speciation and extinction (QuaSSE) likelihood-based method on 20 randomly chosen trees. Our analyses revealed high phylogenetic signal for avian body size (lambda = 0.97), and consistently supported a unimodal relationship between body size and diversification rates, where species with intermediate body size exhibit greater speciation rates.

Consistent patterns of ecomorphology and functional trade-offs in the evolution of discretely different feeding systems in rodents

Dallas Krentzel, Kenneth Angielczyk

Monday, June 23, 2014 -Poster #57

The rodent feeding system is unique among mammals in its combination of antero-posterior jaw movements, spatially segregated dental arcade, and the number of adductor muscle divisions and their numerous orientations. Between different groups of rodents, each of these components are structured and function in discretely different ways, with the obvious and potentially most important difference occurring in masseter muscle configurations (MMCs). There are four main MMCs, one of which is similar to the primitive condition for rodents but belongs to only one extant species, while the other three MMCs are highly derived and each seem to have evolved a number of times independently. Vast ecomorphological radiations, ranging from folivores to piscivores, have occurred within each clade that independently evolved derived MMCs. This pattern challenges the traditional view that each distinct type of MMC is good for a certain feeding style, such as specialized chewing or gnawing. An open question is thus whether functional differences in MMC require morphologically distinct tactics for exploiting the same diets. We used 3D linear morphometrics of mandibles sampled across clades of independently evolved MMCs to assess whether ecomorphology remains consistent despite dramatic qualitative differences in MMC. Our results support ecomorphological similarity across MMCs when using simple characteristics of the dentition and mandible shape in comparison with diet data using canonical discriminate analyses. We also found a consistent evolutionary trade-off in predicted gnawing vs chewing adaptations across MMCs based on the depth of the incisor beam and occlusal surface area of the cheek teeth. A more densely sampled set of taxa across the phylogeny will be necessary to confirm these coarse results, but these data are suggestive of universal patterns in rodent ecomorphology that may be useful for understanding the evolution feeding biomechanics in the morphologically complex rodent masticatory apparatus, as well assessing the ecomorphology of fossil taxa.

DNA-based Species Delimitation of the Agriculturally Important Genus, Ravinia (Diptera: Sarcophagidae)

Evan Wong, Gregory Dahlem, Ronald DeBry

Monday, June 23, 2014 -Poster #58

Members of the genus, Ravinia Robineau-Desvoidy, 1863 (Diptera: Sarcophagidae) are closely associated with man and have a direct impact on the environment with their role in vertebrate waste decomposition. The genus Ravinia is among the most common of all flesh flies collected in North America; comprising ca. 25-33% of all Sarcophagidae specimens in institutional collections. Previous studies within this genus have relied on diagnostic morphological characters, which for many species of Ravinia are variable or have yet to be found that uniquely identify the species. Research we have conducted shows that discordance is present between the morphological characters used to identify species and the mitochondrial DNA (mtDNA) phylogeny inferred using the loci cytochrome oxidase subunit I and II (COI and COII). This conflict could be indicative to the presence of cryptic species, or a result of incomplete lineage sorting or mitochondrial introgression. In order to better understand the relationships among species within this genus, we conducted a species delimitation study using DNA-based coalescent methodologies with a data set of 2 mtDNA loci and 5 nuclear loci. In addition, we compare currently used methods that require a priori species assignments and those that do not, when inferring species limits.

Diversification in the Hexapoda (Insects and their relatives)

James Rainford, Peter Mayhew, Michael Hofreiter, David Nicholson

Monday, June 23, 2014 -Poster #59

Hexapoda (insects and their relatives) is the most diverse terrestrial group of organisms on the planet and collectively comprise over half of all described species. Any attempt to understand the history of life on land and the assembly of terrestrial ecosystems is thus incomplete without consideration of the pattern of hexapod diversification and how the potential drivers of this richness have acted through evolutionary time. Previous work on understanding the history of hexapod diversification has either focused on patterns within the fossil record, which for hexapods is highly incomplete, or has been taxonomically restricted and so unable to consider the wider phylogenetic context. Here I present a first attempt to explore patterns of diversification within hexapods using an explicit dated phylogenetic hypothesis for the group and the application of birth-death models. These models confirm the roles of flight and complete metamorphosis as key innovations driving hexapod diversification. Subsequent reductions in diversification are recovered for several relic groups previously identified as having a higher fossil diversity during the Mesozoic. In addition a number of recently derived taxa are found to have radiated at an elevated rate following the development of flowering plant (angiosperm) floras during the mid Cretaceous. Taken together these results identify key developmental innovations responsible for hexapod richness and differing responses of various hexapod groups to environmental changes from the mid Cretaceous floral transition to the present day.

Following in Wallace's footsteps: investigating species diversity & biogeography of the onchidiid slugs in the Indo-West Pacific

Tricia Goulding, Benoît Dayrat

Monday, June 23, 2014 -Poster #60

In his travels Alfred Russel Wallace noted a sharp biogeographic division in the terrestrial fauna of the Indo-Malay Archipelago, which was later named the "Wallace Line". Modifications of this faunal boundary have been proposed but it has held as an important division between organisms of Asian origin versus those of a mix of Australian and Asian origin. Current data on species distribution of coral reef species (mostly corals and fishes) have not indicated a broad division of marine fauna between the western and eastern regions of the archipelago analogous to Wallace's Line. Instead, they have shown a center of exceptionally high diversity in an area of the archipelago known as the "Coral Triangle." Coral reef diversity patterns have been assumed to apply to the fauna of other marine habitats in the Indo-West Pacific, but many invertebrates of the region are un-studied, especially in mangrove ecosystems. In order to investigate patterns of species diversity and distribution of mangrove invertebrates, extensive fieldwork is being conducted to sample all of the major groups of mangrove gastropods from across the Indo-West Pacific, and DNA sequencing is being used to delineate species. Results will be presented on the slug family Onchidiidae, one of the most abundant and diverse groups of animals in mangroves, as well as other gastropod taxa. Information on species diversity and distribution of mangrove gastropods will be interpreted in light of various historical processes, such as changes in sea level, which might have shaped diversity in this marine system.

Color, not gill number, resolves clade assignments within the Paguristes/Areopaguristes hermit crab complex

Catherine Craig, Darryl Felder

Monday, June 23, 2014 -Poster #61

A large component of the 15,000 species of decapod crustaceans is represented by Anomura, a group with highly modified, non-ambulatory 4th and 5th pereopods. The superfamily Paguroidea includes hermit crabs and king crabs and comprises half of the 2,451 anomuran species. Repeated revisions of the superfamily have relied exclusively on morphological evaluation of adults, larval forms, and spermatophore structure. More recently, molecular markers and modern phylogenetic techniques have been incorporated into decapod systematics. However, as decapod systematics shifts focus to relationships within families and genera, significant conflict between morphological and molecular data is developing. With many traditionally used characters now being of questionable utility, a search for new diagnostic morphological features has ensued. Gill pair number, which has been viewed as a fundamental trait that is unlikely to vary among closely related taxa, has become a key character. An entire genus, Areopaguristes, was erected from within the genus of over 100 species, Paguristes. This new genus accomodates taxa with 12 pairs of gills rather than 13. Because of the assumed stability of gill number, Areopaguristes has been treated as monophyletic, but as molecular evidence mounts, the genus becomes phylogenetically unstable. With recent collections of molecular data ever more tightly clustered, species complexes continue to emerge that include both 12- and 13-gill forms. In contrast to the decreasing utility of gill pair number in delineating species within the Paguristes/Areopaguristes complex, a combination of nuclear and mitochondrial genes tell a story of how color may function as a useful character in systematic analyses. With modern photographic techniques and improved collection methods, color pattern in hermit crabs can be accurately documented and included in analyses. In the present analysis, color and pattern are superimposed on a molecular phylogeny of the Paguristes/Areopaguristes complex and closely related groups are found to be united by shared color schemes, regardless of present genetic assignment. The pattern and coloration of head appendages in particular forms distinct color-sets consistent with underlying molecular phylogeny. In a striking initial case, species with dark banded eyestalks formed a clade distinct from another with primarily blue eyestalks. Color evidence is now found to support at least two further molecular genetic clades of this complex, underscoring the importance of color pattern evolution in this decapod group.

Molecular Phylogenetics of North American Ribbonsnakes

Larimy Brown, Bradley Martin, John Placyk

Monday, June 23, 2014 -Poster #62

The eastern (Thamnophis sauritus) and western (T. proximus) ribbonsnake are currently distinguished solely on morphology (e.g., coloration) and geographic distribution. Both species also currently include multiple subspecies defined on similar grounds. We used mtDNA sequencing and molecular barcoding data to determine if the two currently recognized species and their respective subspecies can be supported using molecular phylogenetic analyses. Our results indicate that 1) the eastern and western ribbonsnakes are separate species, 2) the four eastern subspecies are supported by our analysis, and 3) the five western subspecies are not supported by our analysis. The lack of genetic differentiation in the western ribbonsnake may result from intensive hybridization.

Enhanced phylogeographic information of the Green Woodpecker and the Acorn Woodpecker

UTKU PERKTAS, HAKAN GÜR, TOWNSEND PETERSON

Monday, June 23, 2014 -Poster #63

The late Quaternary glacial–interglacial cycles strongly influenced the demographic pattern and genetic structure of many bird species. Genetic and demographic responses of some bird species such as sedentary woodpeckers against this influence have been recognized differently in various regions of the world. For example, there are similarities and differences in demographic responses between bird species within North America and Europe. In the light of the similarities and the differences, we better investigated the generality of recognized patterns of North American and European phylogeography for two widespread sedentary woodpecker species, one from Europe (the Green Woodpecker Picus viridis), and one from North America (the Acorn Woodpecker Melanerpes formicivorus). For this aim, we reevaluted previously published data for these species using molecular phylogeography and ecological niche modelling (ENM). The molecular phylogeography and the ecological niche modelling results match each other, and indicate that the Green Woodpecker shows contraction pattern during the last glacial maximum (LGM), whereas the Acorn Woodpecker shows expansion during the LGM.

Genetic basis of adaptive developmental traits in Drosophila melanogaster: phenotypic variation and plasticity in natural-derived populations

Alejandra Petino Zappala, Victoria Ortiz, Ignacio Satorre, Julián Mensch, Valeria Carreira, Juan José Fanara

Monday, June 23, 2014 -Poster #64

The study of the genetic basis of phenotypic variation in natural populations is critical to understand the mechanisms and processes involved in adaptation. Here we show results addressed to analyze the genetic variability, phenotypic plasticity and environmental sensitivity for developmental adaptive traits in D. melanogaster. We utilized isogenic lines derived from two nearby natural populations of Argentina located at different altitude as well as isogenic lines of the Drosophila Reference Genome Panel derived from Raleigh (NC) that was considered also as a lowland population.

Larval and pupal Developmental Times (DTs) were estimated in individuals reared at different temperature (25ºC and 17ºC) to investigate developmental plasticity whereas the robustness was calculated by means of their environmental variability. Larval and pupal DT exhibited a particular variation pattern for each population that differs between these developmental stages suggesting a decoupling between larval and pupal DT. Since these results are consistent with previous observations, where lines derived from different populations and mutagenized lines were analyzed, we considered larval and pupal DT as different traits. These two traits presented significant genetic variation among populations as well as differences in their robustness although the levels of plasticity were similar among them. We observed that the populations differ in their DT and that differences are temperature specific. In fact, lines from lowland population of Argentina showed higher DTs when larvae were reared at 17º whereas at 25ºC the highest DT correspond to lines derived from the highland population. Our results indicate that these developmental traits showed specific temperature-populations dynamics. We will perform GWAS in these lines to compare the genetic basis of phenotypic adaptive developmental traits variation among all three populations and associate these variations with ecological diversity.

Quantitative genetics of micro-environmental plasticity in Drosophila melanogaster

Fabio Morgante, Daniel Sorensen, Peter Sørensen, Christian Maltecca, Trudy Mackay

Monday, June 23, 2014 -Poster #65

The term ‘environmental plasticity’ is used to describe changes in the mean of a quantitative trait phenotype associated with a defined change of macro-environmental conditions as well as responses to micro-environmental variation that cannot be attributed to a specific perturbation. Environmental plasticity can have a genetic component. In the case of variation among macro-environments (e.g. temperature, level of nutrition), genetic variation in plasticity gives rise to genotype by environment interaction. Genotype by environment interaction for a quantitative trait can be readily quantified by rearing the same genotypes in different macro-environments. Less well known and readily quantifiable is genetic variation for micro-environmental plasticity, which requires rearing the same genotypes within the same macro-environment, and determining whether the residual, or environmental, variance differs among genotypes. The existence of genetic variance for micro-environmental plasticity has evolutionary implications, as it implies that selection and other evolutionary forces may act on it favouring, for example, genotypes producing a greater or smaller range of phenotypes under the same micro-environmental conditions.

Here, we used the Drosophila melanogaster Genetic Reference Panel (DGRP), a collection of 205 inbred fly lines with complete genome sequence, to estimate the heritability of environmental plasticity for two traits, chill coma recovery time and startle response. Furthermore, we also performed genome wide association studies (GWAS) to map molecular variants associated with micro-environmental plasticity for the two traits.

Estimates of broad sense heritabilities for both traits are substantial (from 0.51 to 0.77), of the same order as the heritability at the level of the trait mean for startle response and even larger for chill coma recovery. Genome wide association analyses identified molecular variants (from 15 to 31 depending on the sex and the trait) associated with micro-environmental plasticity.

Micro-environmental plasticity is thus under strong genetic control in D. melanogaster. This opens to the hypothesis that evolutionary forces may act on micro-environmental plasticity. There is almost no overlap among variants associated with micro-environmental plasticity and variants associated with mean performance for both traits analyzed. The GWAS have suggested candidate genes for future validation using genetic resources available in D. melanogaster.

Testing adaptive plasticity: Are the effects of social density on offspring size consistent over multiple food regimes in Heterandria formosa

David Hoover, Joseph Travis

Monday, June 23, 2014 -Poster #66

Adaptive plasticity has been documented in the least killifish, Heterandria formosa, in their ability to adjust the size of their offspring in response to conspecific density. In this study, we assigned females from a single river to one of four density treatments in order to determine the shape of the reaction norm. The responses of these females to the social density were compared across three food regimes to conclude how consistent this plasticity remains given contextual differences. The results from this project give insight into the nature of adaptive plasticity and the reliability of phenotypic cues upon which evolution can be expected to act.

The origins of adaptive plasticity: Using experimental evolution to examine costs, benefits, and constraints in the evolution of trait plasticity

Noah Gettle, Michael Travisano

Monday, June 23, 2014 -Poster #67

All organisms possess the ability respond to changes in their environment. The range of adaptive plasticity among traits and among organisms, however, can be quite dramatic, suggesting that the adaptive value of plasticity varies across environments. What, then, are the conditions that promote or constrain the evolution of trait plasticity? Theoretical models suggest that plasticity should evolve in heterogeneous environments in which the optimal phenotype varies with the environment, unless constrained by certain costs or limitations. Although, numerous suggestions have been made as to the source of these costs, empirical examinations have remained limited. Using experimental evolution techniques with a new multicellular strain of yeast (Saccharomyces cerevisiae) I am exploring the environmental conditions under which we see the evolution of fixed versus plastic responses. Using this system, I am exploring the relative costs of fixed and plastic adaptive responses to the environmental stressors under which they evolved as well the molecular underpinnings of these adaptations.

