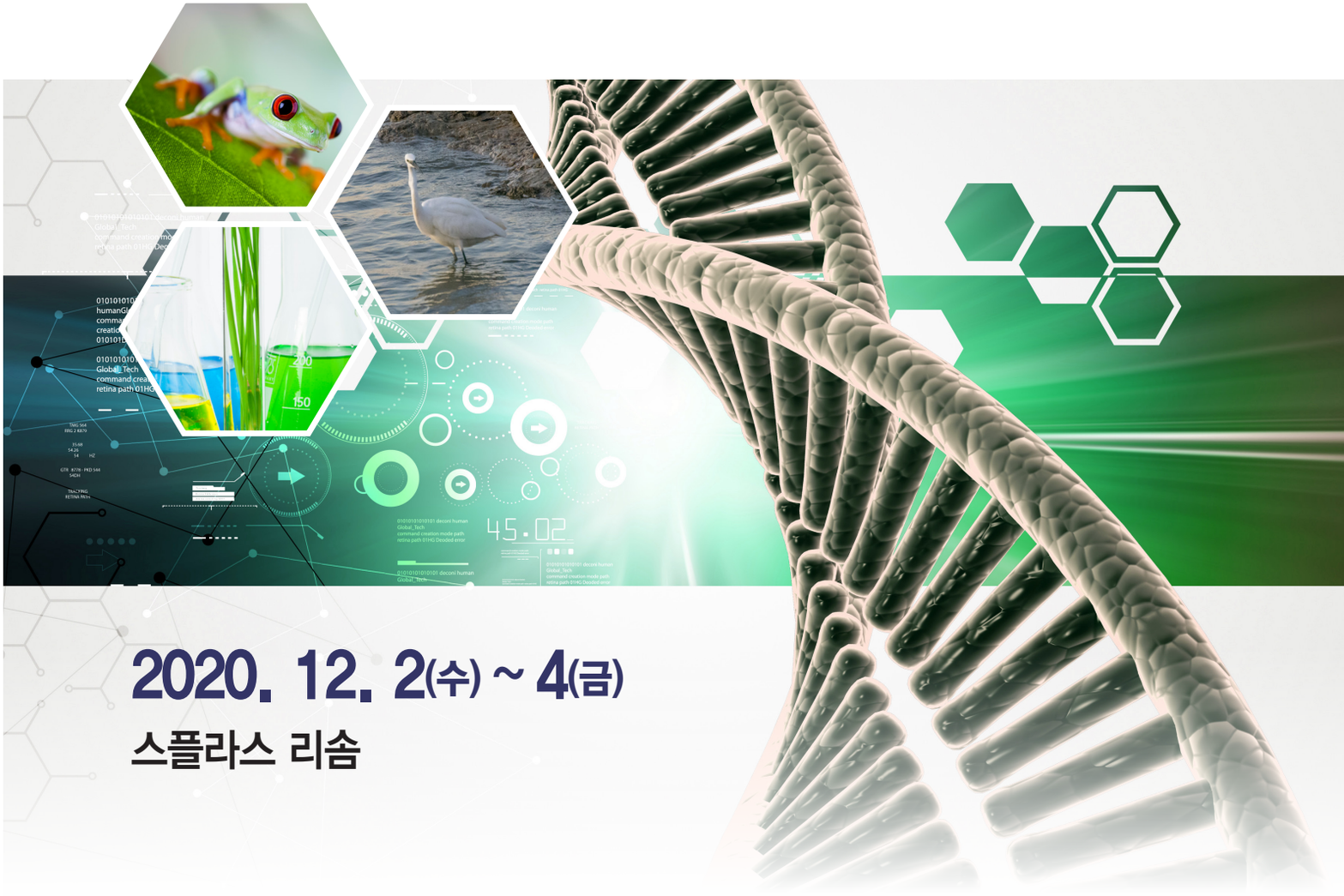
한국통합생물학회

정기학술대회



2020. 12. 2(수) ~ 4(금)

스플라스 리솜

주 최 한국통합생물학회

후 원 KOFST

IBS Institute for Basic Science CGI Center for Genomic Integrity

서울대학교 생물정보연구소 SNU BIOINFORMATICS INSTITUTE

한국통합생물학회

EVENT

"Total RNA Isolation Reagent"

많은 고객들께서 품질로 선택하신 바로 그 제품입니다.

TRI-Solution™

Virginia Tech Bio-Technology

TRI-Solution – High Quality & Low Price & No Bubble 제품입니다.

Event

Cat. No : TS200-001 Size : 200ml Price : 170,000(-Vat)

Dnases, Rnase free Performance Tested

※대학교, 의대, 국가기관, 연구소 등에서 다량 사용하고 있으며 많은 고객분들이 인증한 공인된 제품입니다.

※제품 성능이 궁금하시면 지금 곧 Sample 신청하시면 됩니다.

Feature

- 다양한 조직 및 세포로부터 1 시간 이내 total RNA , DNA, Protein추출 가능
- 색깔을 통해 aqueous phase와 phenol phase의 구분 용이
- 산화를 방지시켰기 때문에, 오랜 시간이 지나도 활성에 영향이 없습니다.
- 순도가 높은 Total RNA를 얻을 수 있습니다.
- RNA 추출을 위한 가장 경제적이며, 최고 제품입니다.

BSK ㈜비에스케이바이오 Bio Science Korea

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한국통합생물학회 정기학술대회 후원사 로고

This work was supported by the Korean Federation of Science and Technology Societies(KOFST) grant funded by the Korean government.

한국통합생물학회
정기학술대회

2020. 12. 2(수) ~ 4(금)
스플라스 리솜

주 최 한국통합생물학회 IBS Institute for Basic Science CGI Center for Genomic Integrity 서울대학교 생물정보연구소 SNU BIOINFORMATICS INSTITUTE

후 원 KOFST

환영사

안녕하십니까?

한국통합생물학회 회장 김철근입니다.

올해 코로나19의 확산 및 재확산으로 인한 사회적 거리두기로 회원님들의 일상 생활에 많은 불편함이 있을 것으로 생각됩니다. 한국통합생물학회 역시 이번 코로나19의 영향으로 인하여 어려움과 시행착오가 있었으나 저희 임원진은 올해 계획된 정기 학술대회 준비를 위해 최선을 다해 노력하고 있습니다.

올해 초 2020년도 정기학술대회를 9월에 개최하기로 의결한 이후 8월부터 코로나19의 재확산이 지속되면서 12월로 정기학술대회를 연기하였고 현장 대면 학회로서 진행하기 어렵다는 판단 하에 온라인 회의와 긴급 비상기획 위원회를 통해 100% 온라인 학회로 전환하기로 결정한 바 있습니다. 무엇보다 한국통합생물학회 회원 분들의 안전을 최우선시 하여 내린 결정이오니 온라인 학회의 불편함이 있으시더라도 넓은 아량으로 양해를 부탁드리겠습니다.

이번 정기학술대회는 12월 2일~4일 덕산 리플라스 리솜 현지에서 기조강연, 키노트 강연, 초청 강연자분들을 모시고 현장에서 온라인 생중계로 진행될 예정입니다. 기조연자로 UNIST 명경재 교수님, 서울시립대 조익훈 교수님, KAIST 허원도 교수님을 초청하였고, 키노트 연자로 한양대 최제민 교수님, 고려대 김윤기 교수님, 아주대 김유선 교수님을 초청하였습니다. 특별 초청 강연으로 한국연구재단 생명과학단장이신 김희수 교수님을 모셨습니다. 특히 한국통합생물학회 비전에 부합하도록 생명과학분야 6개의 다양한 세션 주제로 각 연구분야에서 출중하신 18분의 우수한 강연자 분들을 초청하였습니다. 학술대회를 위해 바쁘신 와중에 자리를 빛내주신 모든 연자분들께 진심어린 감사의 말씀을 올립니다. 이외에도 학생구두 및 학생포스터 발표는 사전 녹화 상영 및 e포스터로 진행되고 협력 기업들의 전시 참여는 온라인으로 구성하였습니다. 무엇보다 올해 초부터 예상치 못한 어려움 속에서도 이번 정기학술대회 준비를 위해 많은 노력과 열정을 아끼지 않으신 학회 운영진분들께 깊은 감사의 말씀을 올립니다.

아무쪼록 알찬 프로그램으로 구성된 정기학술대회를 통해 다양한 연구성과를 공유함과 동시에 회원분들과 함께 코로나 19의 어려움을 함께 극복하고자 합니다. 아울러 한국통합생물학회의 발전과 위상이 보다 확대될 수 있는 계기가 되길 바라며 회원님들의 많은 참여와 성원을 부탁드립니다.

2020년 12월 2일

한국통합생물학회 회장

김 철 근

일정표

날짜	시간	프로그램	
12.2 (수)	09:00 ~ 10:30	**Registration** *[스테이타워 2층 로비]*	
	10:30 ~ 10:40	**Opening remarks** *[스테이타워 2층 SPACE A]*	
	10:40 ~ 11:30	**Plenary lecture I: (명경재, UNIST)** Translation of genomic integrity to clinical application *[스테이타워 2층 SPACE A]*	
	11:30 ~ 12:10	**Keynote lecture I: (최제민, 한양대)** Role of bystander T cells in autoimmune encephalomyelitis *[스테이타워 2층 SPACE A]*	
	12:10 ~ 12:30	Photo time and Notice *[스테이타워 2층 SPACE A]*	
	12:30 ~ 14:00	Lunch time *[스테이타워 1층 더 다이닝]*	
	14:00 ~ 15:30	**Symposium I. Epigenetics: From mechanisms to disease** 김태경(POSTECH), 변상원(KRIBB), 주재열(한국뇌연구원) *[스테이타워 2층 SPACE A]*	**Symposium II. Precision medicine and human disease** 남진우(한양대), 이지훈(DGMIF), 이만렬(순천향대) *[스테이타워 2층 SPACE B]*
	15:30 ~ 17:00	**Poster presentation I**	
	17:00 ~ 18:00	**2021년 한국연구재단 생명과학단 기초연구과제 소개** (김희수, 한국연구재단 생명과학단장) *[스테이타워 2층 스페이스A]*	
	18:00 ~ 18:30	**정기총회** *[스테이타워 2층 스페이스A]*	
	18:30 ~	Banquet &Discussion *[스테이타워 2층]*	
12.3 (목)	07:00 ~ 09:00	**Breakfast** *[스테이타워 1층 더 다이닝]*	
	09:00 ~ 09:50	**Plenary lecture II: Functional analysis of novel regulators of Hippo and Wntsignalings (조익훈, 서울시립대)** *[스테이타워 2층 SPACE A]*	
	09:50 ~ 10:30	**Keynote lecture II: mRNA and polypeptide surveillance pathways (김윤기, 고려대)** *[스테이타워 2층 SPACE A]*	
	10:30 ~ 10:50	Break time	
	10:50 ~ 12:20	**Symposium III. Biodiversity and evolution** 윤성일(중앙대), 박춘구(전남대) 조성진(충북대) *[스테이타워 2층 SPACE A]*	**Symposium IV. Advanced bioimaging** 김두리(한양대), 이성수(KBSI) 김범수(한국뇌연구원) *[스테이타워 2층 SPACE B]*
	12:20 ~ 13:20	**Lunch time** *[스테이타워 1층 더 다이닝]*	
	13:20 ~ 14:50	**Symposium V. Viruses, crossing species** 박수형(KAIST), 이종수(충남대) 이근화(한양대) *[스테이타워 2층 SPACE A]*	**Symposium VI. Neurological disorders and brain injury** 이병대(경희대), 이연종(성균관대), 윤기준(KAIST) *[스테이타워 2층 SPACE B]*
	14:50 ~ 15:20	Break time	
	15:20 ~ 16:10	**Plenary lecture III: Optogenetic control of diverse molecular and cellular processes in the mouse brain (허원도, KAIST)** *[스테이타워 2층 SPACE A]*	
	16:10 ~ 16:50	**Keynote lecture III: Necroptosis in pathophysiology of disease (김유선, 아주대)** *[스테이타워 2층 SPACE A]*	
	16:50 ~ 18:00	**Poster presentation II**	
	18:00 ~ 21:00	Dinner & Group discussion *[스테이타워 1층]*	
12.4 (금)	07:00 ~ 09:30	Breakfast *[스테이타워 1층 더 다이닝]*	
	09:30 ~ 11:30	**Student presentation I.** *[스테이타워 2층 SPACE A]*	**Student presentation II.** *[스테이타워 2층 SPACE B]*
	11:30 ~ 12:30	**Awards** *[스테이타워 2층 SPACE A]*	
	12:30 ~	**Closing remarks** *[스테이타워 2층 SPACE A]*	