Natural variation, plasticity and tradeoffs of ecophysiological traits in the Brachypodium distachyon (Poaceae) ploidy complex

Antonio Manzaneda, Pedro J. Rey, Jill Anderson, Tom Mitchell-Olds

Monday, June 23, 2014 -Poster #68

Water stress is one of the main abiotic factors that limit the distribution and abundance of plants and one of the major selective forces that promote local adaptation in plants. Water use efficiency (WUE) and flowering time are key traits intrinsically related to dehydration avoidance and drought escape, respectively, which have a direct impact on fitness of plants growing in water-restricted environments. However, evolutionary menchanisms that maintain natural variation in those traits are still poorly known. Beyond of variations in the nucleotide sequence, other heritable genomic changes such as genome duplications may influence importantly phenotypic trait variation and be also subjected to natural selection. We used the Brachypodium distachyon ploidy complex as study system. We performed a comprehensive assessment of the inter-individual natural variation and plasticity of ecophysiological drought tolerance-related traits within and between diploids B. distachyon (2n= 10) and allotetraploids B. hybridium (2n =30) accessions collected from multiple wild populations across the Iberian Peninsula and grown under contrasting watering regimens. By documenting the magnitude of variation in ecophysiological drought tolerance-related traits within and between natural Brachypodium populations, we detected adaptive signals in relation to variations in aridity in the pattern of trait and plasticity variation in this system. Furthermore, we uncover extensive genetic differentiation among Brachypodium populations, and this differentiation is geographically structured. Allotetraploids are more drought tolerant than diploids, which is reflected in their ecological distributions and could underlie the ecogeographical segregation of cytotypes in nature. Our results show that ploidy variation, adaptation and plasticity play an important role in explaining natural variation in drought-tolerance related traits in Brachypodium distachyon complex. Although we found significant genetic variation in most ecophysiological traits, adaptive evolution of drought tolerance-related traits could be constrained by the presence of low levels of standing genetic variability and significant genetic correlations, in particular within B. distachyon diploid populations. Finally, our study corroborates the hypothesis that the divergence in ecological tolerance to water stress between Brachypodium ploidy lineages is a driver of ecogeographical differentiation in this species complex.

Incipient speciation between two races of Drosophila athabasca

Roman Yukilevich

Monday, June 23, 2014 -Poster #69

Here I study a recent case of divergence within Drosophila athabasca, a temperate forest species in North America containing partially overlapping geographical races. I characterize sexual isolation between these races, determine the intrinsic fitness costs of hybrids both at the behavioral and fecundity levels, and characterize phenotypic and pheromonal divergence that has occured in this species. These results provide a context for understanding the underlying mechanism by which this species has speciated into multiple behavioral races.

Fine-scale Local Adaptation: case study of thermal tolerance of Tigriopus californicus

Lori Luers, Ricardo Pereira, Ron Burton

Monday, June 23, 2014 -Poster #70

Extrinsic differentiation evolves prior to the establishment of intrinsic incompatibilities among neighboring populations of Tigriopus californicus.

Both extrinsic and intrinsic factors may play a role in speciation. Extrinsic selection can lead to local adaptation and pre-mating isolation while intrinsic selection can result in post-zygotic reproductive isolation. Whether these processes can occur at a fine spatial scale, where populations diverged recently or experience gene flow, remains a topic of debate. Previous studies of the intertidal copepod Tigriopus californicus have shown that F1 hybrids between populations as little as 8 km apart (Bird Rock and San Diego) show reduced fitness (hybrid breakdown). Here we consider population differentiation at even a finer scale. We sampled every outcrop inhabited by T. californicus from La Jolla (LJ) to Bird Rock (BR) - a total of 25 sites sampled over 5 km of coastline. Sequencing of one mitochondrial gene and at least one nuclear gene will be used to determine population differentiation and connectivity. Hybrid crosses were performed to examine intrinsic selection, while heat stress experiments were performed to examine extrinsic differentiation. Significant differences in thermal tolerance were observed among populations only 1.6 kilometers apart. Despite these observed ecological differences, interpopulation hybrids between LJ and BR, did not show any evidence of hybrid breakdown. Therefore, our preliminary results suggest that populations of T. californicus may exhibit ecological differentiation (and possibly local adaptation) prior to exhibiting evidence of intrinsic incompatibility.

The Genetic Basis of an Incident of Incipient Speciation in Nasonia Wasps

Ashley Saulsberry

Monday, June 23, 2014 -Poster #71

Hybrid incompatibilities are thought to evolve over long periods of time, which prevents biologists from studying the speciation process as it happens. In our lab we have discovered a novel hybrid incompatibility between two species of Nasonia wasps, thereby giving us an unprecedented chance to study speciation and how reproductive barriers can evolve in a short period of time. When Nasonia wasps are cured of their natural Wolbachia infections, the different species can normally interbreed to produce viable F1 hybrid offspring. However, crosses between females of the N. longicornis strain IV7R3-1b and N. vitripennis males have recently been observed in the lab to result in a new F1 hybrid mortality. The F1 mortality is unidirectional, suggesting the incompatibility arose between N. vitripennis nuclear DNA and either N. longicornis maternal effect genes or mitochondrial genes. In order to test the hypothesis that a cyto-nuclear interaction causes the incompatibility, the affected IV7R3-1b strain and an unaffected N. longicornis strain (NAS_NLUT 230A) were used to create two inter-strain N. longicornis hybrid lines; each of these lines contained the cytoplasm of the respective pure strains, but both had the same nuclear DNA, half IV7R3-1b and half NAS_NLUT 230A. Crosses between N. vitripennis males and females with the original NAS_NLUT 230A mitochondria exhibited less mortality than crosses between N. vitripennis males and females with the original IV7R3-1b mitochondria despite the similarity in the nuclear genomes of these inter-strain N. longicornis hybrid lines. However, mortality was not complete as originally seen in the IV7R3-1b strain, suggesting hybrid vigor or a nuclear-by-mitochondria interaction rescues some of the hybrid inviability. Future experiments will resolve these two possibilities as well as deploy whole mitochondrial sequencing to decipher the substitutions that underscore this newly evolved hybrid incompatibility.

Genetic architecture of hybrid "less-function" in the nematode Caenorhabditis briggsae

Joseph Ross, Kevin Pham, Jordan Montgomery, Brandon Ortega

Monday, June 23, 2014 -Poster #72

Two biological species can be established when genetic variants in two populations cause dysfunction (loss of viability or fertility) when combined in hybrids by mating. Although the study of species formation has been pursued for generations, identifying the genes that interact to produce hybrid dysfunction has often been difficult. Traditional genetic mapping is not a feasible approach for identifying genes causing inviability or sterility. Further, it is likely that speciation is a multi-step process and that alleles typically identified as speciation genes do not represent the variants that might initially have caused hybrids to have lower fitness than their parents. Thus, a useful approach for studying the evolution of speciation is to identify genes that epistatically interact to cause not hybrid dysfunction (fitness = 0), but hybrid "less-function."

In the nematode Caenorhabditis briggsae, a close relative of C. elegans, two such phenotypes have been identified. In one case, a fraction of F2 hybrids experiences a developmental delay. Results of crosses meant to probe the genetic architecture of developmental delay suggest either a complex basis or non-Mendelian inheritance. Efforts to identify the genetic basis of developmental delay include both near-isogenic line (NIL) and advanced-intercross recombinant inbred line (AI-RIL) mapping approaches.

In the other case, hybrid genotype data suggest that a mitochondrial-nuclear incompatibility exists between two populations of C. briggsae. To support this hypothesis, phenotype data including life history and mitochondrial traits have been collected from the two populations as well as from cytoplasmic-nuclear hybrids. Indeed, fecundity and reactive oxygen species levels are often affected in these hybrids. Future efforts to identify the loci involved will entail genetic mapping and deep sequencing approaches. Additional directions common to both research projects are to identify the evolutionary history of the underlying variants and to test the hypothesis that mitochondrial dysfunction is involved in producing hybrid developmental delay.

Colocalizing quantitative trait loci control pre- and post-mating female choice in Drosophila

Cheng-Ruei Lee, Cheng-Lin Li, Shun-Chern Tsaur, Shu Fang, Chau-Ti Ting

Monday, June 23, 2014 -Poster #73

Speciation is the process in which inter-mating populations become reproductively isolated lineages. While gene flow homogenizes the genetic differentiation among populations, reproductive isolation is essential to reduce gene flow among lineages. Separated by the mating and zygote formation events, reproductive isolation consists of three components: pre-mating, post-mating pre-zygotic, and post-zygotic isolation. Although genetic mapping studies have identified many separate genomic regions or individual genes controlling these traits, whether or how the existence of genetic correlation among different components of reproductive isolation may constrain or facilitate speciation remains unknown. Here we investigated the genetic architecture of female choice in the pre-mating and post-mating pre-zygotic components of reproductive isolation. We performed quantitative trait loci (QTL) mapping on observable (mating latency and duration) and cryptic (conspecific sperm precedence) female choices between D. simulans and D. mauritiana via backcrossing hybrid F1 females to parental D. mauritiana males. Interestingly, 'copulation latency to D. simulans males' and 'proportion of progeny sired by D. simulans males' have colocalizing QTL, with largely overlapping confidence intervals and QTL peaks differing by merely 4 cM. In addition, the QTL effects act consistently towards reproductive isolation: having a D. simulans allele in the QTL confers faster mating to D. simulans males by ~10 minutes and higher proportion of progeny sired by D. simulans males by ~0.2, while D. mauritiana homozygotes have the opposite. This colocalizing QTL contributes significantly to the correlation between these two traits, suggesting that one genomic region can simultaneously promote reproductive isolation in two different stages of female choice. The widespread and consistent effects of this QTL are shown in two independent experiments with different genomic backgrounds and experimental procedures, where the D. simulans allele significantly increased the proportion and number of progeny sire by D. simulans while having no effect on the number of progeny sired by D. mauritnana. In addition, cryptic female choice is controlled by a few other genomic regions with varying effects. In summary, we identified a genomic region with synergistic effects promoting reproductive isolation in two different stages of female choice, and this dual-effect QTL controls cryptic female choice in different D. simulans genomic backgrounds. Finally, the genetic architecture of cryptic female choice between these two species is complex, with multiple genomic regions each with different effects on the number of progeny sired by D. simulans or D. mauriana.

Sex, flies, and videotape: behavioural phenotypes of adaptation in Certititis capitata

William Nash

Monday, June 23, 2014 -Poster #74

The role played by ecological adaptation in the promotion of speciation is currently receiving renewed interest. There is growing support for the importance of indirect effects of adaption to divergent environments in the induction of reproductive isolation. We use experimental evolution to examine the role that adaptation to larval dietary nutrients can have on the instigation of reproductive isolation in the highly polyphagous Mediterranean fruit fly, Ceratitis capitata. Using selection lines reared from high and low nutritional backgrounds, we tested for isolation between treatments using quartet mating tests. We also employed video analysis of courtship behaviour to examine the effect of adaptation to diet on behavioural phenotypes. We show that the diets selected for different courtship strategies and adaptive physiological changes over the duration of selection. However, there was no diet-induced reproductive isolation. The results are important as they demonstrate how nutritional background can effect behaviour. They also highlight candidate behaviours on which future divergence leading to reproductive isolation could be based.

Comparative phylogeography of three rock dwelling lizard species gives unparalled insights into the speciation process in southern Africa.

Stuart Nielsen, Brice Noonan, Krystal Tolley, Aaron Bauer

Monday, June 23, 2014 -Poster #75

Geology, geography and changing climate have all played a role in shaping the distribution of organisms in southern Africa, particularly for species spanning the arid/semi-arid Karoo biome. Using comparative phylogeography, we explored patterns within three co–distributed yet distantly related, rock-dwelling lizard species: the southern rock agama, Agama atra; Bibron's gecko, Chondrodactylus bibronii; and the Karoo girdled lizard, Karusasaurus polyzonus. All three taxa are saxicolous, greatly utilizing the geologically complex, ancient, rock formations found throughout the subcontinent; yet differ in period of daily activity, social structure, and microhabitat use (although C. bibronii has been observed inhabiting the same rock cracks with either K. polyzonus or A. atra). In many regards C. bibronii could be considered a 'rock generalist,' often living in rocky habitat unsuitable for either A. atra or K. polyzonus. This habitat 'leniency' could potentially erase significant, informative genetic signal, as it would allow for better individual dispersal throughout this species' range. In light of this, we hypothesized that there would be a degree of shared evolutionary history across the subcontinent between the three, particularly at recognized barriers to gene flow for other rock-dwelling organisms (e.g. the Knersvlatke plain) due to shared distribution and gross ecological requirements. Employing genetic data we asked: 1) what is the structure of 'populations' within a species, and what are the geographic boundaries of those groupings; 2) are these clusters/populations isolated (or conversely, is gene flow ongoing between them), and for how long; and 3) how have climatic shifts affected species/population distributions? The species-specific patterns granted unparalleled insight into the processes of speciation in the poorly understood arid zones of the southern hemisphere.

Molecular and behavioral correlates of premating isolation in Mus

Abby McClellan, Heather Martin, Polly Campbell

Monday, June 23, 2014 -Poster #76

Behavioral barriers to gene flow between species are difficult to measure and even harder to dissect to the level of genes. However, genes required for normal reproductive behavior are compelling candidates for assortative mating between species. In rodents, chemical communication dominates, and chemoreceptors in the vomeronasal organ (VNO) are essential for reproductive and defensive behaviors. The vomeronasal receptor (VR) gene family has undergone a major expansion in Mus (house mice and their wild relatives) with >250 putative members; individual VRs are narrowly tuned to distinct chemical compounds present in urine and other excretions, and different receptors are activated by conspecific vs. heterospecific cues. Species differences in degree of geographic range overlap, the costs incurred by females who mate with males from the wrong species, and the prevalence of hybridization in nature, provide a natural experiment in which to study the genetics and evolution of premating isolation. We present results from preliminary molecular and behavioral experiments whose goal was to quantify the acuity of VNO-mediated discrimination among male chemosignals. We exposed females from two house mouse subspecies to male chemical cues from consubspecifics, heterosubspecifics, or co-distributed heterospecifics. In experiment 1 we measured the relative expression of a suite of VRs previously identified as responding with high specificity to conspecific vs. heterospecific male cues. In experiment 2 we used a spatial memory test to compare innate female preference for the three classes of male cues. We find that females exhibit stronger molecular and behavioral response to conspecific vs. heterospecific male cues. These results provide preliminary support for VNO-mediated species discrimination in mice, and motivate future work on this system.

Selection Response for Stamen Accuracy (Precision and Bias) in Brassica rapa

Carolina Diller, Charlie Fenster

Monday, June 23, 2014 -Poster #77

Introduction: Trait variability may result from developmental noise and lack of genetic and environmental canalization as well as from conflicting selective pressures which deviate the population mean from the adaptive optimum. In the literature, these two sources of variation have been described mathematically as: accuracy = precision + bias. Precision is the variance of a trait and bias is the difference between the mean of the trait to the mean of the optimum. The goal of this study was to select for these two sources of variation independently and verify whether: 1. there was a selection response 2. if there was a correlated response across whorls. For this purpose, we focused on the trait precision of the two whorls that are directly involved in the pollination performance and reproductive success: the androecium and the pistil. The developmental stability and positioning of these two whorls will determine the efficiency of pollen removal and deposition. To facilitate the analysis we focused on male fitness, i.e stamen variability in relation to pistil variability. Stamen precision is the variability in the stamens' height within a flower. Stamen bias is the difference between the stamen mean height to its optimum.

Methods: We selected for increased and decreased stamen bias and stamen precision in Brassica rapa. We performed two replicates. In the first replicate, we selected for 5 generations and performed a within family selection design with 49 families. We measured two flowers per individual, and had two individuals per treatment. For replicate 2, we selected for 2 generations and applied a mass selection design with a base population of 100 individuals. Here we measured 5 flowers per individual and selected top/bottom half of the population (50 individuals for the first generation and 25 individuals for the second). In addition to stamen and stigma height, we also measured petal length, petal width, corolla tube length and sepal length to check for correlational response.

Results/Conclusion: We found no significant selection response for any of the treatments in both replicates as well as no clear correlational response.

Parasite modification of predator functional response

William Newsome, Benjamin Toscano, Blaine Griffen

Monday, June 23, 2014 -Poster #79

Parasite alteration of the host (predator) functional response provides a mechanism by which parasites can alter predator–prey population dynamics and stability. We tested the hypothesis that parasitic infection of a crab (Eurypanopeus depressus) by a rhizocephalan barnacle (Loxothylacus panopei) can modify the crab's functional response to mussel (Brachidontes exustus) prey and investigated behavioral mechanisms behind a potential change in the response. Infection dramatically reduced mussel consumption by crabs across mussel densities, resulting in a decreased attack rate parameter and a nearly eightfold reduction in maximum consumption (i.e. the asymptote, or inverse of the handling time parameter) in a type II functional response model. To test whether increased handling time of infected crabs drove the decrease in maximum consumption rate, we independently measured handling time through observation. Infection had no effect on handling time and thus could not explain the reduction in consumption. Infection did, however, increase the time that it took crabs to begin handling prey after the start of the handling time experiment. Furthermore, crabs harboring relatively larger parasites remained inactive longer before making contact with prey. This behavioral modification likely contributed to the reduced mussel consumption of infected crabs. A field survey revealed that 20 % of crabs inhabiting oyster reefs at the study site (North Inlet estuary, Georgetown, South Carolina, USA) are infected by the barnacle parasite, indicating that parasite infection could have a substantial effect on the population level crab-mussel interaction.