발표일정

Plenary Lecture I

일시: 2020. 12. 2. (수) 10:40-11:30
장소: 스플라스 리솜 스테이타워 스페이스 A
좌장: 조 익 훈 (서울시립대학교)

10:40-11:30__**Translation of genomic integrity to clinical application**
Kyungjae Myung (Center for Genomic Integrity, IBS and Department of Biomedical Engineering, UNIST)

Plenary Lecture II

일시: 2020. 12. 3. (목) 09:00-09:50
장소: 스플라스 리솜 스테이타워 스페이스 A
좌장: 조 성 진 (충북대학교)

09:00-09:50__**Functional analysis of novel regulators of Hippo and Wnt signalings**
Eekhoon Jho (University of Seoul)

Plenary Lecture III

일시: 2020. 12. 3. (목) 15:20-16:10
장소: 스플라스 리솜 스테이타워 스페이스 A
좌장: 기 윤 (강원대학교)

15:20-16:10__**Optogenetic control of diverse molecular and cellular processes in the mouse brain**
Won Do Heo (Department of Biological Sciences, Korea Advanced Institute of Science and Technology (KAIST))

Keynote Lecture I

일시: 2020. 12. 2. (수) 11:30-12:10
장소: 스플라스 리솜 스테이타워 스페이스 A
좌장: 조 익 훈 (서울시립대학교)

11:30-12:10__**Role of bystander T cells in autoimmune encephalomyelitis**
Je-Min Choi (Department of Life Science, Hanyang University)

Keynote Lecture II

일시: 2020. 12. 3. (목) 09:50-10:30
장소: 스플라스 리솜 스테이타워 스페이스 A
좌장: 조 성 진 (충북대학교)

09:50-10:30__**mRNA and polypeptide surveillance pathways**
Yoon Ki Kim (Division of Life Sciences, Korea University)

Keynote Lecture III

일시: 2020. 12. 3. (목) 16:10-16:50
장소: 스플라스 리솜 스테이타워 스페이스 A
좌장: 기 윤 (강원대학교)

16:10-16:50__**Necroptosis in pathophysiology of disease**
You-Sun Kim (Department of Biochemistry, Ajou University School of Medicine & Department of Biomedical Sciences, Graduate School, Ajou University)

Symposium I. Epigenetics: From mechanisms to disease

일시: 2020. 12. 2. (수) 14:00-15:30
장소: 스플라스 리솜 스테이타워 스페이스 A
좌장: 이 화 선 (UNIST)

14:00-14:30__**Functional coordination of BET family proteins in brain plasticity and diseases**
Tae-Kyung Kim (Department of Life Sciences, POSTECH)

14:30-15:00__**Fasting-induced FGF21 signaling activates hepatic autophagy and lipid degradation via JMJD3 histone demethylase**
Sangwon Byun (Personalized Genomic Medicine Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB))

15:00-15:30__**Big data-based novel Alzheimer's disease diagnostics target genes**
Jae-Yeol Joo (Neurodegenerative Disease Research Group, Korea Brain Research Institute)

Symposium II. Precision medicine and human disease

일시: 2020. 12. 2. (수) 14:00-15:30
장소: 스플라스 리솜 스테이타워 스페이스 B
좌장: 조 정 희 (단국대학교)

14:00-14:30__**Ultra-fast prediction of somatic structural variations by reduced read mapping via pan-Genome *k*-mer sets**
Jin-Wu Nam (Department of Life Science; Research Institute for Convergence of Basic Sciences; Research Institute for Natural Sciences, Hanyang University)

14:30-15:00__**The development of protein-protein interaction modulators using peptidomimetic compound**
Ji Hoon Lee (New Drug Development Center, Medicinal Chemistry Support Department, Daegu Gyeongbuk Medical Innovation Foundation (DGMIF))

15:00-15:30__**Metabolic restructuring and cell fate conversion through controlling cellular organelles**
Man Ryul Lee (Soonchunhyang Institute of Medi-bio Science (SIMS), Soon Chun Hyang University)

Symposium III. Biodiversity and evolution

일시: 2020. 12. 3. (목) 10:50-12:20
장소: 스플라스 리솜 스테이타워 스페이스 A
좌장: 지 성 길 (고려대학교)

10:50-11:20__**The evolutionary origin of phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS)**
Seong-il Eyun (Department of Life Science, Chung-Ang University)

11:20-11:50__**Is phylotranscriptomics as reliable as phylogenomics?**
Chungoo Park (School of Biological Sciences and Technology, Chonnam National University)

11:50-12:20__**Insights into marine animal genomics and regeneration from Lophotrochozoa**
Sung-Jin Cho (School of Biological Sciences, College of Natural Sciences, Chungbuk National University)

Symposium IV. Advanced bioimaging

일시: 2020. 12. 3. (목) 10:50-12:20
장소: 스플라스 리솜 스테이타워 스페이스 B
좌장: 민 경 진 (인하대학교)

10:50-11:20__**Super-resolution microscopy study of platelet activation and release**
Doory Kim (Department of Chemistry, Hanyang University)

11:20-11:50__**Holotomography : Dynamic imaging for label-free living cell**
Seongsoo Lee (Korea Basic Science Institute Gwangju Center)

11:50-12:20__**Live imaging of a type of cell in the nervous system using a fluorescent chemical probe**
Beomsue Kim (Korea Brain Research Institute)

Symposium V. Viruses, crossing species

일시: 2020. 12. 3. (목) 13:20-14:50
장소: 스플라스 리솜 스테이타워 스페이스 A
좌장: 윤 성 일 (중앙대학교)

13:20-13:50__**A vaccine for severe fever with thrombocytopenia syndrome virus (SFTSV) than can confer complete protection against lethal infection**
Su-Hyung Park (Graduate School of Medical Science and Engineering, KAIST)

13:50-14:20__**Negative regulator of IFN signaling and IFN evasion of virus**
Jong-Soo Lee (College of Veterinary Medicine, Chungnam National University)

14:20-14:50__**Epidemiology of severe fever with thrombocytopenia syndrome virus**
Keun Hwa Lee (Department of Microbiology, Hanyang University College of Medicine)

Symposium VI. Neurological disorders and brain injury

일시: 2020. 12. 3. (목) 13:20-14:50
장소: 스플라스 리솜 스테이타워 스페이스 B
좌장: 김 정 목 (한양대학교)

13:20-13:50__**The pathological functions of LRRK2 in brain injury**
Byoung Dae Lee (Department of Physiology, Kyung Hee University School of Medicine, Department of Neuroscience, Kyung Hee University)

13:50-14:20__**Conditional mouse model of Parkinson's disease refined for preclinical application**
Yunjong Lee (Department of Pharmacology, Sungkyunkwan University School of Medicine)

14:20-14:50__**Deciphering the neural epitranscriptome using mouse and human brain organoid models**
Ki-Jun Yoon (Department of Biological Sciences, KAIST)

Student Presentation I

일시: 2020. 12. 4. (금) 09:30-11:30
장소: 스플라스 리솜 스테이타워 스페이스 A
좌장: 이 연 종 (성균관대학교)

09:30-10:20__**Linalool has neuroprotective effects on suppressing ROS production and inflammation of Linalool in Aβ42-induced *Drosophila* model of Alzheimer's disease**
Myeongcheol Shin (Konkuk University)

Characterization of Alzheimer's disease-associated genes using *Drosophila* model
Seokhui Jang (Konkuk University)

Newly recorded sea star *Henricia oculata* (Asteroidea: Spinulosida: Echinasteridae), in the East Sea, Korea
Michael Dadole Ubagan (Sahmyook University)

Effect of Th2 differentiation control through formation of skin lipid barrier on *Coptidis Rhizoma*, *Glycyrrhiza uralensis* and and fermameted *Glycine max* extract
Seong Eun Kim (Semyung University)

Study of amyloid-β-induced fragmentation of lamin A and B
Il-Seon Park (Chosun University)

TTF-1 action in leptin-induced development of hypothalamic neurons
Dasol Kang (University of Ulsan)

Stress-induced NEDDylation promotes cytosolic protein aggregation through HDAC6 in a p62-dependent manner
Soyeon Kim (Ajou University School of Medicine)

10:20-10:30__Break

10:30-11:20__**CITESDB: A centralized portal for accessing detailed information on endangered species of wild fauna and flora**
Bo Kyeng Hou (Korea Research Institute of Bioscience and Biotechnology)

CNS-specific expression pattern of *rnf126* in zebrafish embryos
JiHun Baek (Chungnam National University)

Fine-tuning UDSMProt model for anti-CRISPR prediction
Chan-Seok Jeong (Korea Institute of Science and Technology Information)

***trim46* is associated with the zebrafish neurogenesis via Foxa2**
Jaehun Kim (Chungnam National University)

Development of a tetracycline regulatable conditional mouse model of Parkinson's disease expressing parkin substrate, ZNF746
Hyojung Kim (Sungkyunkwan University School of Medicine)

Poly (ADP-ribose)-dependent Ubiquitination of Heterochromatin protein 1 alpha (HP1α) by RNF4 E3 ligase suggests a functional role for homologous recombination repair
Sangwook Park (Ajou University School of Medicine)

Student Presentation II

일시: 2020. 12. 4. (금) 09:30-11:30
장소: 스플라스 리솜 스테이타워 스페이스 B
좌장: 주 재 열 (한국뇌연구원)

09:30-10:20__**Transcriptomic analysis of the pathogenesis of Parkinson's disease by FAF1 in A53T mouse model**
Jangham Jung (Chungnam National University)

Formation of amyloid β oligomeric forms enhanced or reduced its cytotoxicity
Il-Seon Park (Chosun University)

전통발효 식품으로부터 분리한 항균활성을 가진 유산균의 바이오필름 특성
김종희 (국립축산과학원)

Metagenomic analysis of the DNA viral communities in fermented food kimchi
Jae Yon Chang (Chungnam National University)

The role of commensal microbes on the longevity effect of dietary restriction
Ji-Hyeon Lee (Inha University)

Odontogenic demineralized dentin matrix powder based bio-ink without compromise between biofunctionality and printability for 3D bioprinted dental constructs
Jonghyeuk Han (Ulsan National Institute of Science and Technology)

USP39, a new poly (ADP-ribose)-binding deubiquitinase, drives non-homologous end-joining repair by liquid demixing
Yiseul Hwang (Ajou University School of Medicine)

10:20-10:30__Break

10:30-11:20__**Imaging of astrocyte-to-neuron conversion using aptamers**
Eun-Song Lee (Hanyang University)

발효식품으로부터 박테리오신 유전자를 보유한 바실러스균의 스크리닝 및 동정
김종희 (국립축산과학원)

Probiotic *Lactobacillus reuteri* extends the lifespan of *Drosophila melanogaster* through a mechanism dependent on dSir2 and insulin/IGF-1 signaling
Hye-Yeon Lee (Inha University)