Genetic and epigenetic response to the Deepwater Horizon oil spill in S. alterniflora

Marta Robertson, Aaron Schrey, Ashley Shayter, Christina Meals, Christina Richards

Monday, June 23, 2014 -Poster #80

In 2010, the Deepwater Horizon oil spill contaminated ecosystems along the Gulf Coast, including native stands of Spartina alterniflora. Although tragic, this event offers a unique opportunity to study population genetic and epigenetic response to stress in natural populations. Spartina alterniflora is highly stress tolerant in the salt marsh, inhabiting salt pans devoid of other species, and populations of S. alterniflora have recovered quickly from this disaster. However, no study has examined the genetic or epigenetic basis for this rapid response. We suggest that both genetic and epigenetic mechanisms may contribute to the resilience of S. alterniflora in response to the oil spill. Epigenetics is the study of changes to gene expression without alterations of the DNA sequence. DNA methylation is a commonly studied epigenetic mechanism, which can affect phenotype by modulating gene expression. Importantly, DNA methylation can be induced by the environment and can be inherited across generations. Despite growing evidence that epigenetic mechanisms are important in determining phenotype, epigenetic response to stress remains understudied. In concert with genetic variation, DNA methylation may offer an explanation for the high diversity and evolutionary potential in S. alterniflora, and may explain a mechanism of response to environmental challenges, like the Deepwater Horizon oil spill. To explore this hypothesis, we collected new growth from oil-contaminated and uncontaminated sites along the Gulf coast following the Deepwater Horizon oil spill. We examined global genetic and epigenetic changes in response to the oil spill using AFLP and MS-AFLP and found high genetic and epigenetic variation within and among contaminated and uncontaminated sites. We identify several MS-AFLP outlier loci correlated with oil exposure, suggesting a role for DNA methylation in stress response.

Analysis of the cultivated sunflower methylome

Adam Bewick

Monday, June 23, 2014 -Poster #81

Cytosine DNA methylation is an epigenetic modification that is important to genome stability and regulation of gene expression. Advancements in next generation sequencing technology are allowing us to elucidate the extent and impact of variation and patterns in DNA methylation between individuals, tissues and across the (plant) tree of life. Thus, we sought to contribute, characterize and explain the cultivated sunflower (Helianthus annuus [L.]; Compositae) methylome – an important agricultural and taxonomic species/group missing from the plant "pan-methylome". We found similar patterns of cytosine methylation within and flanking genes and long terminal repeat (LTR) retrotransposons compared to other studies. However, we showed variation of methylation among LTR families and that certain families could potentially influence methylation of neighboring genes differently. Also, certain types of genes are hyper- or hypomethylated and some characteristics of genes are significant predictors of methylation. This work contributes to our understanding of methylation in plants and provides opportunities to investigate patterns of methylation across the (plant) tree of life.

When super-organisms collide: thermal adaptation at the colony level in two ant species

Clint Penick, Sarah Diamond, Rob Dunn

Monday, June 23, 2014 -Poster #82

Unlike solitary organisms, social insects respond to environmental change as a collective. Selection may act on thermal performance traits of individual group members to produce an adaptive response at the colony level. Here we examine how two ant species–Aphaenogaster rudis and Temnothorax curvispinosus–differ in their response to temperature change with a focus on colony-level traits. Both species are broadly distributed in eastern forests in the United States, but colonies of A. rudis tend to perform better under cooler conditions compared to T. curvispinosus. We conducted a large-scale common garden experiment to determine how changes in temperature affect individual traits and lead to differences in colony growth and survival. At the colony level, survival decreased under high temperatures (up to 30ºC) for A. rudis, while the opposite pattern was observed for T. curvispinosus. Similarly, A. rudis colonies exhibited increased growth parameters under cooler conditions compared with T. curvispinosus. Changes in growth rate were associated with queen egg-laying rate, worker mortality, and brood development rate, which all co-varied with temperature. The strongest effect of temperature on colony growth was associated with brood development. A change in only 3ºC could nearly double development time. Our results begin to tease apart how selection can act on individual components of a super-organism to produce adaptive phenotypes at the colony level.

Quantitative Genetics of Food Intake in Drosophila melanogaster

Megan Garlapow, Trudy Mackay

Monday, June 23, 2014 -Poster #83

Food intake is an essential animal activity, regulated by signaling pathways, nutrient perception, taste perception, and other processes. To identify factors associated with food intake and its variation in a model system, we performed genome wide association studies (GWAS) in the Drosophila melanogaster Genetic Reference Panel (DGRP). The DGRP population is 205 wild-derived, inbred, fully sequenced D. melanogaster lines, enabling GWAS where all variants are known. We assessed food intake in 182 DGRP lines, finding highly significant genetic variation among the lines, sexual dimorphism in feeding behavior, and genetic variation in sexual dimorphism. The top hits from a GWAS for food intake were significantly enriched for components of the Epidermal Growth Factor signaling (EGFs) pathway. The role of EGFs in invertebrate food intake remains largely unexplored. Validation experiments will improve understanding of the components of the EGFs cascade that affect food intake. Next we computed the coefficient of environmental variation (CVE) of food intake within each DGRP line. CVE quantifies the variability of food intake between individuals in genetically uniform lines. We performed a GWAS of CVE and found significant genetic variation and a distinct genetic basis from average food intake, indicating genetic control of variance in food intake. Individuals within some DGRP lines consistently consume similar amounts of food, while other lines' individuals consume widely varying volumes of food. Validation experiments on the CVE GWAS-predicted genes will further elucidate its genetic underpinnings. The DGRP allows us to explore the fundamental genetic bases of food intake and its CVE in a genetically tractable population.

Long term selection experiments: The role of epistasis in the response to selection

Charles Goodnight

Monday, June 23, 2014 -Poster #84

Long term selection experiments typically show a roughly linear response to selection that can go on for extended periods, often a hundred or more generations; however, these responses this response to selection is frequently punctuated by intermediate selection plateaus. These plateaus are periods of often ten or more generations in which there is no response to selection, after which the response resumes. Typically, the explanation for these two behaviors has been on-going quantitative genetic mutations. In this study I use a two locus additive-by-additive epistatic system to show that this same behavior can be observed in a simple genetic system with gene-gene interactions. In particular, I show that in a deterministic epistatic system the response to selection can continue far longer than expected for a comparable additive system. I also show that for some starting conditions there will be intermediate selection plateaus that occur. For both the extended response to selection and the selection plateaus can be attributed to changes in the additive genetic variance and changes in the local average effects of the underlying alleles. Both of these phenomena are the result of the characteristics of epistatically interacting genetic systems, and are cannot be observed in traditional models that consider only additive effects.

A Comparison of Effective Population Size and Census Size in Three Coastal Shark Species

Hayley DeHart, Gavin Naylor

Monday, June 23, 2014 -Poster #85

Sharks are widely held by the scientific community to be threatened with extinction, and yet they remain some of the most poorly understood marine vertebrate organisms. There is belief among marine conservation biologists that population genetics based approaches can be used to distinguish species, populations, and even population sizes for these threatened animals. Estimating population sizes using multiple estimates, as well as multiple species, is critical to understanding true population sizes and life history traits that skew these estimates. This study aims to estimate census population size (Nc) from mark and recapture data in the program MARK and compare these estimates to next generation sequencing based contemporary estimates of effective population size (Ne). Utilizing a cross-species gene capture method that collects DNA sequence data from hundreds of loci from hundreds of samples in a single sequencing run, genotypic information can be used in effective population size estimates using the program NeEstimator. These methods will be executed on three separate shark species; bonnethhead sharks (Sphyrna tiburo), finetooth sharks (Carcharhinus isodon), and sandbar sharks (Carcharhinus plumbeus). These species all exhibit different population structure, life history, and recapture rates, which may in turn affect their Ne/Nc ratio. It is believed that the comparisons between these estimates and species may be utilized for conservation and management of coastal shark species.

Apocynum (Apocynaceae) through time and space: dispersal, divergence, and adaptations to temperate habitats

Elizabeth McHone, Tatyana Livshultz

Monday, June 23, 2014 -Poster #86

How species come to be distributed across the globe and what causes them to diverge or hybridize are fundamental questions in evolutionary biology. Apocynum is an excellent system for the study of these questions, in part because three (including the hybrid A. medium) out of seven species occur in North America and the rest in temperate Eurasia, all herbaceous plants with pollen in tetrads. In contrast, the majority of species in the 27 genera of tribe Apocyneae grow in tropical East Asia as lianas with pollen in monads. Preliminary phylogenetic evidence suggests that Apocynum may have colonized North America twice, but when and by which route(s) has yet to be determined. Apocynum is also a useful model system for study of the evolution and adaptive value of pollen aggregation, as it represents one of three independent origins of aggregated pollen in Apocynaceae. Aggregated pollen has been linked to higher pollen transfer efficiency (PTE) and may be adaptive in seasonal climates with unreliable or infrequent pollinators and/or more synchronous flowering and interspecific competition for pollination. Our first measurements of A. cannabinum indicate the species has a PTE intermediate to flowering plants with more- and less-aggregated pollen. Here we review previous studies of Apocynum ecology, hybridization, biogeography, and evolution, and delineate a research plan for answering questions concerning Apocynum's shift to temperate habitats, colonization of North America, and reproductive barriers between North American species.

Deep mRNA sequencing of the central nervous systems of six Nudipleura molluscs: molecular homologies and animal phylogeny.

Adriano Senatore, Neranjan Edirisinghe, Paul Katz

Monday, June 23, 2014 -Poster #87

Introduction:

Sea slugs from the Nudipleura clade (Mollusca, Gastropoda, Heterobranchia) are highly advantageous for studying the evolution of behavior because they have individually identifiable neurons that form circuits underlying simple forms of swimming. There is evidence that two different forms of swimming, dorsal-ventral (DV) and left-right (LR), may have evolved independently several times. We have previously shown that often similar subsets of neurons are used to build swimming circuits, however, there can also be significant differences in synaptic connectivity and overall circuit organization. Notably, although many important contributions have been made using these preparations, the absence of genetic information has impeded exploration at the molecular level.

Methods:

An important pre-requisite for elucidating the genetic mechanisms underlying convergent evolution of swimming behavior is the availability of gene sequences. We therefore performed deep mRNA sequencing of the central nervous systems of six Nudibranch species with different forms of swimming behavior: Tritonia diomedea (DV); Melibe leonina (LR); Hermissenda crassicornis (LR); Pleurobranchaea californica (DV); Flabellina iodinea (LR); and Dendronotus iris (LR).

Results:

This effort has provided the full length sequences of a majority of neuronal genes for all six species. We are also using the data for phylogenetic analyses aimed at resolving the phylogeny between these species, to build upon the hypothesis that DV and LR swimming arose independently in distinct phylogenetic lineages of the Nudipleura.

Consequences of hybridization for mountain bog pitcher plants and their phytotelma communities

Elise Powell, Steven Jaslow, Rebecca Hale, Jennifer Rhode Ward, Caroline Kennedy, Mara Alexander

Monday, June 23, 2014 -Poster #88

The phytotelma communities of the purple pitcher plant, Sarracenia purpurea, have been extensively described and 165 species have been found living within its pitchers. In western North Carolina, S. p. var. montana hybridizes with the endangered S. jonesii, the pitchers of which do not hold phytotelma communities but instead appear to digest prey like more carnivorous species. The pitchers of hybrids are morphologically intermediate between the two parent species in both height and diameter. Both S. p. var. montana and the hybrid hold fluid and host both mosquito and midge larvae. The goal of our research is to compare the phytotelma communities of S. p. var. montana and the S. p. var. montana x S. jonesii hybrids. S. jonesii appears to be carnivorous, digesting its prey with endogenously produced enzymes. Therefore, we hypothesize that the phytotelmata of hybrids may contain higher levels of digestive enzymes than those of S. purpurea and may be a less hospitable environment for aquatic invertebrates. Here, we describe results of a 2013 field study in which we sampled monthly the pitchers of both S. p. var. montana and the hybrid and quantified the invertebrate community.

The origin of gap junction proteins

Stephen Bond, Andreas Baxevanis

Monday, June 23, 2014 -Poster #89

Gap junctions (GJs) are a nearly ubiquitous feature of metazoan life, coupling the cytoplasm of adjacent cells into a partially selective syncytium. The range of physiological and pathophysiological processes that GJs partake in is extensive — a feature mirrored by an equally extensive diversity in the primary sequence of GJ-forming proteins. A particular curiosity is the presence of two distinct families of GJ proteins within the animal kingdom. In chordates, connexins (Cxs) are responsible for coupling adjoining cells, while the “invertebrate analogs of connexins”, namely innexins (Inxs), perform the function across most of the remaining phyla; Inx genes are also found alongside the Cxs in chordates. The three-dimensional structures of Inxs and Cxs are thought to be quite similar, but they share very little identity at the sequence level, which has left it unclear whether the two families are homologous.

This study explores the relationship between Inxs and Cxs, testing among three candidate scenarios that are consistent with the phylogenetic distribution of these protein families: 1) Cxs and Inxs are derived from completely unrelated ancestor sequences, and have undergone convergent evolution; 2) Cxs are descendent from Inxs, but experienced a burst of very rapid sequence divergence early in their history; or 3) Cxs and Inxs share a common non-GJ ancestor, and have undergone parallel evolution.

As genomics has advanced, it is now possible to analyze thousands of GJ protein sequences from across all metazoan phyla. We have supplemented publicly available databases of profile hidden Markov models with additional sequence data from basal metazoans, and calculated ‘relatedness’ values between the GJ families and hundreds of other transmembrane protein families. These values are being used to test the three evolutionary models suggested above.

The origin of Cxs and Inxs has been debated for over 15 years, and resolving the issue will inform our future experimental initiative to characterize the biophysics of the various channels each family can form. For example, evidence of convergent evolution will strengthen the inferred importance of shared biophysical properties, while evidence of a common non-GJ ancestor could allow us to reconstruct a ‘consensus channel’ for testing new therapeutics.

Molecular patterns of conflict in imprinted genes of Arabidopsis

Katherine Geist, Joan Strassmann, David Queller

Monday, June 23, 2014 -Poster #90

The successful outcome of sexual reproduction depends on the cooperation of male and female genomes as gametes unite. This is reflected in Mendelian inheritance, in which the expression of an allele is independent of the sex of the parent from which it comes. Genomic imprinting, or parent-of-origin-specific gene expression, deviates from this view of life. Under the kinship theory, genomic imprinting evolves as a consequence of conflict between maternal and paternal genomes over maternal investment. This conflict has the potential to create arms race dynamics that drive patterns of rapid evolution and positive selection in imprinted loci, but is not a necessary outcome. In imprinted loci, such as those in the angiosperm Arabidopsis thaliana, the patterns of molecular variation remain an open question. Our work builds on that of previous researchers to provide a more comprehensive view of the molecular evolution of imprinted genes in Arabidopsis. We test the prediction that imprinted loci show patterns of molecular evolution consistent with historical or ongoing conflict. Using sets of empirically validated and putative imprinted loci in A. thaliana from the literature, we performed a battery of analyses both within and among species to examine the potential roles of positive and diversifying selection in imprinted vs. unimprinted genes. We specifically address whether patterns of molecular variation differ between matrigenes and patrigenes.

QTL studies of transcription factors that control opsin expression in cichlid fishes.

Sri Pratima Nandamuri, Jane Schulte

Monday, June 23, 2014 -Poster #91

One of the key mechanisms contributing to phenotypic evolution is gene regulation. African cichlids provide an ideal platform for studying the genes responsible for species divergence. These highly speciose fishes exhibit substantial variation in the expression of seven distinct cone opsin genes. Each species expresses a subset of these seven genes leading to extensive diversity in their visual sensitivities. In a genetic cross between two Lake Malawi cichlid species with varying visual palettes, we previously identified two quantitative trait loci (QTLs) responsible for the differential expression of the SWS2A (short wavelength sensitive 2A) opsin gene. Using fine-mapping and RNA-seq in retinal transcriptomes, we identified that RX1 (retinal anterior neural fold homeobox-1) gene on linkage group 23 is the causative gene for the first QTL. The present study focuses on the second QTL on linkage group 5 with the aim of finding another causative factor. We hypothesize that MITF1 (micropthalmia-associated transcription factor 1) might be involved with the difference in SWS2A expression between the parental species. This gene is in the center of the fine-mapped QTL region. Transcriptome data indicates that the MITF1 gene is differentially expressed between the parents and is correlated with SWS2A expression (R2=44%) in five other cichlid species. An analysis of the SWS2A promoter shows the presence of MITF1 binding sites. We propose that regulatory changes in the promoter of the MITF1 gene affect its expression and are therefore responsible for the abundance of the SWS2A visual pigment in the parents as well as the entire Malawi flock. These changes might have arisen early in the Lake Malawi lineage and are randomly being sorted between species, thereby contributing to their divergence.

The evolution of plant carnivory: insights into morphological diversification and prey partitioning in the carnivorous pitcher plant genus Sarracenia

Jessica Stephens, Ron Determann, Russell Malmberg

Monday, June 23, 2014 -Poster #92

Ecological interactions among closely related species are thought to be significant drivers of adaptive evolution and diversification of species. How these interactions have shaped rates and patterns of speciation and morphological divergence is therefore of interest in ecology and evolutionary biology. The North American carnivorous plant genus Sarracenia is an attractive model system to investigate how interactions between closely related species, specifically competition over a limited resource, have shaped diversification. These plants have evolved highly modified leaves (i.e. pitchers) used in attraction, trapping, retention, and digestion of insect prey to obtain nutrients. Moreover, carnivorous plants are dependent on insects for nutrients, creating intense competition for prey among sympatric species. This competition scenario is predicted to cause strong selection on traits related to prey attraction potentially leading to resource partitioning and variation in trapping morphology. Here, we created a common garden containing the 11 species and 4 putative infraspecific taxa. Preliminary data from six species (S. minor, S. minor var. okefenokeensis, S. flava, S. rosea, S. psittacina, and S. leucophylla) was collected in the fall of 2013 and prey identified to order and family. Multivariate analyses highlight significant differences in prey captured across these six species/varieties. In addition, various leaf traits were measured and multivariate analyses show differences in height, trichome densities, and peristome width between pitchers of the six species sampled. Moreover, prey community differences are correlated with leaf traits. For example, taller pitcher plant species attract flying prey more often (e.g. Lepidoptera, Coleoptera, Hymenoptera, Diptera), while shorter pitcher plant species trap ground crawling prey (e.g. Formicidae, Diplopoda). These differences in prey communities may have been an important ecological driver of speciation in this genus. Future work will examine these leaf traits and prey communities within a phylogenetic context to further assess this hypothesis.

The effects of pitcher plant hybridization on oviposition of the pitcher plant midge

Steven Jaslow, Rebecca Hale

Monday, June 23, 2014 -Poster #93

Flies of the family Chironmidae produce lots of offspring and, as they provide no parental care, the initial choice of where they eggs is crucial to their offspring's survival. Although Chironomid adults are terrestrial, their larvae are aquatic and adult females may use multiple factors to help select an ideal pool of water for eggs, including the pool's likelihood of evaporating, its available nutrients, and the presence of predators. One Chironomid species, Metriocnemus knabi, is so particular that it only lays eggs in the leaves of the purple pitcher plant, Sarracenia purpurea, a pitcher plant species that hosts a large community of invertebrates in its pitchers instead of digesting them as prey. In this study, we build on data collected in 2013 to examine whether female M. knabi preferentially select S. purpurea pitchers over the pitchers of hybrids between S. purpurea and the carnivorous S. jonesii. We test two hypotheses: 1) that hybrids provide a less hospitable environment for M. knabi larvae because they contain higher levels of digestive proteases and 2) that female M. knabi preferentially select S. purpurea pitchers based on the properties of the water collected in the pitchers.

Seeing the forest by interpreting the trees: An assessment instrument for evaluating undergraduate student understanding of evolutionary trees

Louise Mead, David Baum, Kristin Jenkins, Kristy Halverson

Monday, June 23, 2014 -Poster #94

Trees, figures showing ancestor-descendant relationships, are used all the time by biologists to reconstruct evolutionary history, to test specific hypotheses about trait evolution, and to evaluate the evidence for evolution. All science education reform acknowledges the key role of descent with modification from common ancestors in understanding biological diversity. While evolutionary biologists may feel completely comfortable reading and interpreting evolutionary trees, it is not clear that our students feel the same level of comfort or are capable of extracting key information. The ability to interpret trees and use them for organizing knowledge of biodiversity was initially discussed by Baum et al. (2005) in The Tree Thinking Challenge, and included two quizzes of varying difficulty. Evidence of validity and reliability for these questions was not included. We have been working to redesign this instrument so that it tests student understanding of a number of key concepts associated with tree thinking. We report our progress and some initial findings.

Moving the mountain: How to transform comparative anatomy into computable anatomy?

Wasila Dahdul, Alex Dececchi, Nizar Ibrahim, Hilmar Lapp, Paula Mabee

Monday, June 23, 2014 -Poster #95

The diverse phenotypes of animals have been described for centuries, and though they may be digitized, they are not available in a computable form. Using over 100 morphological studies, the Phenoscape project has demonstrated that by annotating characters with community anatomy ontology terms, links between novel species anatomy and the genes that may underlie them can be made. But given the enormous size of the legacy literature, how can this largely unexploited wealth of complex, expressive descriptive data be rendered amenable to large-scale computation? To identify the bottlenecks, we quantified the time involved in the major aspects of phenotype curation as we annotated 2,543 fin and limb characters for 2,347 vertebrate taxa from 68 phylogenetic systematic publications. This process involves attaching fully computable logical expressions consisting of ontology terms to the natural language character and state descriptions found in character-by-taxon matrices. The workflow consisted of three parts: 1) data preparation, 2) phenotype annotation, and 3) ontology development. Preparing phenotypic data from phylogenetic matrices required significant manual data entry. This is because most matrices are not available electronically, and those that are often require manual entry of character and state descriptions. Subsequent annotation of phenotypes with ontology terms is streamlined by the Phenex software, which includes a feature that decouples annotation from the ontology editing process.

Our results showed that the completion of this work required two person-years by a team of post-docs, data curators, and undergraduate students. Manual data preparation by students and supervision of their work required close to 20% of the effort. This part in particular could be reduced substantially with better community data practices, such as depositing fully populated matrices in public repositories. Phenotype annotation required approximately 40% of the curatorial effort. We are working to make this more efficient with Natural Language Processing (NLP) tools. Ontology development (40% of effort), however, remains a highly manual task requiring domain (anatomical) expertise and expert use of complex and specialized software. The large overhead required to prepare data files and update ontologies contributed to a low rate of annotation of less than one character per hour, compared to 13 characters per hour when curatorial activity was restricted to phenotype annotation only.

In summary, fully unlocking the potential of the vast literature stores of descriptions of morphological biodiversity will require both better tools for efficiently processing natural language, and better community data practices towards a born-digital morphology.

Size matters: a laboratory exercise on the allometric analysis of avian eggs

Henry John-Alder, Allison Anholt

Monday, June 23, 2014 -Poster #96

Body size is a fundamental organizing theme in biology. Size constrains virtually all aspects of form and function and explains much of the diversity of life. Moreover, changes in size have profound consequences in both developmental and evolutionary time. However, a formal consideration of size is typically a minor digression if not entirely absent from undergraduate curricula in organismal biology. We redressed this shortcoming by developing an undergraduate laboratory exercise involving an allometric analysis of avian eggs. This exercise couples simple laboratory measurements with the retrieval of supplementary oological information from journal articles and online resources, and it provides a platform for students to increase their proficiency in data management and manipulation. Described as self-contained life-support systems, eggs are particularly well-suited for this exercise because their autonomy and multifunctionality – as protective exoskeletons, as respiratory diffusion surfaces, and as units of reproduction – emphasizes interrelationships of form, function, and fitness. Furthermore, while an actual egg collection is undeniably alluring, the exercise can be supported entirely by readily accessible published records. Our exercise utilizes Rutgers University's collection of thousands of eggs representing 160 species, varying by four orders of magnitude in body mass. Students use calipers and an electronic balance to measure length, breadth, and mass of the shells of 15 species, and they use online and published resources to retrieve information on species body size and reproductive life history traits (clutch size, clutch frequency, incubation period). Students use Excel functions and published formulae to calculate fresh egg mass, egg volume and surface area, shell thickness, breaking force, water loss, annual reproductive investment, and other parameters of interest. The students use these data for various allometric analyses, including (but not limited to) 1) egg size versus body size, 2) the constancy of water loss versus incubation period, 3) a safety factor against shell breakage, and 4) annual and lifetime reproductive fitness. Taxonomic information can be included to enhance the exercise. These allometric analyses illustrate the interdependence of size constraints on form (length and mass), function (diffusivity, protection), and fitness (reproductive life history traits), with or without phylogenetic control. This exercise introduces students to the importance of size as a key evolutionary, functional, and analytical constraint, and it provides a platform for much-needed practice in everyday methods of data collection, management, analysis, and graphing.

Synthetic morphological supermatrices: revealing unknown knowns and reducing missing data

James Balhoff, Alex Dececchi, Hilmar Lapp, Paula Mabee

Monday, June 23, 2014 -Poster #97

Comparative descriptions of morphology have been formalized in the phylogenetic systematic literature for years. Despite this, they remain difficult to integrate across studies or with developmental or genetic data. A major reason is the lack of a common vocabulary for common descriptive concepts. By representing phenotypes using anatomy and quality ontologies, and taxa using a taxonomy ontology, we have combined different anatomical and taxonomic slices of morphological data to generate morphological supermatrices, using new software tools developed for the Phenoscape Knowledgebase. A coarse default phylogeny for the relevant taxa, derived from the referenced taxonomy, can be generated to examine patterns of character evolution. Using the logic inferences enabled by ontologies, the presence or absence of anatomical entities can be inferred even when they are not directly asserted by authors. For example, reference to the length of a manual digit allows one to infer the presence of a forelimb. Likewise, absence of digits entails the absence of claws. Data inferred in this way can substantially supplement those directly asserted. Conflicting presence/absence assertions or inferences among publications are readily discovered for taxa through this machine-based synthesis. These conflicts can point to changes in the level of knowledge (i.e. differences in specimens examined) between studies or suggest poor semantic construction of the characters and states in the original publication, which can suggest improved scoring practices for future publications.

Whole exome capture in species without a sequenced genome

Matthew Jones, Joel Alves, Ted Cosart, Paulo C. Alves, Jose Melo-Ferreira, Frank Jiggins

Monday, June 23, 2014 -Poster #98

Recent advances in genomics allow for massively parallel target enrichment and high-throughput sequencing of a priori regions of interest (e.g., all exons) in species with reference genomes. However, most species still lack the powerful genomic resources necessary for the design of genome-wide target enrichment experiments. Here we demonstrate the utility of using a divergent genomic reference to enable whole-exome capture in the non-model species snowshoe hares (Lepus americanus). We captured a single snowshoe hare exome using probes designed from the European rabbit (Oryctolagus cuniculus) genome, which is ~15 million years diverged. This initial exon capture included 20,478 genes (~185,000 exons) across 30.9 Mb. We recovered ~176,00 targeted exons (95%) comprising ~28 Mb of the hare exome. From this snowshoe hare exome we have designed a snowshoe hare-specific exon capture to perform additional capture experiments in this species. These resources will enable population genomic inquiries into diverse questions on the evolution of this important ecological model.

UNPAK: using a knockout library to quantify variation in whole-organism phenotypes, and to test ideas about phenotypic and genome evolution

Hilary Callahan, Courtney Murren, Matt Rutter, Allan Strand, Michael Wolyniak

Monday, June 23, 2014 -Poster #99

The UNPAK project – Undergraduates Phenotyping Arabidopsis Knockouts – aims to detect and characterize phenotypic variation quantitatively, re-phenotyping a large sample of T-DNA mutant lines (N > 2000 to date). Although the project focuses on a model species in plant genomics, and on a key resource from the functional genomics community, it also addresses major themes in evolutionary ecology. For example, we examine traits expressed at the whole plant level, throughout the life cycle, and relevant to fitness, such as vegetative size, timing of reproduction, fruit production, fruit size, etc. Additionally, to account for inevitable environmental sources of phenotypic variation, every one of UNPAK's many experiments grows knockouts alongside not only a wild-type but also a carefully selected set of 10 ecotypes (i.e., "phytometers"). Data from UnPAK's first three years demonstrate the project's ability to successfully and frequently uncovered phenotypic variants within this focal T-DNA mutant library. In addition to discussing analyses of UNPAK's current database, we compare UNPAK's protocols, objectives and successes with previous screens in A. thaliana and with similar efforts employing other model species.

Evaluating the application of high-throughput sequencing for the identification of fish eggs collected in the Northern Gulf of Mexico

Matthew Greenwold, Joseph Quattro, Shrujan Amin, Mark Roberts

Monday, June 23, 2014 -Poster #100

Fishery managers use fishery dependent and independent data to perform stock assessment for fishery management. An often overlooked source of fishery independent data is fish eggs, which have the potential to provide valuable information on spawning and can lead to better estimates of population size for stock assessments. However, fish eggs are often disregarded due to difficulties in accurately identifying species with morphological analyses. When morphological identification is impracticable or uncertain, barcoding genes such as 16S rRNA or cytochrome oxidase subunit I (COI) coupled with high-throughput sequencing have been instrumental in evaluating bacterial community composition by providing accurate identification and species quantification. Here we evaluate the practicality and cost effectiveness of using Illumina paired-end sequencing and the 16S rRNA region of mitochondria to identify and quantify commercially important fish species from eggs sampled in the Northern Gulf of Mexico. We assess count accuracy and reproducibility and estimate the fold coverage needed for future applications using known and unknown samples of fish eggs.

Development of microsatellite markers for two Orconectid crayfishes via Illumina paired-end genomic sequencing

Angela Roles, Dyani Sabin

Monday, June 23, 2014 -Poster #101

Molecular markers, particularly microsatellites, have historically been costly and time-consuming to develop and are largely lacking for crayfishes. However, the relatively low cost of next generation sequencing makes marker development possible - and fast - for many non-model species. We generated Illumina barcoded paired-end libraries for two species of crayfish, Orconectes rusticus and O. sanbornii. From the resulting sequence data, we searched for 4-mer repeat motifs using msatcommander and chose 50 candidate loci to test for each species using VARscores generated by SERV to select those most likely to be variable. Primers were designed via msatcommander. We then tested amplification of the primers in multiple populations of both species, noting between-species length variation visible on an agarose-gel for some loci. We genotyped individuals from several populations of each species to assess the utility of the markers for studying patterns of genetic variation within and among these species. These markers are a valuable resource for others interested in crayfish population genetics with potential uses including species identification, paternity analysis, conservation genetics, and assessing population structure.

Connections between Neotropical Rainforests revealed by Araneus venatrix (Araneae: Araneidae)

Elen Peres, Vera Solferini, da Silva Márcio José

Monday, June 23, 2014 -Poster #102

Amazonia and Atlantic Rainforests exhibit similar climatic conditions and biotic composition, although separated by a large dry corridor of open vegetation. Geomorphological and paleopalinological data suggest an historical connection between these rainforests, but few phylogeographic studies focus on this question. We investigated the phylogeographic patterns of Araneus venatrix (Araneae: Araneidae), a spider widely distributed in Brazilian humid environments, to study the formation and diversification of Neotropical Rainforests. We sequenced mitochondrial COI and nuclear ITS2 regions of samples from 30 populations located along the species distribution. The concatenated phylogenetic inference showed a deep divergence between Southern Atlantic Rainforest populations (clade I) and all other samples (clade II), a pattern corroborated by haplotype networks and population structure analyses (FST and AMOVA) conducted for COI and ITS2 separately. This node was dated on Late Miocene (6.9 Mya, 95% HPD = 2.8–12.9 Mya) and the diversification of each clade has occurred in Pleistocene. Clade II is composed by three main lineages, each with a predominant geographical distribution in Amazonia, Northern Atlantic Rainforest or South-Central region of Brazil. Demographic analyses showed signs of recent expansion in the Amazonia group (~0.2 Mya), and bayesian analyses of population structure for the mitochondrial region indicate connections between Amazonia and the other two groups, but not with clade I. The evidence that Amazonia is closely related to Northern Atlantic Rainforest strongly suggest that the formation of this biome was not uniform along its distribution. Our results show that the biogeographic history of Neotropical region is complex and the evolutionary events underlying the diversification of Amazonia and Atlantic Rainforests are not completely independent. Investigating organisms widely distributed in Neotropics is extremely important to reveal patterns that may remain unclear or biased in studies that focus on only one specific biome.