Intein-mediated protein cyclization for improved intracellular delivery into cancer cells
Duc Long Nguyen (Hanyang University)

The control of bakanae disease caused by *Fusarium fujikuroi* based on the interaction of plant-derived *Burkholderia* species with *F. fujikuroi*
Seongeom Jeong (Pusan National University)

Self-assembled hyaluronic acid nanoparticles protect against osteoarthritic development by targeting CD44
Juhwan Yoon (Ajou University)

The roles of LRRK2 in excitotoxicity-and oxygen and glucose deprivation-induced neuronal toxicity
Tae-Young Kim (Kyung Hee University)

목 차

Plenary Lecture

PL1

Translation of genomic integrity to clinical application

Kyungjae Myung

Center for Genomic Integrity, IBS and Department of Biomedical Engineering, UNIST, Ulsan 44919, Korea

Mutations in *BRCA1* or *BRCA2* cause cells susceptible to breast and ovarian cancers. Tumors with a *brca1* or *brca2* mutation are defective in the homologous recombination DNA repair. Due to defects of the homologous recombination, tumors carrying *brca1* or *brca2* mutation heavily rely on the single strand break repair pathway to deal with DNA damage during proliferation. PARP1 inhibitor which blocks the single strand break repair becomes a promising treatment option for tumors with a *brca1* or *brca2* mutation. However, tumors become resistant to PARP1 inhibitor. To identify small molecules inhibiting DNA replication stress response, we found a leading compound, UT2 and its derivative 418, which silence DNA replication stress response. Interestingly, 418 as well as UT2 could selectively kill *parp1* deficient cells. Furthermore, PARP1 inhibitor-resistant cancer cells derived from *brca2*-deficient ovarian tumors were highly sensitive to treatment of 418. Consistently, treatment of 418 successfully inhibited the growth of *parp1*-deficient tumors in vivo. We found that treatment of 418 in cells inhibited cellular autophagy pathway and triggered selective proteolysis of proteins in recombination repair and DNA replication stress response by the molecular crosstalk between autophagy and proteasome pathways. Taken together, we identified a novel small molecule selectively killing PARP1 inhibitor-resistant tumors by enhancing proteolysis of recombination proteins through the inhibition of autophagy pathway.

▶ **Keywords:** Genomic integrity, BRCA, PARP1 inhibitor

PL2

Functional analysis of novel regulators of Hippo and Wnt signalings

Eekhoon Jho

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Hippo signaling controls organ size by regulating cell proliferation and apoptosis. YAP is a key downstream effector of Hippo signaling and its nuclear localization is essential for the activation of target gene expression. However, the mechanism for the nuclear localization of YAP, which does not have nuclear localization signal, is unknown. Data which show that MAML1 is essential for the nuclear localization and transcriptional activation of YAP will be presented. Controlled cell growth and proliferation are essential for tissue homeostasis and development. Wnt and Hippo signaling are well known as positive and negative regulators of cell proliferation, respectively. Regulation of Hippo signaling by the Wnt pathway has been previously shown, but how and which components of Wnt signaling are involved in the activation of Hippo signaling during nutrient starvation are unknown. I will present data that show “LRP6 has unexpected roles as a nutrient sensor and Hippo signaling regulator”.

▶ **Keywords:** Hippo signaling, YAP, MAML, LRP6, Merlin, Wnt signaling

PL3

Optogenetic control of diverse molecular and cellular processes in the mouse brain

Won Do Heo

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My group has been developing various bio-imaging and optogenetic tools for the study of cell signaling in live cells as well as neuronal functions in vivo. Novel optogenetic toolkit developed by my group is highly advantageous compared with conventional approaches in that it allows finely manipulated signaling pathways in a spatial and temporal resolution, thereby making it possible to dissect and analyze the transient dynamics of signaling processes within a defined period. These tools are very useful not only for imaging based researches in cell biology, but also for the studies in neuroscience. Recently developed optogenetic strategies have brought significant changes the way in which signaling in living cells is studied in neurobiology and other disciplines. Novel optogenetic toolkit my group has been developing are capable of providing what channelrhodopsins could not offer previously, contributing in a disparate perspective of neuroscience. We are applying the new technologies to the study of spatiotemporal roles of signaling proteins and second messengers in learning and memory in normal and disease mouse models.

Keynote Lecture

KL1

Role of bystander T cells in autoimmune encephalomyelitis

Je-Min Choi

Department of Life Science, Hanyang University, Seoul 04763, Korea

T cells generate antigen-specific immune responses to their cognate antigen as a hallmark of adaptive immunity. Despite the importance of antigen-specific T cells, here we show that antigen non-related, innate-like bystander-activated $CD4^+$ T cells are significantly contributing to autoimmune pathogenesis. Single cell RNA sequencing analysis reveals naturally occurring $CD44^{high}$ memory phenotype cells which contains various effector-like memory clusters. Transcriptome analysis demonstrates that interleukin (IL)-1β- and IL-23-prime T cells that express pathogenic T_H17 signature genes such as RORɣt, CCR6, and granulocyte macrophage colony-stimulating factor (GM-CSF). Importantly, when co-transferred with myelin-specific 2D2 TCR-transgenic naive T cells, unrelated OT-II TCR-transgenic memory-like T_H17 cells and/or CCR6high natural memory phenotype cells infiltrate the spinal cord and produce IL-17A, interferon (IFN)-ɣ, and GM-CSF, increasing the susceptibility of the recipients to experimental autoimmune encephalomyelitis in an IL-1 receptor-dependent manner. In humans, $IL\text{-}1R1^{high}$ memory $CD4^+$ T cells are major producers of IL-17A and IFN-ɣ in response to IL-1β and IL-23. Collectively, our findings reveal the innate-like pathogenic function of antigen non-related memory $CD4^+$ T cells, which contributes to the development of autoimmune diseases.