Mitochondrial phylogeography of the web spider Aglaoctenus lagotis (Araneae, Lycosidae) in Brazil

Fernanda Fontes, Vera Solferini, da Silva Márcio José

Monday, June 23, 2014 -Poster #103

The Atlantic and Amazon Rainforests are currently separated by a drier area comprised by Caatinga and Cerrado biomes; however, there is evidence that these two forests were continuous in the past. This study aimed to add knowledge about the history of these forests. We studied the web spider Aglaoctenus lagotis, with an extensive neotropical distribution and populations spread over almost all Brazilian biomes. Were collected 267 individuals from 28 populations across the area of known occurrence of this species; DNA was extracted and a fragment of COI mitochondrial region was sequenced. In the bayesian phylogenetic inference the 51 haplotypes coalesce around 2.5 Mya (95% HPD= 1.4 to 4.1), on the beginning of the Pleistocene. Both the phylogenetic tree and the haplotype network showed three well resolved clades with strong geographic structure. One clade consists of haplotypes from the Southern Atlantic Forest, another comprises haplotypes located in the Southwest of the country and the third clade groups the haplotypes from the other sample sites. The radiation within the clades occurred between the middle and late Pleistocene. The third clade comprising the samples from the Amazon, the Northern Atlantic Forest and the Cerrado shows no substructure, indicating a connection between these biomes, despite the great geographical distance among populations. Our results indicate a common history for these Neotropical biomes and a complex history for the formation of the Atlantic Forest, which was only detected by the study of a widely distributed species.

Comparative Phylogeography in Atlantic forest and Brazilian Savanna: Pleistocene fluctuations and dispersion shaping the patterns of two bumblebees

Elaine Françoso, Alexandre Zuntini, Ana Carolina Carnaval, Maria Cristina Arias

Monday, June 23, 2014 -Poster #104

Bombus morio and B. pauloensis are simpatric species, occupying a large area mainly it the two major Brazilian biomes, Atlantic forest and Savanna, and their transition zones. Differences among dispersion capacity, higher in B. morio, may infuence their phylogeographic patterns. These bees are good models to test hypotheses for biodiversity diversification in the Neotropics that includes the Pleistocene refuges, tectonics theory, rivers, uplift of hills and mountains as barrier and the ecological gradient theory. The objectives were describe the phylogeographic patterns for B. morio and B. pauloensis and to relate them to biogeographical hypotheses that properly explain the pattern and the phenomena that shaped the populations and eventual lineages and their distribution; and to test if the different dispersion capacity can generates different phylogeographic patterns. We worked with a large sample size, covering most of the total distribution in Brazil. We used mitochondrial DNA to reconstruct the Bayesian Coalescent phylogeny with molecular clock and the haplotype network; microsatellite markers were applied for historical demography; and ecological niche modeling to construct geospatial histories. Our results suggest that climatic oscillations during the Pleistocene have directly influenced the population structure of both species. Warm periods in Last Inter Glacial (~120,000–140,000 years BP) should have contributed to the demographic retraction, while strong expansion could have happened in Last Glacial Maximum (~21,000 years BP), since bumblebees are cold adapted. Topologic congruence was not observed, as expected, probably due to higher dispersal capacity of B. morio. While B. morio is morphologically and genetically very homogeneous, B. pauloensis showed three distinct clades. Parapatric diversification, with different climate conditions and higher elevations may limit and shape the three current clades. The eastern São Paulo state, in which different breaks were found for many organisms, as frogs, birds, bats and snakes, again seems to be very complex and with another phylogeographic scenario. Furthermore, for being the center of genetic diversity in B. pauloensis and stable over the climatic change for both species, is priority for conservation.

Evolution of Mandirola (Genesriaceae, Lamiales) species complex in Neotropical Savanna

Cecilia Fonseca Fiorini, Andréa Onofre, Vera Solferini, da Silva Márcio José

Monday, June 23, 2014 -Poster #105

The genus Mandirola has three species and an intricate history of taxonomic redefinitions, due to a continuum of phenotypic variation that difficult the establishment of clear boundaries between them. The individuals of Mandirola are found along the Brazilian Savanna (cerrado), forming isolated populations with low phenotypic diversity, despite distinct flower patters between populations. We aimed to study genetic structure of Mandirola populations, what can contribute to the understanding of the processes of population differentiation in this species complex. We visited all known areas of Mandirola occurrence and the 25 populations where individuals were found were sampled. The intergenic region of cpDNA psbA-trnH was sequenced, providing 281 monomorphic and 26 polymorphic sites. The intrapopulational variation is very low: from 18 populations analyzed, 15 are monomorphic. However, interpopulational variation is high, as most haplotypes are exclusive to one population, indicating very restricted seed flow. Our data point to the existence of lineages that are not exclusively related with the morphs, but primarily to the spatial distribution of populations, and that Mandirola was established by gradual dispersion from the center of its distribution.

Unveiling the evolutionary history of an Atlantic forest passerine bird using ABC

Ana Cristina Fazza, Michael Hickerson, Cristina Miyaki

Monday, June 23, 2014 -Poster #106

Ana Cristina Fazza[1], Michael J. Hickerson[2], Cristina Y. Miyaki[1]

[1]Instituto de Biociências, Universidade de São Paulo, São Paulo, Brazil

[2]Biology Department, City College of New York, New York, United States

Here we investigate the phylogeography of the scaled antbird, Drymophila squamata (/family Thamnophilidae, class Aves), a passerine bird endemic of the endangered Atlantic forest. We analyzed 53 samples collected along the species' distribution area, from the state of Bahia to the northeast of the state of Rio Grande do Sul and a disjunct population in the state of Alagoas. Three genetic markers were sequenced: one mitochondrial gene (ND2) and two nuclear introns (FIB7 and G3PDH). ND2 revealed at least three lineages with phylogeographic breaks close to two rivers (Doce and Jequitinhonha). Based on this result, we used approximate Bayesian computation to investigate historical scenarios of three populations derived from two splits that occurred on different times. The results of this analysis suggest that around 20 kya (during the last glacial maximum) the scaled antbird experienced a population split and a 50% reduction of its total population size. This is congruent with a possible retraction of the distribution of the humid forest which may have resulted in isolated forest patches with smaller areas. The oldest split was dated at around 261 kya, which could also be related to Milankovitch cycles of glaciations that could have contributed for this diversification. Thus, the mitochondrial lineages observed in the scaled antbird seem to have diverged during the Pleistocene and the glacial cycles that occurred in this period could have some influence on this pattern. Finally, some authors consider that the scaled antbird has two subspecies (D. s. squamata from Alagoas and Bahia states and D. s. stictocorypha from southeastern Brazil), that can be distinguished by plumage differences. As the distributions of these taxa are not coincident with the genetic lineages identified here, further investigations on plumage and voice are needed. Funds: FAPESP (2009/12989-1, BIOTA 2013/50297-0), NSF (DOB 1343578), NASA, CAPES, CNPq, Research Center on Biodiversity and Computing of the Universidade de São Paulo.

Evaluating the level of endemism and isolation in the avifauna of the Central mountain range in Córdoba province, Argentina

Belen Bukowski, Pablo Lavinia, Natalia Trujillo-Arias, Cecilia Kopuchian, Pablo Tubaro, Dario Lijtmaer

Monday, June 23, 2014 -Poster #107

The Andes mountains constitute without doubt one of the main factors that have promoted Neotropical diversification. However, the role of other highland regions in the southern cone of South America has been barely studied. We analyzed the level of endemism in the avifauna of the Central mountain range in Córdoba province, an isolated high region in central Argentina, to evaluate the possible effect of its geographic isolation from the Andes. There are 11 species in this region that include subspecies endemic to the area, but all of them have been designated due to differences in morphology (mainly coloration) and none has been evaluated yet using molecular markers. We performed the first genetic analyses of these species and, combining fresh tissue samples with toe pad samples, were able to analyze mitochondrial DNA sequences (cytochrome c oxidase subunit I and cytochrome b) of 7 of these species and an assortment of other 10 species that could have cryptic differentiation in the area. The analysis of genetic divergence and haplotype networks have shown that in 5 (Cinclodes atacamensis, Muscisaxicola rufivertex, Asthenes sclateri, Catamenia inornata and Phrygilus unicolor) of the 7 species with endemic subspecies in the Central mountain range, the specimens from this area possessed some degree of differentiation from those of other subspecies of Argentina. In the 2 other species results suggested a lack of isolation in this area (Phrygilus plebejus and Sturnella loyca, being the latter the only one occupying lowland areas and therefore having a continuous, not disjunct distribution). None of the species without endemic subspecies showed signs of isolation in the region, although both Turdus chiguanco and Troglodytes aedon presented high intraspecific variation. While further analyses including more molecular markers, morphological characters and vocalizations are needed, these results suggest that most species that have disjunct distributions, with a population in the Central mountain range of Córdoba province isolated geographically from the Andes, show differentiated genetic lineages in this region that suggest an evolutionary isolation from other populations of the species.

Population genetic structure of Argiope argentata (Araneae: Araneidae)

Jair Francisco Mendes Júnior, Vera Solferini, da Silva Márcio José

Monday, June 23, 2014 -Poster #108

The Amazonia and the Atlantic Rainforests are separated by a region of open vegetation, also known as the large South American disjunction. This separation may isolate populations from the two forests, resulting in genetic structure between populations of these two biomes. To test this, we sampled populations of Argiope argentata (Araneae: Araneidae), a spider species with a wide geographical distribution in all biomes of the neotropical region. Individuals were collected in sites at the Amazonia, at the Atlantic Rainforest and at the Brazilian Savanna (cerrado). The partial sequencing of the mitochondrial gene Cytochrome Oxidase I revealed 626 polymorphic and 34 monomorphic sites. The haplotype network shows the occurrence of a clade with haplotypes exclusive of the Central Amazonia. The remaining haplotypes do not have any detectable geographic structure. Pairwise FST shows significant values between populations of Central Amazonia and the others. Results of AMOVA showed that around 70% of the variations are within populations and around 28% between the group of populations of Central Amazonia and the other group. We found evidence of structuring between Central Amazonia populations and all other; however, there is no differentiation between populations separated by the open vegetation area, indicating that Argiope argentata is a very efficient dispersor.

Recent structuring of lineages of the golden orb-weaver spider Nephila clavipes, a neotropical Nephilidae (Araneae).

Luiz Filipe Macedo Bartoleti, Vera Solferini, da Silva Márcio José

Monday, June 23, 2014 -Poster #109

There are relatively few studies about the evolutionary histories of Neotropical species, in spite of their importance to understanding the processes responsible for the biodiversity of this region. We conducted a phylogeographical study of Nephila clavipes, a widely distributed spider species in order to understand the connections among the Brazilian biomes. We sampled 31 populations along Amazonia and Atlantic Rainforests and also on the drier areas between them. Phylogenetic inference and haplotype network of partial COI mitochondrial sequences from 236 individuals showed four groups, geographically structured. One group contains all the Amazonian haplotypes; another is mostly found in the Atlantic populations; the third group contains haplotypes from the Central part of Brazil and the fourth group comprises haplotypes sampled in all parts of the country. All four groupings are well supported, but the only well resolved branch in the phylogenetic tree is the separation of the fourth group around 870 kya. There are strong signals of recent expansion on Amazonia and Atlantic groups around 400 to 260 kya. Our data indicate a recent divergence of N. clavipes lineages during Pleistocene, with the radiation of all fours groups at about the same time, and no geographical substructure within the groups. Alta Floresta, the southernmost Amazonian population, located in a transitional area between Amazonia and Cerrado (Brazilian savanna), comprises haplotypes of three groups. This indicates that the transitional areas maintain connectivity among populations from different groups. This is a first step of a deeper study. Even though, it highlights the importance of using widely distributed species to better comprehend biodiversity evolution.

Incipient speciation related to mimetic divergence in the poison frog Ranitomeya imitator

Evan Twomey, Kyle Summers, Jacob S. Vestergaard

Monday, June 23, 2014 -Poster #110

Mimicry has been long-celebrated in evolutionary biology as a powerful visual example of convergent evolution among unrelated species. However, in a mimetic radiation—when a single species evolves to resemble different model species—mimicry can drive within-species morphological diversification, and, potentially, speciation. While mimetic radiations have occurred in a variety of taxa, their role in speciation remains poorly understood. We studied the Peruvian poison frog Ranitomeya imitator, a species that has undergone a dramatic radiation into four distinct mimetic morphs. Using a combination of colour pattern quantification, landscape genetics, and mate choice experiments, we show that a mimetic shift in R. imitator is likely driving incipient speciation among two of these mimetic morphs. Analyses of colour pattern clines show that these two morphs form a narrow transition zone approximately 1–2 km wide composed of phenotypic intermediates. Landscape genetic analyses indicate that neutral genetic divergence between morphs is primarily associated with divergence in mimetic colour pattern, rather than geographic distance, suggesting that mimetic divergence has reduced gene flow between morphs. Using mate choice experiments, we found evidence for assortative mating in one of the mimetic morphs. This mating preference is only present near the transition zone, consistent with reproductive character displacement. Taken together, these results suggest that divergent selection to resemble different model species has led to a breakdown in gene flow between these two populations, potentially facilitated by assortative mating. These results extend the effects of mimicry on speciation into a vertebrate system and characterize an early stage of speciation where reproductive isolation between mimetic morphs is incomplete but evident.

RNAseq Analysis of Wing Pigmentation in Papilio glaucus

Maria Gutin, Molly Schumer, Matthew Aardema, Iva Fuková, Peter Andolfatto

Monday, June 23, 2014 -Poster #111

Within the Papilio genus of butterflies, there are a number of species that display mimicry in wing coloration and patterning to avoid predation. The Eastern tiger swallowtail -(Papilio glaucus) is one such species, exhibiting female-limited mimicry of Battus philenor, a poisonous species within the Lepidoptera. All male individuals of the species are yellow, whereas females can either take on a yellow pigmentation pattern resembling the males, or a dark mimetic morph. Using RNA-Seq data extracted from wing discs of yellow and dark morphs of P. glaucus, differential gene expression analyses can be used to elucidate which genes underlie differences in female pigmentation within P. glaucus.

Predator learning and toxicity in a Müllerian mimicry complex of poison frogs in Peru

Adam Stuckert, Ralph Saporito, Kyle Summers

Monday, June 23, 2014 -Poster #112

Recent research suggests that distinct color pattern morphs of the mimic poison frog, Ranitomeya imitator, are Müllerian mimics of different sympatric model species in different geographic regions of northern Peru. We experimentally tested a central tenet of this hypothesis: that predators will learn to avoid the mimic when exposed to the model and vice-versa. Chickens (Gallus domesticus) exposed to a spotted morph of R. imitator learned to avoid the putative model, R. variabilis, and vice-versa, supporting the claim that this system functions as a Müllerian mimicry complex. Tests with a distinct striped morph indicate that some predators may generalize aversion to the spotted and striped morphs of R. imitator. We further investigated the hypothesis of Müllerian mimicry in this system by testing the prediction that all morphs and species involved in the complex are toxic. Analysis of extracts from the skin of the four major morphs of R. imitator and four putative model species/populations demonstrated the presence of alkaloid toxins in all cases, consistent with a key tenet of Müllerian mimicry. Surprisingly, there was a trend for R. imitator to have higher diversities and quantities of alkaloids than the putative models. We discuss these results in light of recent investigations of population genetic structure and color pattern diversity in R. imitator, and we highlight the potential importance of automimicry in this system.

Mimicry on the wing: flight morphology and kinematics in a mimetic butterfly and its model

Krushnamegh Kunte, Deepa Agashe, Stacey Combes

Monday, June 23, 2014 -Poster #113

Batesian mimicry is known to exert very strong natural selection on visual resemblance between aposematic toxic prey and the species that mimic them. How do sexual and species differences between models and mimics influence other dimensions of mimicry such as flight and behavior? To find out, we recorded flights of the toxic Pachliopta aristolochiae butterfly and its mimic Papilio polytes. Papilio polytes is a female-limited polymorphic mimic, i.e., males are monomorphic and non-mimetic whereas females are polymorphic, with a male-like (non-mimetic) form and one or more mimetic forms resembling locally available Pachliopta models. We found significant differences in body weight, investment in thorax versus abdomen, and several important flight kinematic parameters between males and females of each species. Thus, the sexes of both species had their own flight morphological differences that affected their flight kinematics, suggesting that selection pressures faced by the sexes may be different. When we compared models (Pachliopta males and females), mimic (Papilio mimetic female form) and non-mimics (Papilio male and non-mimetic female form), we found that the mimic had diverged from its ancestral kinematic background (the non-mimics of the same species) to resemble the models for the majority of flight kinematic parameters that we studied. These included important parameters such as wing loading, maximum turning rate and average radius of curvature of the flight path, which may influence the speed and escape flight of butterflies. However, the morphology of the mimic was indistinguishable from its ancestral morphological background. That is, morphology of the mimic was conserved but its flight kinematics had evolved substantially under directional selection to match that of its models. Thus, female-limited mimicry in Papilio polytes extends to flight behavioral dimensions despite the mimic’s ancestral flight morphology.

Avian coloration along an Andean elevation gradient: Interspecific patterns in Thraupidae

Laura Natalia Céspedes Arias, Oscar Laverde, Daniel Cadena

Monday, June 23, 2014 -Poster #114

Interspecific variation in color has been broadly studied in association with contrasting light environments and humidity gradients. However, the effect of other environmental variables and biotic conditions on the patterns of interspecific variation in coloration remains highly unexplored. Elevational gradients are useful settings to understand how environmental and biotic variables may affect the evolution of coloration in birds. Temperature, humidity, forest structure, and biotic variables such as nest predation pressure vary with elevation, but the effects of such variation on the evolution of avian coloration have not been assessed. We examined whether elevational distribution of species partially explains the interspecific variation in coloration in a speciose family of Passeriformes: Thraupidae, which is highly diverse in the Colombian Andes. We included a total of 49 species that live in three localities at different elevation in the Colombian Andean region. We used reflectance spectrometry to evaluate how plumage conspicuousness and other characteristics of the color pattern changes in relation to the elevational distribution of species. We measured museum skins and characterized foraging strata and habitat occupied by each species, and also incorporated data on the coloration of background elements (e.g., leaves, litter and wood) to fully characterize plumage conspicuosness relative to background color. Also we obtained the color volume, mean color span and mean hue disparity, for both males and females. We found, for example, that hue disparity (i.e color heterogeneity) appears to be higher in localities at higher elevation for females but not males. Our data suggest that elements of plumage coloration have likely been shaped by contrasting selective pressures along elevational gradients, however, we did not find strong evidence for the idea that such pattern is related with differences in predation pressure.

Environmentally induced background matching in spadefoot toads

Antonio Serrato-Capuchina, Dylan Carroll, David Pfennig

Monday, June 23, 2014 -Poster #115

Coloration in animals serves numerous functions, including concealment, thermoregulation, and communication. For species occupying variable environments, selection is often expected to favor physiologically flexible coloration, in which individuals alter their coloration in response to present ecological circumstances. We asked whether such phenotypic plasticity in coloration exists among different life stages of spadefoot toads, Spea bombifrons, which occupy habitats that differ dramatically in substrate coloration and light intensity. We found that this species can indeed actively alter body coloration in response to changes to background coloration and light intensity. Background was more important than illumination in triggering color change, however, suggesting that flexible color change has evolved as an adaptation to facilitate background matching, thereby presumably enhancing concealment from potential predators. We discuss possible genetic mechanisms of this plasticity, as well as its potential role in facilitating the colonization of new habitats.

Evolution of morphological diversity and sexual dimorphism in Argynnis butterflies

Gaurav Agavekar, Jahnavi Joshi, Krushnamegh Kunte

Monday, June 23, 2014 -Poster #116

Natural and sexual selection strongly influence the evolution of morphological diversity, including intraspecific traits such as sexual dimorphism. The predominant theory regarding the evolution of sexual dimorphism is that directional sexual selection on male traits is responsible for divergence of phenotypes between the sexes. However, the role of natural selection on divergent female phenotypes was recently highlighted in mimetic Papilio swallowtail butterflies. In Papilio, female-limited mimicry, rather than directional selection on male traits, has largely been responsible for the evolution of sexual dimorphism. Here, we test whether this pattern of female divergence under natural selection is more widespread, or whether the pattern observed in Papilio is an artifact of the special case of natural selection for female-limited mimicry. Specifically, we test whether morphological evolution in unrelated and equally brightly colored Argynnis butterflies shows female-biased accelerated rate of morphological (wing pattern) evolution similar to Papilio, and whether this drives the evolution of sexual dimorphism. For this purpose, we built a multi-locus (mitochondrial and nuclear genes, ~3kb), species-level molecular phylogeny of Argynnis to reconstruct the evolutionary history of sexual dimorphism using likelihood approach. On the resulting well-supported molecular phylogeny, we mapped the evolution of wing patterns and found out that male wing patterns were phylogenetically conserved in this entire genus. However, there were three phylogenetically independent instances of the evolution of sexual dimorphism where females had diverged from the ancestral bright wing colors to become cryptically colored (unrelated to mimicry). In one instance (in two species), sexual dimorphism was induced by evolution of female-limited mimicry. This suggests that the evolution of sexual dimorphism due to natural selection on female traits is not necessarily linked with specific selection for female-limited mimicry in butterflies. This opens up the possibility that this phenomenon is more widespread than previously thought, and deserves extensive consideration.

The genomic basis of adaptive coat color variation in a population rock pocket mice (Chaetodipus intermedius)

Noelle Bittner, Megan Phifer-Rixey

Monday, June 23, 2014 -Poster #117
Finding the genes that underlie adaptive traits allows us to understand how evolution shapes natural populations. Rock pocket mice, Chaetodipus intermedius, display variations in coat coloration throughout their range in association with the substrate they inhabit. Mice living on the dark lava flows scattered throughout the desert southwest often have a much darker pelage than congeners living on lighter desert rock substrate. Each lava flow population that has been studied has a unique mutation underlying coat color polymorphism, suggesting a high occurrence of convergent adaptive evolution, although the precise genetic basis remains unknown in many populations. Here, we use a transcriptomic approach to look for gene expression level variation in a population of dark mice from a lava flow Kenzin, New Mexico across the genome to pinpoint the genes involved in adaptive melanism in this population.

The genetic basis of coat color change in the snowshoe hare, Lepus americanus: an RNA-seq approach

Ana Mafalda Sousa Ferreira, Paulo C. Alves, Colin Callahan, L. Scott Mills, Jeffrey M. Good, Jose Melo-Ferreira

Monday, June 23, 2014 -Poster #118
The ability of some boreal species to change their coat color to mimic the change in the habitat's background with seasonal snow cover is one of the most fascinating biological adaptations. Yet, the genetic basis of this mechanism remains poorly understood. Such understanding is particularly important at a time when climate warming is inducing dramatic decreases in snow cover in the northern habitats, which will affect the capacity of these species to survive. In this work we use the snowshoe hare, Lepus americanus, a North American species adapted to the boreal forest, as model to tackle this question. Differential gene expression in several skin tissues collected in animals undergoing the winter molt was assessed using RNA-seq and the results obtained will be here presented and discussed.

Molecular phylogeny, phylogeography, and anti-predatory eyespot evolution in Eumorpha caterpillars (Lepidoptera: Sphingidae)

Francesca Ponce

Monday, June 23, 2014 -Poster #119
Many animals possess conspicuous external circular markings, or "eyespots". Eyespots typically function to startle or otherwise deter predators, and are thought to have evolved primarily in response to natural selection. However, surprisingly few studies have examined how eyespots have evolved. We study the evolution of the posterior larval eyespot in the charismatic New World hawkmoth genus Eumorpha. While Eumorpha has a range of posterior larval eyespot shapes and sizes, little is known of how this trait has changed over time because phylogenetic relationships and phylogeography of the genus remains unknown. In this study, we sampled 59 individuals from 23 Eumorpha species, and sequenced four genes (CAD, EF-1α, Wingless and CO1), totaling 3,789 base pairs. Maximum likelihood and Bayesian phylogenetic methods produced largely congruent trees, many relationships of which had robust branch support. Our analyses reveal that Eumorpha had an ancestor with a posterior larval eyespot and that the eyespot was subsequently lost in at least three lineages. Eumorpha appears to have originated in South America and shifted its distribution northward to Central and North America. We found little correlation between the presence or absence of the larval eyespot and geographic distribution, which might indicate that Eumorpha larvae have found alternate adaptations that are equally effective against visual predators.

Identification of genomic underpinnings of spot polymorphism in Harmonia axyridis

Lindsay Havens, Matthew MacManes

Monday, June 23, 2014 -Poster #120
Though biologists have long been fascinated by the variety of colors and patterns animals naturally exhibit, the mechanism underlying color polymorphism is largely unknown. One particularly striking example of polymorphism can be found in the color and spot polymorphism of the Asian Multicolored Ladybird (Harmonia axyridis). This research project aims to tease apart the genomic underpinnings of color differences and spot number using high throughput DNA and RNA sequencing, while simultaneously attempting to understand how selection (e.g. natural selection versus sexual selection) may shape phenotype. This poster will present data on the degree of phenotypic variation in both spot number and color patterns in H. axyridis, as well as a draft genome and transcriptome data. Together, these data will further our aims of understanding how selection shapes color patterning.

Differential predation on the two color morphs of Nicaraguan Midas cichlid fish: implications for the maintenance of its gold-dark polymorphism

Julián Torres Dowdall, Gonzalo Machado-Schiaffino, Jimena Golcher-Benavides, Andreas F. Kautt, Henrik Kusche, Axel Meyer

Monday, June 23, 2014 -Poster #121

Predation can play an important role in the evolution and maintenance of prey color polymorphisms. Several factors are known to affect predator choice, including the prey's relative abundance and conspicuousness. In polymorphic prey species, predators often target the most common or most visible morphs. To test if predator choice can explain why in Midas cichlid fish the most visible (gold) morph is also more rare than the inconspicuous dark morph, we conducted predation experiments using two differently colored wax models in Nicaraguan crater lakes. Contrary to expectations, we observed an overall higher attack rate on the much more abundant, yet less conspicuous dark models, and propose frequency-dependent predation as a potential explanation for this result. Interestingly, the attack rate differed between different types of predators. While avian predators were biased towards the abundant and less colorful dark morphs, fish predators did not show a strong bias. Subsequent experiments showed that attacks by predatory fish are tree times as frequent as attacks by birds, suggesting that predatory fish might have a more significant impact in the dynamic of Midas cichlid population. Moreover, most of the attacks occurred on wax models set deep in the water column compared to models set close to the surface of the water; and smaller models were the most commonly attacked models. The relative differential predation rates on different morphs might impact the relative abundance of both color morphs and thus explain the maintenance of the color polymorphism.

Historical and Geographic Variation in wing melanin in an alpine butterfly in relation to climate

Heidi MacLean, Jessica Higgins, Lauren Buckley, Joel Kingsolver

Monday, June 23, 2014 -Poster #122

Colias butterflies adapt to local climate conditions along latitudinal and elevational gradients through differences in hindwing melanin, allowing them to achieve the body temperatures needed for flight, mating and oviposition. Alpine areas in Colorado have seen greater increases in temperature over the past fifty years than other parts of the country on the order of 0.4 C per decade. We used Colias meadii, a species restricted to subalpine and alpine habitats in the Rocky Mountains, to explore geographic variation and historical changes in wing melanin. We sampled museum specimens of C. meadii from across their geographic range for the last 120 years, focusing on past 50-60 years. We photographed each specimen to measure grey level as a metric of hind-wing melanin. By mapping the location of these data and relating grey level values to summer temperatures, Our preliminary results suggest that melanin increases with elevation, but not with latitude, across the range of this species. Ongoing analyses will evaluate whether wing melanin has changed in association with climate changes over the past 50 years in the region.

Candidate genes and SNPs for body size related traits in Drosophila melanogaster

Victoria Ortiz, Juan José Fanara, Valeria Carreira

Monday, June 23, 2014 -Poster #123

Body size is a complex character which is associated to many important fitness related traits. In order to study its genetic basis, we analyzed face width (FW), thorax length (TL) and wing length (WL) in 40 lines of the Drosophila Genetic Reference Panel (i.e. isogenic lines of D. melanogaster derived from a natural population whose nuclear genomes were completely sequenced). We identified 19, 20 and 114 Single Nucleotide Polimorphisms (SNPs) associated to variation in FW, TL and WL respectively, most of which are located in intronic and intergenic regions. These candidate SNPs are associated to 18, 15 and 89 genes for FW, TL and WL respectively. Some SNPs are related to more than one candidate gene as well as multiple SNPs affect a single gene in many cases. We found only two genes, A2bp1 and axo, affecting two traits simultaneously (i.e. TL and WL) and no gene affecting all of them at the same time. Furthermore, SNPs affecting both traits simultaneously were different for each gene. These results suggest a low level of pleiotropy regarding the studied characters. The distribution of these genes through the genome departed from a random one as we found far less candidate genes located in the 3R chromosome than expected. Finally, a gene ontology analysis associated 93 annotated genes with 118 terms of Biological Process including anatomical structure morphogenesis, organ development, locomotion, tissue development, imaginal disc morphogenesis and imaginal disc-derived appendage morphogenesis. Most candidate SNPs associated to TL and WL showed sex-specific results although an important number of SNPs were associated to WL variation in both sexes simultaneously. Several of these SNPs are associated to genes as fruitless, which have been related to inter-male aggressive behavior. On the other side, most SNPs associated to FW were related to the SNP by sex interaction, although some of them showed sex-specific results. One of the two genes related to variation in males´s FW, Gr39a, has been associated to courtship behavior in males. Finally, our results confirmed five candidate genes which have been related to different morphological traits using other type of isogenic lines (e.g. CG9171, CG42684, bif, bol and ed), many of which have been associated to inter-male aggressive behavior. These results greatly contribute to the knowledge regarding the genetic basis of body size traits as well as they raise interesting questions concerning its relationship with characters related to sexual behavior.

Evolutionary conservation of genes for male size at maturity in poeciliid fishes

Tyler Collins, Margaret Ptacek, Brian Langerhans, Elizabeth Lange, Felix Breden, Shawn Shaji

Monday, June 23, 2014 -Poster #124

Animals have evolved remarkably variable reproductive strategies, but we currently know very little about their underlying genetic basis in most taxa. Poeciliid fishes are well known for their great diversity in male secondary sexual characteristics including body size, fin ornamentation, coloration and courtship behaviors, and in many species males exhibit size-linked alternative mating strategies of courting versus sneaking. Recent work uncovered a link between allelic variation and copy number of the melanocortin 4 receptor (mc4r) gene in some species of swordtails (Xiphophorus) and differences in male size at maturity and expression of size-associated alternative mating behaviors. To test whether mc4r variants are evolutionarily conserved over a wide range of poeciliid fishes, we characterized allelic diversity at mc4r in 18 species from four genera; each genus contains species that have considerable variation in male size and age at maturity and exhibit alternative mating strategies. We found homologous alleles to those described for mc4r in swordtails in every poeciliid species examined, suggesting strong conservation of these alleles over evolutionary time. When mapped onto a phylogeny constructed from the mitochondrial ND2 gene, these results suggest an ancient origin (> 40 MYA) of mc4r mutant alleles, likely pinpointing a major contributing factor in the diversification of male size and size-associated mating signals observed in poeciliid species today.

Quantitative genetics of an evolutionary innovation and diagnostic trait in the Drosophila affinis subgroup

Ryan Mulqueen, Spencer Koury

Monday, June 23, 2014 -Poster #125

Genetic architecture is the pattern and organization of genetic effects controlling phenotypic variation. Genetic architecture is the most important factor in predictions for the evolution of any trait. Here, we study the genetic architecture of an evolutionary innovation and species diagnostic trait in the Drosophila affinis subgroup. Sex comb morphology originated in Sophophora, varies widely across species, and is evolutionarily labile. To determine if genetic architecture is also evolving, we apply quantitative genetic analyses to both within and between species variation in sex comb morphology. We established inbred lines for five species within the D. affinis subgroup (D. athabasca, D. algonquin, D. azteca, D. narragansett and the appellative D. affinis). Due to the fact that these species are interfertile, we can experimentally test the evolution/conservation of sex comb genetic architecture. In contrast to the vast phenotypic diversity of sex combs, both within species, between species and in hybrids, the organization of genetic effects underlying this variation remains similar.