KL2

mRNA and polypeptide surveillance pathways

Yoon Ki Kim

Division of Life Sciences, Korea University, Seoul 02841, Korea

It is important that eukaryotic genes are expressed at the right time and place, and at an appropriate level. However, gene expression is not without errors: abnormally synthesized gene products routinely arise as a consequence of mistakes made during gene replication, gene transcription, pre-mRNA processing, and/or mRNA translation. These mistakes can result in the production of improperly functional or nonfunctional polypeptides that could be deleterious to normal cell functions. To ensure mRNA and protein homeostasis, eukaryotic cells have evolved highly sophisticated mechanisms of quality control. Nonsense-mediated mRNA decay (NMD) is the best-characterized mRNA surveillance mechanism by which faulty mRNAs harboring premature termination codons (PTCs) are selectively degraded. It remains an essential issue to understand how NMD machinery specifically recognizes and degrades their target transcripts. In this talk, I will update our recent understanding on NMD mechanism with emphasis on a molecular role of UPF1. I will also discuss the roles of UPF1 in a variety of mRNA and protein quality control pathways.

KL3

Necroptosis in pathophysiology of disease

You-Sun Kim

Department of Biochemistry, Ajou University School of Medicine & Department of Biomedical Sciences, Graduate School, Ajou University, Suwon 16499, Korea

Necroptosis is distinguished from apoptosis in that it does not require caspases, and unlike apoptosis, necroptosis directly results in plasma membrane rupture. Repression of necroptosis by apoptotic proteins is essential for proper mammalian development and prevents spontaneous cell death and inflammation, underscoring the physiological relevance of necroptosis. Receptor-interacting protein kinase-3 (RIP3, or RIPK3) is an essential protein for necroptosis, along with its upstream sister kinase RIPK1, which it interacts with via a homotypic interaction motif (RHIM). Mixed Lineage Kinase Domain-like protein (MLKL) is an essential target of RIP3 kinase activity in necroptosis. The kinase activity of RIP3 is required for downstream signaling events in necrotic cell death which is canonical function. Over the years, our understanding of a core necroptotic pathway consisting of RIP3 activation increased substantially, but the recent discovery indicates that RIP3 kinase may functions through non-canonical pathway, and also suggests tissue-specific roles of RIP3. In this meeting, I will discuss about the functions of RIP3 in necroptosis-mediated human diseases.

▶ **Keywords:** Necroptosis, RIP3, Cell death

Symposium I

Epigenetics: From mechanisms to disease

일시: 2020. 12. 2. (수) 14:00–15:30

S1-1

Functional coordination of BET family proteins in brain plasticity and diseases

Tae-Kyung Kim

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Bromodomain and extraterminal proteins (BET) are epigenetic readers that play critical roles in gene regulation. BET inhibition is a promising therapeutic strategy for various diseases. We investigated three major BET family members (BRD2/3/4) for their functional contributions to neuronal activity-dependent gene expression and the responses to BET inhibition. Individual BET proteins showed significant differences in the sensitivity to BET inhibition, recruitment kinetics, and interdependency. All three BET proteins functionally participated in memory formation, and in a mouse model of Fragile X syndrome (FXS), BRD2/3 and BRD4 showed oppositely altered expression and chromatin binding, resulting in transcriptional dysregulation. Acute inhibition of CBP/p300 histone acetyltransferase (HAT) activity restored the altered binding patterns of BRD2 and BRD4, and rescued memory impairment in FXS. We propose that dysregulated coordination of BET proteins might underlie altered gene expression associated with many diseases.

S1-2

Fasting-induced FGF21 signaling activates hepatic autophagy and lipid degradation via JMJD3 histone demethylase

Sangwon Byun

Personalized Genomic Medicine Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Daejeon 34141, Korea

Autophagy is essential for cellular survival and energy homeostasis under nutrient deprivation. Despite the emerging importance of nuclear events in autophagy regulation, epigenetic control of autophagy gene transcription remains unclear. Here, we report fasting-induced Fibroblast Growth Factor-21 (FGF21) signaling activates hepatic autophagy and lipid degradation via Jumonji-D3 (JMJD3/KDM6B) histone demethylase. Upon FGF21 signaling, JMJD3 epigenetically upregulates global autophagy-network genes, including *Tfeb, Atg7, Atgl,* and *Fgf21*, through demethylation of histone H3K27-me3, resulting in autophagy-mediated lipid degradation. Mechanistically, phosphorylation of JMJD3 at Thr-1044 by FGF21 signal-activated PKA increases its nuclear localization and interaction with the nuclear receptor PPARα to transcriptionally activate autophagy. Administration of FGF21 in obese mice improves defective autophagy and hepatosteatosis in a JMJD3-dependent manner. Remarkably, in non-alcoholic fatty liver disease patients, hepatic expression of JMJD3, ATG7, LC3, and ULK1 is substantially decreased. These findings demonstrate that FGF21-JMJD3 signaling epigenetically links nutrient deprivation with hepatic autophagy and lipid degradation in mammals.

S1-3

Big data-based novel Alzheimer's disease diagnostics target genes

Jae-Yeol Joo

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Alzheimer's disease (AD) is one of the age-related disorders that is most common degenerative disorders today, and strongly involved memory consolidation and cognitive in the brain. Amyloid-β and tau proteins are trigger for AD pathogenesis, and usually use for AD candidate biomarkers in the clinical research. Especially, clinical exam, brain imaging and molecular biological methods are being used to diagnosis for AD. Genome-wide association study (GWAS) is new biomedical method, and use contribute to understanding of many human diseases included brain diseases. Blood contains various type of RNAs, such as mRNA, miRNA and other ncRNA. Theses circulating RNAs play a crucial role in disease and important potential biomarkers. Studies of risk factors, such as the Aβ and tau, provide a possible regulatory mechanism for AD progression. However, links to the other functions have not been fully established. While potent biomarkers in AD has been extensively identified, less is known about the detection of these molecules in AD diagnosis, despite its obvious importance in AD treatment and outcome. Based on the analysis of blood from AD patients who were classified as normal, mild, and severe, we identified various gene expression in blood such as *Ube2h*, *Ace2*, and *CDK* subfamilies. These data may provide information of diagnosis or clinical approach, and suggest that circulating *Ube2h, Ace2*, and *CDK* subfamilies mRNA are novel potential biomarker for AD.