Self-incompatibility and the maintenance of cleistogamy in T. perfoliata, an annual herb

Beth Ansaldi, Steve Franks, Jennifer Weber

Monday, June 23, 2014 -Poster #126

One of the central challenges in evolutionary plant biology concerns the ecological and evolutionary significance of mixed mating systems. Mixed mating refers to reproduction in hermaphroditic individuals wherein both self-fertilization (selfing) and mating with other individuals (out-crossing) produce offspring. Some evolutionary theories and genetic models predict that only fully selfing or fully outcrossing strategies are stable because the two represent separate peaks of an adaptive landscape (Lande and Schemske 1985), yet mixed mating systems have evolved in as many as 49% of plant species (Vogler and Kalisz 2001, Goodwillie 2005). Despite knowledge that plant mating systems are prone to adaptive evolution, mating systems are often studied at the species level. Examining intraspecific variation across populations can elucidate mechanisms behind mating system evolution. This study will determine the extent to which self-incompatibility, the primary mechanism plants use to prevent selfing, varies across four populations of T. perfoliata. Triodanis perfoliata (Campanulaceae) is a hermaphroditic annual herbaceous plant, containing both male and female reproductive parts within each individual flower. Triodanis perfoliata confers a mixed mating system, but utilizes specialized (cleistogamous) flowers for exclusive selfing and chasmogamous flowers that have potential to both self and outcross. By means of hand-pollination, I am producing selfed progeny (both from cleistogamous flowers and selfed chasmogamous flowers) and outcrossed offspring from 4 populations, 17 maternal plants each. For each maternal plant, fruits will be collected and seeds will be counted and weighed. Results showing that seed production from manually selfed flowers varies with population, would suggest that adaptive self-incompatibility varies with populations. This study is part of a larger study examining inbreeding depression in T. perfoliata.

Cleistogamy affects the direction and extent of gene flow between subspecies of an annual plant

Carol Goodwillie, Emily R. Stewart, Evan Arthur

Monday, June 23, 2014 -Poster #128

The evolution of self-fertilization is often argued to be one of the most common trends in plant evolution, and the selective factors driving mating system evolution are well-studied; yet the role of mating systems in evolutionary divergence has received considerably less attention. This study addresses the role of dimorphic cleistogamy, the production of both open, cross-pollinated (chasmogamous, CH) flowers and closed, obligately selfing (cleistogamous, CL) flowers, in limiting gene flow between two widely co-occurring subspecies of the annual plant, Triodanis perfoliata that have diverged in their allocation to CH and CL flowers. Genetic marker analysis of three contact zones in North Carolina supports the presence of distinct subspecies but reveals a low to moderate degree of hybridization. A local study of the relative strength of sequentially acting reproductive barriers quantified the effects of habitat isolation, cleistogamous flower production, asynchrony in chasmogamous flower production, pollinator fidelity and F1 viability and fertility in limiting gene flow between the subspecies. Postzygotic barriers were found to be weak. Cleistogamy is the predominant prezygotic factor limiting hybridization. Despite the weedy nature of both subspecies, divergence in preference for soil and light conditions also appears to limit their co-occurrence to some degree. Genetic analysis suggests that gene flow may be asymmetric, and dominance of high CH flower production in F1s may be the causal factor. Thus, cleistogamy appears to play a key role in limiting and determining the direction of gene flow between sympatric subspecies.

Correlates of gut community composition across an ant species (Cephalotes varians) elucidate causes and consequences of symbiotic variability

Yi Hu, Piotr Lukasik, Corrie Moreau, Jacob Russell

Monday, June 23, 2014 -Poster #129

Insect guts are often colonized by multi-species microbial communities that play integral roles in nutrition, digestion, and defense. Community composition can differ across host species with increasing dietary and genetic divergence, yet gut microbiota can also vary between conspecific hosts and shift/change during an individual's lifespan. Through exploration of such intraspecific variation and its correlates, molecular profiling of microbial communities can generate and test hypotheses on the causes and consequences of symbioses. In this study, we used 16S rRNA amplicon sequencing and TRFLP analysis to achieve these goals in an herbivorous ant, Cephalotes varians, exploring variation in bacterial communities across colonies, populations, life stages and workers reared on different diets. We found that C. varians bacterial communities were dominated by 16 core species present in over two-thirds of the sampled colonies. Core bacteria hailed from ant-specific clades, with most having close relatives in other Cephalotes species. In spite of their prevalence and long-standing relationships with Cephalotes ants, the relative abundance of core species varied across colonies and individuals. We demonstrate that diet influences the microbial community composition, with pollen-based diets altering the relative abundance of certain bacteria. Furthermore, microbial communities shift in a predictable manner as workers age. Additional factors such as host genetics, chance, or natural selection must therefore shape natural variation. Future studies on these possibilities and on bacterial contributions to the use of pollen, a widespread food source across Cephalotes, will be important steps in developing C. varians as a model for studying widespread social insect-bacteria symbioses.

Differentiation of sex allocation strategies between terminal and lateral inflorescences in Aconitum kusnezoffii

Xing-Yue Ge

Monday, June 23, 2014 -Poster #131

Flowering plants have evolved more diverse sexual systems than any other organisms on this planet. Fitness of a individual hermaphroditic plant is the sum of its male and female reproductive success. Sex allocation theory predicts fitness maximizing strategies in terms of allocation of resources to male and female function. Due to modular growth, studies on plant sex allocation may be performed on different scales, such as within flower, among flowers, among inflorescences, among ramets or among individuals. Most prior studies have considered only within flowers or within inflorescence scales while few studies have considered among inflorescences or among ramets scales. We investigated the sex allocation patterns within flower and among inflorescences in a self-compatible, bee-pollinated clonal perennial plant, Aconitum kusnezoffii. Special attention was paid to the differences between terminal and lateral inflorescences.

We found that early-flowering terminal inflorescences have more female reproductive success than late-flowering lateral inflorescences, and inflorescences near the terminal position produced larger seeds. We also investigated the initial male and female reproductive investment between terminal and lateral inflorescences. We collected mature anthers before pollen dispersal, counted the pollen grains using particle analyzer, and counted the stamen and ovule numbers under microscope. We found that flowers of terminal inflorescences produced more ovules, while flowers of lateral inflorescences tended to produce more stamens and more pollen grains per stamen. During the fruiting phase we compared female reproductive success between terminal and lateral inflorescences, the results showed that the lateral ones had comparatively lower female fertility than terminal inflorescences. A further experiment was conducted to test whether pollen and/or resource limitation led to the reduced female reproductive success of lateral inflorescences. Aconitum kusnezoffii gender dynamics during its whole flowering period showed that early-blooming terminal inflorescences had a female biased sex allocation while later-blooming lateral inflorescences had a male biased sex allocation. This flowering-time dependent pattern resulted in flowers of terminal inflorescences bearing more female gametes and while lateral inflorescences bore more male gametes, leaving less resources for the female reproduction of lateral inflorescences.

Impact of male: female ratio on male mating behaviors in Poecilia latipinna

Shane Gorbett, Shala Hankison

Monday, June 23, 2014 -Poster #132

Studies on intersexual mating competition show that an increase in the proportion of males leads to increased male-male aggression and decreased courtship. Mating behaviors of the U.S. sailfin molly (Poecilia latipinna) have been studied in depth, however primarily in a 1:1 male: female ratio. We hypothesized that in a more female biased ratio males would exhibit a higher frequency of female-oriented mating and courtship behaviors and in more male biased ratios males would demonstrate a decrease in courtship behaviors and mating frequency and an increase in male competition. We observed male P. latipinna in four differing male: female ratios of 1:1,1:5, 2:4, and 3:3 for mating, courtship, and competition behaviors. As predicted there was a significant increase in male courtship displays and nibbling in the 1:5 male: female ratio compared to the more male biased ratios. However, contrary to our hypothesis there was no difference in thrusting frequency between the various male: female ratios. Males in more male biased groups showed slightly, but not significantly, more aggression and competition behaviors (eg. male-male displays) compared to males in more female biased environments, suggesting that there may be a threshold for the benefits of competition. In male biased environments, male competition increased, as males competed more vigorously for a lower number of potential mates. This study demonstrated that in a social environment with an increased proportion of competitors male P. latipinna put less time and energy into courtship displays and nibbling behaviors directed at females, and more time and energy into competing with other males, but that thrusting, a behavior that potentially can pass sperm to the female, did not change.

The influence of male and female genotype on copulatory plug breakdown

Rachel Mangels, Matt Dean

Monday, June 23, 2014 -Poster #133

In a wide diversity of taxa, the male's ejaculate coagulates to form a structure known as the copulatory plug, which in mice completely fills and adheres to the vaginal-cervical canal. One functional hypothesis is that the copulatory plug is a male's adaptation for blocking access of other males to a mated female's reproductive tract. This dynamic potentially places the copulatory plug in sexual conflict, where the structure benefits males to the detriment of females. However, little is known about the dynamics of the plug following mating, and whether plug survivorship depends on male and female genotypes. Here we mated multiple males from 10 genetically distinct strains of mice to multiple females from 2 genetically distinct strains in all combinations. We show that plugs survive in the female reproductive tract for 24-48 hours following mating, consistent with an interpretation that the plug is effective at blocking future matings. The survivorship trajectory is significantly influenced by male genotypes. In our study, we did not detect an effect of female genotype. The male genotypes in our study did not differ in terms of seminal vesicle size, the organ that is primarily responsible for the manufacture of copulatory plug proteins in mice. Male genotypes also did not differ in protein sequence of candidate copulatory plug genes. The explanation for the effect of male genotype therefore remains unexplained, but nevertheless reveals that males make plugs that degrade at different rates.

The role of social and dietary environment on growth and life history trait expression in sailfin mollies, Poecilia latipinna

Elizabeth Lange, Grant Davidson, Kelly Hogan, Margaret Ptacek

Monday, June 23, 2014 -Poster #134

Understanding the genetic and environmental factors responsible for differences in growth and life history traits, such as size and age at maturity, can aid in determining how alternative male mating strategies evolve and persist in natural populations. Both social and dietary environment are important environmental factors as they can influence the development of an individual and result in differences in survival and reproductive success. In sailfin mollies, Poecilia latipinna, male size is fixed at maturity, highly variable within populations and correlated with the expression of alternative male mating behaviors. Early maturation confers natural selection benefits through earlier reproduction, but reaching maturity later confers sexual selection benefits since females prefer to mate with larger males, which result from a longer growth period. In this study, we used a breeding design to determine the genetic (G), environmental (E) and GxE effects on the development of life history traits including growth rate and age and body size at maturity. We raised half siblings from three sire size classes (small, intermediate and large to approximate genotype) in isolation on two different diets (high protein versus low protein) and in three social groups (in isolation, in sibling groups that lacked an adult male and in sibling groups with an adult male present) while being fed the high protein diet. There was no effect of genes (sire size class) or dietary environment on age or size at maturity. Diet did, however, have a significant effect on growth rate as measured by mass, with control fed individuals increasing in mass faster than half-sibs reared in the low protein diet treatment. There was also a strong effect of social environment on these life history traits. Male offspring reared in the presence of an adult male took nearly three times longer to reach maturity and were twice as large as male offspring reared alone, or in sibling groups in the absence of an adult male. Adult males appear to provide cues (chemical and/or visual) that delay maturity and allow juvenile males to mature at larger sizes. Future work will examine the role of social environment at a finer scale by investigating how the size of the adult male social competitor and timing of exposure to social competitors affects these life history traits, as well as, the development of alternative mating strategies in these fish.

Sexual size dimorphism and reproductive isolation in two island populations of Anolis sagrei

Eric Wice, Anastasia Arkhipova, Christopher Noble-Molnar, Andrew Schurtz, Thomas Wood, Robert Cox

Monday, June 23, 2014 -Poster #135

Sexual selection may favor speciation both by leading to phenotypic divergence among populations and contributing to reproductive isolation. Here, we present results from a study of two island populations of Anolis sagrei that show strong differences in the extent of sexual dimorphism, a pattern likely driven by differing histories of sexual selection. We mated lizards in the lab both within and between populations to assess the potential for reproductive isolation. Between-population crosses produced significantly fewer eggs, but did not differ in hatching success, which suggests the potential for prezygotic isolation. Between-population crosses involving larger males showed the largest decline in fitness, suggesting that females from the low-dimorphism population may be intimidated by larger males. Our results indicate the presence of reproductive isolation between these divergent populations. Future work will be needed to quantify prezygotic vs. postzygotic isolation and to test whether the pattern seen in these two populations is general.

Testing for cryptic female choice in monarch butterflies

Andrew Mongue

Monday, June 23, 2014 -Poster #136

Sexual selection is an important force in shaping the evolution of species. Although many studies have focused on pre-copulatory female choice, it is increasingly clear that females may choose paternity following copulation with multiple males. Such cryptic female choice may be especially common in species where females have limited ability to choose pre-copulation. We tested for cryptic female choice in the monarch butterfly (Danaus plexippus). Whereas most butterfly species have elaborate pre-copulatory courtships, mating in monarchs is coerced by males, suggesting females only have post-copulatory opportunities to affect the fatherhood of their offspring. We used a mating design consisting of pairs of females, both mated to the same two males. Using microsatellite markers, we determined P2, the proportion of offspring fathered by the second male. In three treatments, we varied the relatedness of females and males, and calculated the repeatability of P2 values of the first and second female in a replicate. Assuming cryptic female choice, we predicted more repeatable P2 values for genetically related female pairs than unrelated pairs. In addition, we predicted that females should favor paternity by unrelated males over brothers to avoid potential inbreeding depression. Our results revealed no differences in repeatability of P2 values between treatments and no differences in paternity of brothers and unrelated males. These results suggest that monarch butterflies do not employ cryptic female choice and do not avoid inbreeding. Moreover, we did not find significant sperm precedence; neither the first nor second male obtained higher paternity. However, our results did indicate that interactions between male and female genotypes affected offspring paternity, suggesting that genetic compatibilities may affect sexual selection in this species. We also found a bimodal paternity distribution, confirming that monarchs follow the Lepidopteran pattern of paternity, despite pre-copulatory behavioral differences.

Multimodal Signaling and Mating Success in Drosophila saltans

Cynthia Odu, Kaila Colyott, Jennifer Gleason

Monday, June 23, 2014 -Poster #137

A variety of signals produced by the male and female contribute to courtship and are instrumental in mate choice and mating success within a species. These signals are produced and received through a variety of sensory channels, including visual, auditory, gustatory, and olfactory organs. In the genus Drosophila, the evolution of these sensory modalities may contribute to speciation through changes in courtship signals and their reception. Within the Drosophila saltans species group, courtship song has evolved quickly, leading us to ask what role audition and the other sensory modalities play in the courtship and mating. We tested the role of sensory modalities in mating success for D. saltans, the nominate species of the saltans group. We compared courtship variables of individuals with ablated and intact senses to test the hypothesis that individual sensory modalities are important for recognition of a compatible mate. Vision was ablated by both covering eyes and placing potential mating pairs in the dark, olfaction by removing the antennae, gustation by removing the foretarsi and midtarsi (the location of pheromonal receptors), and audition by both removing the males wings (sound production organ) and the females aristae (sound reception organ). All tested sensory modalities affected copulation success and the only individual sense that was required for copulation to occur was olfaction. In conclusion, the tested sensory modalities both increase mating success and facilitate copulation.

Patterns of selection on floral traits important for male fitness in the gynodioecious Geranium maculatum

Dorothy Christopher, Shu-Mei Chang

Monday, June 23, 2014 -Poster #138

A major transition in angiosperm evolution that has occurred multiple independent times is the evolution of separate sexes from a hermaphroditic ancestor. Theoretical studies have posited that separate male and female plants, dioecy, evolve from hermaphroditism via a gynodioecious intermediate stage, in which populations have separate female and hermaphroditic plants. For dioecy to evolve, several conditions must be met. First, the presence of females causes hermaphrodites to gain more of their fitness through male function. This puts selective pressure on hermaphrodites to invest more in traits related to male fitness at the expense of ovule production. The selective pressure should increase as female frequency increases. Additionally, the spatial structuring of the sexes found in gynodioecious populations can influence the functional maleness of a hermaphrodite. Hermaphrodites surrounded by other hermaphrodites will acquire fitness equally through male and female function. Hermaphrodites surrounded by females will acquire fitness more through male function. This creates favorable conditions for the successful establishment of a female sterility mutant. We tested this theory in Geranium maculatum, a gynodioecious perennial herb. In populations that span the range of female frequencies in this species (0-50%), we created a dispersal kernel to define an area within which individuals mate. We then estimated the sex ratio within the dispersal kernel. Floral traits important for male fitness were measured in hermaphrodites. We examined the pattern of selection on floral traits using a multivariate phenotypic selection analysis. We predict that at high female frequency, hermaphrodites will acquire less of their total fitness through male function, and more through female function. This study provides an empirical analysis of the gynodioecy-dioecy evolutionary transition.

Characterisation of the Manduca sexta Sperm Proteome

Emma Whittington, Qian Zhao, Stephen Dorus, James Walters, Stuart Reynolds

Monday, June 23, 2014 -Poster #139

Mass spectrometry (MS) based proteomic analyses have greatly improved our understanding of sperm cell composition. Here we present the analysis of the Tobacco Hornworm (Manduca sexta) sperm proteome, the first Lepidoptera sperm proteome to be characterised. Using MS-based techniques 1070 proteins were identified from 3 biological replicates, using high stringency peptide and protein identification parameters. Comparative analysis with the Drosophila melanogaster sperm proteome showed considerable overlap and correlations in protein abundance. Phylogenetic comparisons revealed 173 proteins unique to the Lepidoptera, 11 of which were among the top 25 most abundant proteins in the proteome. Expanding these methods into further Lepidoptera species and analysing eupyrene and apyrene sperm types separately may give insight into the function of parasperm in this sperm heteromorphic group.

The Relationships Between Female Throat and Egg Carotenoids in Threespine Sticklebacks from a Population with Red-Throated Females

Ruqing Guo, Michele Pierotti, Lenny Yong, Jeffrey McKinnon

Monday, June 23, 2014 -Poster #140

The male threespine stickleback (Gasterosteus aculeatus) has been studied extensively for the orange-red nuptial color that results mainly from carotenoids, a class of pigments that also possess important functions as immunostimulants, as antioxidants, and potentially in other capacities. Although orange-red throat coloration has now also been documented in the females of some stickleback populations, female coloration has only lately begun to be studied, and the role of carotenoids in female coloration has not been examined. We investigated female throat carotenoids and the potential trade-offs between carotenoid content of throat skin tissue and of eggs. HPLC was used to identify and quantify carotenoids in both tissues for field-collected females, and reflectance measurements were made to assess throat coloration. We found (a) female throat carotenoids mainly comprise astaxanthin and closely related pigments, and lutein and closely related pigments; (b) there are strong positive correlations between throat carotenoids and egg carotenoids; (c) correlations between reflectance-based measures of throat coloration and carotenoid measures (total, astaxanthin only, lutein only, or astaxanthin/lutein ratio) are non-significant, although these analyses continue. To our knowledge, this is the first study of female throat color and pigment composition in the threespine stickleback and the first to document that females possess the same throat pigments as males. Moreover, the positive correlation between carotenoid concentrations in throat and egg tissues argues against a clear trade-off for carotenoid allocations. This contrasts with previous findings that document a negative relationship between the red intensity of female pelvic spines and gonad carotenoids (Nordeide et al. 2006). The absence of robust relationships between throat coloration and carotenoid concentrations is unexpected and contradicts some results for male sticklebacks. In sum, relationships between color patterns and carotenoids may vary by sex and possibly population, suggesting that few assumptions can be made about the pigments underlying color patterns without direct investigation of the pigments themselves.

Sperm heteromorphy in Danaus plexippus: a molecular approach to an unsolved phenomenon

Desiree Harpel, James Walters

Monday, June 23, 2014 -Poster #141

In Lepidoptera there occurs a phenomenon of sperm heteromorphy, in which males produce both fertilizing (eupyrene) and non-fertilizing sperm (apyrene). Furthermore, apyrene sperm lacks DNA and a nucleus and is produced in higher quantities than eupyrene sperm. Why do males invest in producing vast amounts of sperm that do not fertilize? This question has spurred numerous research efforts to begin to understand the role of apyrene sperm, but all have been inconclusive in pinning down apyrene function. This study is the first to perform a molecular approach to characterize the protein content in both sperm types, leading to new insight in the investigation in the purpose of apyrene sperm. A novel method for separating apyrene from eupyrene sperm was developed and applied to sperm samples of Danaus plexippus, the Monarch Butterfly. Liquid chromatography/mass spectrometry (LC/MS) proteomic techniques were then applied to characterize the two sperm morphs.

Multi-model analysis of biased birth sex ratios in captive prosimians

Elizabeth Berkeley, Sarah Zehr

Monday, June 23, 2014 -Poster #142

Certain life history traits and environmental cues are suspected to strongly link with offspring sex based on sex allocation (SA), or provision of resources by the parents towards their offspring. Several theories have been proposed to explain the observed variation including the Trivers-Willard hypothesis; local resource competition; and its corollary, local resource enhancement. In the past ten years, it has been suggested that the physiological mechanisms responsible for sex allocation may involve changes in circulating glucose or steroid hormone concentrations around the time of conception. Part of the confusion in understanding SA is that many different species and both proximate (i.e. physiological, endocrinological) and distal types of variables (i.e. evolutionary and ecological) have been analyzed. The Duke Lemur Center database provides a fortuitous opportunity to conduct a comparative analysis of evolutionary theories on causes for biased birth sex ratios in a large group of closely related prosimians primate species. We tested competing hypotheses of sex allocation using multimodel hierarchical analyses. Data was tabulated according to published predictors including life history traits. Sex ratio variation was calculated both as deviation from parity and from averaged population birth sex ratios. Multiple models were constructed and a Bayesian-type analysis was performed in JMP to identify the variables that best explain the variation in the SA response.

Structure and function of bursal spines in the female internal genitalia of false blister beetles (Coleoptera: Oedemeridae)

Kosei Hashimoto, Hirotaka Sugawara, Fumio Hayashi

Monday, June 23, 2014 -Poster #143

Antagonistic coevolution between the sexes has been considered to be responsible for the rapid evolution of male reproductive traits in insects. However, its impact on female reproductive morphologies is not fully understood because the female reproductive organs are soft and simply membraneous. Females of the false blister beetle, Nacerdes caudata (Coleoptera: Oedemeridae), have numerous sclerotized spines in their bursa copulatrix. In this species, males transferred a large spermatophore to the female, and then the spermatophore was eventually broken and consumed within the female spiny bursa copulatrix. In contrast, males of the congeneric species, N. waterhousei, formed a small spermatophore. The females had no spines in the bursa copulatrix in this species. Thus, spines in the bursa copulatrix were assumed to break and consume large spermatophores transferred from males at mating. To clarify the matching between the evolutionary patterns of bursal spines and spermatophore sizes, we examined presence or absence, sizes, and numbers of the sclerotized spines in the bursa copulatrix and sizes of spermatophores in 25 species of false blister beetles. Also we constructed a molecular phylogenetic tree for these oedemerid species inferred from mitochondrial 16S and nuclear 28S rRNA gene sequences. Comparisons of male and female reproductive traits on the phylogenetic tree suggested that (i) oedemerid species originally have no spines in the bursa copulatrix, and then female bursal spines have evolved independently, (ii) males transfer larger spermatophores in the lineages with more spiny bursae, and that (iii) there is a trade-off between the number and size of bursal spines. Such evolutionary trends may be explained as sexually antagonistic coevolution between their reproductive traits. That is, males enlarge their spermatophores not to be consumed easily by the well-developed bursal spines of the females.

A test of inbreeding avoidance in multiple populations of the redheaded pine sawfly, Neodiprion lecontei

Katherine Harper, Robin Bagley, Catherine Linnen

Monday, June 23, 2014 -Poster #144

Many members of the order Hymenoptera, including sawflies, bees, wasps and ants, possess a haplodiploid, single-locus complementary sex determination system. Under sl-CSD, the allelic state of a single locus determines sex, with hemizygous haploid individuals developing into males, and heterozygous diploids developing into females. Although the presence of haploid males should allow rapid purging of deleterious recessive alleles, inbreeding avoidance has been detected in a wide range of Hymenoptera. While there are typically many alleles at the sex determining locus, under inbreeding, homozygous diploid individuals which develop into males may be produced. There is likely considerable selection pressure against inbreeding to avoid production of these diploid males, as they are often inviable or sterile. Here, we investigate multiple populations of the red-headed pine sawfly, Neodiprion lecontei, a pest species theorized to possess sl-CSD, for evidence of inbreeding avoidance. Under no-choice conditions, we examined the willingness of females from three populations of differing initial genetic diversity to mate with sibling versus non-sibling males. Preliminary analyses suggest significant inbreeding avoidance may exist, but the mechanism behind this behavior is unknown. If we are sure that our results are consistent with our predictions they could provide insight into the mating behaviors of sawflies and also carry implications for speciation processes. Future work will look into specific mechanisms behind kin recognition.

Transcriptional co-regulation of linked genes in Daphnia and its (epi?)genetic variability

Lev Yampolsky, Michael Pfrender, John Colbourne

Monday, June 23, 2014 -Poster #145

We show that transcriptional activity in linked genes in plankton crustacean Daphnia is co-regulated along long stretches of chromosomes (>5 Mbp), with areas of low CG content, low CpG density and high occurrence of low complexity regions containing mostly genes with low expression. Within the areas of high expression, on the other hand, mean expression correlates positively with CG content within 50Kbp windows. No significant clusters of genes co-regulated by high temperature have been found. On the other hand, numerous differences among distinct genotypes in co-regulation of linked genes can be observed, indicating either genetic or multigenerational epigenetic variation for local transcriptional activity. We analyze functional compositions of genes located in regions of low transcriptional activity and discuss possible roles of nucleosome positioning and chromatin remodeling in the observed patterns.

HIF (Hypoxia Inducible Factor) transcription factor family expansion and diversification in Eukaryotes

Allie Graham, Jason Presnell

Monday, June 23, 2014 -Poster #146

Hypoxia inducible factor (HIF) transcription factor genes are known to play a key role in cellular response to low oxygen tension in a variety of organisms, and are frequently associated with adaptations to high altitude and other oxygen limited environments. In Humans, the HIF-1, HIF-2/EPAS, and HIF-3 gene products encode alpha subunits, while the three ARNTs encode for the beta subunits that form functional heterodimers to regulate transcription.

All HIF genes are characterized by the presence of a bHLH DNA binding domain and two oxygen sensing PAS domains. HIF-1α and HIF-2α/EPAS are additionally characterized by the presence of the HIF-C-terminal domain (HIF-CTAD). Despite their important role in oxygen sensing, very few studies have focused on the evolutionary history of the HIF gene family, with even fewer analyses outside of the vertebrate lineage. Therefore, we have assessed the expansion and diversification of the HIF gene family in 35 eukaryotic genomes. We have also investigated the separate evolutionary histories of each of the three domains that characterize the HIF family.

Our results show that the combination of bHLH and PAS domains first appeared early in the metazoan lineage. However, the HIF-CTAD does not appear with the bHLH + PAS domains until after the divergence of the Bilateria. We also find that HIF-CTAD does not appear in combination with any other domain groups before, or after, its appearance in Bilaterians. We demonstrate that the invertebrate HIF/ARNT genes are divergent compared to their vertebrate counterparts. We also show that HIF-2α/EPAS appears soon after the divergence of Vertebrata, most likely as a result of the whole genome duplication event in the vertebrate stem lineage.

Thus, our results suggest that the HIF-CTAD domain evolved do novo in the Bilaterian stem lineage, and is specific to a subset of the HIF genes. We also show that both HIF- α and their –β (ARNT) complements, appear at the base of the metazoans. Our results also suggest that the appearance of the HIF-2α/EPAS domain architecture is correlated with the evolution of closed-circulatory system/endothelial vasculature, and it thus heavily constrained.

Bulk segregant RNA-sequencing reveals insights into the genetic basis for the loss of anthocyanin pigmentation in the genus Iochroma

Daniel Gates, Bradley Olson, Stacey Smith

Monday, June 23, 2014 -Poster #147

When multiple mutations can achieve the same adaptive phenotype, evolutionary theory predicts that the genetic change that incurs the smallest reduction in overall fitness will be preferentially fixed. Flower color provides a powerful system for testing this prediction because a wide array of mutations in pigment genes can result in similar phenotypes, and there are many cases of convergent shifts in color. In this study, we use a bulk segregant RNA-sequencing approach to identify the genetic basis for the transition from the blue ancestral state to white flowers in Iochroma loxense. Convergent evolution of white flowers in other lineages commonly involves mutations in R2R3 MYB transcription factors, allowing for the coordinated loss of expression of pigment genes in flowers without affecting the activity of these genes in other tissues. In I. loxense, however, we find no association of R2R3 MYBs with the loss of anthocyanin pigmentation. Instead, one R3 MYB transcription factor, which is orthologous to known regulators of the anthocyanin pathway in Mimulus, Petunia, and Arabidopsis, strongly predicts the phenotypes segregating in backcross populations. Although the developmental effect is similar to that of R2R3 mutations (i.e. downregulation of pathway genes), the R3 acts as a repressor of anthocyanin production and thus the derived I. loxense allele is nearly dominant in segregating populations. The similar developmental effects of these different classes of mutations lends support to the idea that regulatory changes are preferentially fixed during evolutionary transitions from pigmented to unpigmented flowers.

Untangling selection and mutation in non-coding RNA

Joshua Martin, Adam Smith

Monday, June 23, 2014 -Poster #148

Over 90% of the human genome is transcribed but never translated. This presents a problem when the techniques for tracking and determining if selection has occurred assumes that the nucleotide sequence codes for a protein. We present a method for determining when a change in sequence is the result of natural selection or random mutation. It is expected that natural selection should optimize the structure, lowering the number of structures that populate the ensemble of structures. For a non-coding RNA, the number of different structures in the ensemble of structures can be estimated with the Shannon entropy. By comparing the effect of the Shannon entropy from random changes, we are able to determine if a nucleotide sequence is the result of random mutations or natural selection. We applied this methodology to 73 sequences of the small subunit of the ribosome from E. coli and identified which sequences were the result of natural selection or random mutation. These results show what is expected to be a general pattern in the evolution of RNA; a single or a few mutations increase structural diversity which is then followed by multiple mutations that decrease structural diversity. We expect this methodology to be useful and informative for all non-coding RNA and especially for those that are highly structured.

Survival of the Curviest: Selection for Robustness and the Origins of Epistasis

Jon Wilkins

Monday, June 23, 2014 -Poster #149

Many common, heritable diseases are complex, in that additive genetic variation appears to account for only a small fraction of the overall phenotypic variability. Many of these diseases are likely to result from strong epistatic interactions among multiple loci. Using a simple, but biologically relevant "Limiting Reagent" model, we show how selection for robustness to phenotypic noise selects for strong epistasis, and we characterize how various features of the system affect the magnitude of epistasis observed. Previous studies have observed similar patterns, but have focused on the mean effect on epistasis. Our focus is on the probability and magnitude of epistasis in the most severe phenotypes, which are the set that is most relevant to understanding human disease. The characterized patterns may be useful in the identification of epistatic interactions in genome-wide association studies.

Variation in Genetic Robustness

Dana Opulente, Isaak Heon, Christopher Morales, Joshua S. Rest

Monday, June 23, 2014 -Poster #150

Genetic robustness, the maintenance of phenotypic stability in the presence of genetic perturbations, has long been hypothesized as an important evolutionary force. Two key questions about genetic robustness we address are: 1. Is there genetic variation in genetic robustness? 2. Is variation in genetic robustness and environmental robustness correlated? We generated mutant lines by subjecting wild strains of Saccharomyces cerevisiae to mutagenesis with ethylmethane sulfononate or UV light. We measured the survivorship and growth rate of both the ancestral cells, which were not treated with a mutagen, and mutant cell lines. We quantified variation in genetic robustness by comparing the distribution of growth rates of the mutant lines to the ancestral wild strains. We also measured the environmental robustness of each strain by measuring its growth across various nutrient and stress conditions. This allowed us to determine the extent of correlation between genetic robustness and environmental robustness. Our results suggest there is genetic variation in genetic robustness among strains.