Symposium II

Precision medicine and human disease

일시: 2020. 12. 2. (수) 14:00–15:30

S2-1

Ultra-fast prediction of somatic structural variations by reduced read mapping via pan-Genome *k*-mer sets

Min-Hak Choi[#,1], Jang-il Sohn[#,1,2], Dohun Yi[#,1], A Vipin Menon[1], Yeon Jeong Kim[4], Sungkyu Kyung[5], Seung-Ho Shin[5], Byunggook Na[6], Je-Gun Joung[4], Sungro Yoon[6], Youngil Koh[7], Daehyun Baek[8], Tae-Min Kim[9], and Jin-Wu Nam[c,1,2,3]

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Genome rearrangements often result in copy number alterations of cancer-related genes and cause the formation of cancer-related fusion genes. Current structural variation (SV) callers, however, still produce massive numbers of false positives (FPs) and require high computational costs. Here, we introduce an ultra-fast and high-performing somatic SV detector, called ETCHING, that significantly reduces the mapping cost by filtering reads matched to pan-genome and normal *k*-mer sets. To reduce the number of FPs, ETCHING takes advantage of a Random Forest classifier that utilizes six breakend-related features. We systematically benchmarked ETCHING with other SV callers on reference SV materials, validated SV biomarkers, tumor and matched-normal whole genomes, and tumor-only targeted sequencing datasets. For all datasets, our SV caller was much faster (^{3}15X) than other tools without compromising performance or memory use. Our approach would provide not only the fastest method for largescale genome projects but also an accurate clinically practical means for real-time precision medicine.

S2-2

The development of protein-protein interaction modulators using peptidomimetic compound

Ji Hoon Lee

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Daegu Gyeongbuk Medical Innovation Foundation (DGMIF), Daegu 41061, Korea

Interactions between proteins play a key role in nearly all biological process, and therefore, disruption of such interactions may lead to many different types of cellular dysfunctions. Hence, pathologic protein-protein interactions (PPIs) constitute highly attractive drug targets and hold great potential for developing novel therapeutic agents for the treatment of incurable human diseases. Unfortunately, most such interactions cannot be readily disrupted by typical 'drug-like' small molecules, since protein interfaces are fairly large and shallow. To target PPIs, we focus on the development of different types of molecules, such as conformationally constrained macrocyclic molecules and protein surface mimetics. The resulting compounds will not only serve as highly useful research tools to elucidate the functions of target proteins, but also have a great potential as novel therapeutic candidates. Our goal is to develop novel synthetic molecules that can modulate cellular signaling pathways with an emphasis on protein-protein interactions (PPIs). To this end, we take a multidisciplinary approach including synthetic organic chemistry, combinatorial chemistry, high-throughput screening, biochemistry, and molecular biology.

S2-3

Metabolic restructuring and cell fate conversion through controlling cellular organelles

Man Ryul Lee

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Even though there have been lots of researches and attention on transcriptome and epigenome, efficiency of cell transformation is still low and many parts of the mechanism of determining the fate of cells are not entirely known. The reason is that the transformation mechanism of cell fate occurring mainly on a nucleus and the changes of many cell organelle within cytoplasm are not sufficiently identical, and in particular that there are few researches or understanding about changes of mitochondrial metabolism and stress of endoplasmic reticulum. In the process of transformation of cell fate, the changes of transcriptome which changes within a nucleus are relatively dynamic, and it is known that morphological/ functional changes of cell organelle existing in cytoplasm also occur simultaneously. We gave it a new name of cytoplasmic reprogramming or cytoplasmic synchronization. It is urgently required to find the mechanism which is comprehensively moderated when the cell fate is transformed through the research on the changes of cell organelle and understanding about the control of cell stress when the cell fate is transformed.

Symposium III

Biodiversity and evolution

일시: 2020. 12. 3. (목) 10:50–12:20

S3-1

The evolutionary origin of phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS)

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The bacterial phosphoenolpyruvate:sugar phosphotransferase system (PTS) is one of the most influential regulatory cascades in bacterial physiological processes such as carbohydrate transport and metabolism, carbon storage, and the coordination of carbon and nitrogen metabolism. The four paralogs of PTS gene families have been identified in the bacterial genomes. However, their evolutionary origin and history have remained unexplored. To address this question, we selected two PTS genes (*ptsG* and *nagE*); *ptsG* transports glucose into a cell and *nagE* transports *N*-acetyl-glucosamine (GlcNAc) which is the monomer form of chitin. The exhaustive data-mining of two genes are performed from all bacterial orders. Total 252 genes were obtained from the genomic sequences using BLAST searches and phylogenetic relationships were reconstructed using the maximum-likelihood method. We found that almost all bacterial orders have *ptsG* and *nagE* except for Fusobacteria and Synergistetes which has only *ptsG* genes and are known as the most primitive bacteria clades. In order to confirm the hypothesis and examine the patterns of evolutionary constraints, the ratio of nonsynonymous to synonymous distances (ω or d_N/d_S) is estimated for two PTS genes. The average ω for *nagE* genes is ~5.14 times higher than that in *ptsG* genes, indicating that *nagE* have been subject to relaxed purifying selection. Our finding suggests that *ptsG* genes is preceded in early bacteria.

S3-2

Is phylotranscriptomics as reliable as phylogenomics?

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Phylogenomics, the study of phylogenetic relationships among taxa based on their genome sequences, has emerged as the preferred phylogenetic method because of the wealth of phylogenetic information contained in genome sequences. Genome sequencing, however, can be prohibitively expensive, especially for taxa with huge genomes and when many taxa need sequencing. Consequently, the less costly phylotranscriptomics has seen an increased use in recent years. Phylotranscriptomics reconstructs phylogenies using DNA sequences derived from transcriptomes, which are often orders of magnitude smaller than genomes. However, in the absence of corresponding genome sequences, comparative analyses of transcriptomes can be challenging and it is unclear whether phylotranscriptomics is as reliable as phylogenomics. Here we respectively compare the phylogenomic and phylotranscriptomic trees of 22 mammals and 15 plants that have both sequenced nuclear genomes and publicly available RNA sequencing data from multiple tissues. We found that phylotranscriptomic analysis can be sensitive to orthologous gene identification. When a rigorous method for identifying orthologs is employed, phylogenomic and phylotranscriptomic trees are virtually identical to each other, regardless of the tissue of origin of the transcriptomes and whether the same tissue is used across species. These findings validate phylotranscriptomics, brighten its prospect, and illustrate the criticality of reliable ortholog detection in such practices.

S3-3

Insights into marine animal genomics and regeneration from Lophotrochozoa

Sung-Jin Cho

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In this talk, I will describe recent advances in the field of metazoan comparative genomics and regeneration, the insights into the marine animal genomic and annelid regeneration. The scientific questions arising from the ability of certain species, but not others, to massively regenerate their bodies are among the most fascinating and challenging confronting modern cell and developmental biologists today. The tremendous implications of this research area for human medicine and tissue engineering are obvious. Yet many other animals exhibit robust regenerative capabilities, including "lower" vertebrates such as amphibians, and invertebrates such as echinoderms, flatworms and annelids. In the extreme case, some species can reproduce vegetative indefinitely. Such animals must contain the operational equivalent of immortal, totipotent somatic stem cells. From invertebrates to the higher vertebrates, their metabolic pathway, developmental regulatory genes, and intercellular signaling pathways are evolutionary conserved. With these, study on regeneration is an ingenious, powerful model system for studying the post-embryonic development, innate immunity mechanisms, and primordial germ cells (PGCs).

Symposium IV

Advanced bioimaging

일시: 2020. 12. 3. (목) 10:50–12:20

S4-1

Super-resolution microscopy study of platelet activation and release

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Platelets are anucleate cytoplasmic fragments generated from megakaryocytes and have major roles in hemostasis. Recent emerging evidence demonstrates that platelets are equipped with elaborate intracellular machinery,and their organization is far more complex than previously regarded. However, their ultrastructural organization in platelets in the different stages of activation or maturation process remains unclear due to the difficulty in determining and quantifying the ultrastructure of platelets by diffraction-limited conventional light microscopy. To overcome this limit, we used stochastic optical reconstruction microscopy toresolve the native ultrastructure and their interaction of different organelles in platelets. The recent development of super-resolution fluorescence microscopy allows the location of molecules to be determined with nanometer-scale spatial resolution. Moreover, correlative super-resolution microscopy, the integration of the high spatial resolution of super-resolution fluorescence microscopy with other imaging platforms, offers intriguing opportunities to probe multiple aspects of a given system. By using these approaches, we quantitatively characterized nanoscale localization changes of organelles,including cytoskeletal elements, mitochondria, endoplasmic reticulum, and granules in a platelet during its activation and releaseprocess. Our results highlight how different organelles are spatiotemporally organized in the different intermediate stages duringthe platelet activation and releaseprocess. We anticipate that these techniques would open up a new way to study ultra-structures of organelles in platelets, and will shed light on the fundamental molecular mechanisms of platelet structure and function.

S4-2

Holotomography : Dynamic imaging for label-free living cell

Seongsoo Lee

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Holotomography (HT) has emerged as a valuable live-cell imaging technique that reconstructs 3D refractive index (RI). HT images can be quantitatively analyzed to provide biophysical parameters such as cell volume and dry mass in label-free live cell. Here, we will present recently developed 3D correlative system combining the RI tomogram and fluorescence images. We will also show various biomedical applications including diagnosis, therapeutic approach and environmental inspection.

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S4-3

Live imaging of a type of cell in the nervous system using a fluorescent chemical probe

Beomsue Kim

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The nervous system controls our body, processes sensory information, and generates a memory through the orchestration of multiple cell types, including glia as well as neurons. However, visualizing a type of live cells in nervous tissues often require transgenic animals labeled with fluorescence proteins, causing common challenges to apply due to the cost and the complexity of techniques. Herein, I will present the development of a chemical fluorescent probe for labeling live microglia, a type of glial cells specialized for maintaining the nervous tissue environment. Adding the compound before observation enables the visualizing and tracking of microglia at tissue levels. The developed probe, named CDr20, detect microglia *in vivo* through simple intravenous injection if BBB has slightly altered. The mechanism study revealed that CDr20 label microglia through the Ugt1a7c-mediated fluorescence turn-on process of the chemical. Because of its simplicity and specificity, developing novel fluorescent chemical probes for targeting other types of cells by the described platform will be very useful in basic neuroscience and further in biomedical applications.

Symposium V

Viruses, crossing species

일시: 2020. 12. 3. (목) 13:20–14:50

S5-1

A vaccine for severe fever with thrombocytopenia syndrome virus (SFTSV) than can confer complete protection against lethal infection

Su-Hyung Park

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Although the incidence of severe fever with thrombocytopenia syndrome virus (SFTSV) infection has increased from its discovery with a mortality rate of 10-20%, no effective vaccines are currently available. In this study, we developed a SFTSV DNA vaccine and examined its immunogenicity and protective efficacy. Vaccine candidates induced both a neutralizing antibody response and multifunctional SFTSV-specific T cell response in mice and ferrets. When the vaccine efficacy was investigated in aged-ferrets that recapitulate fatal clinical symptoms, vaccinated ferrets were completely protected from lethal SFTSV challenge without developing any clinical signs. A serum transfer study revealed that anti-envelope antibodies play an important role in protective immunity. Our results suggest that Gn/Gc may be the most effective antigens for inducing protective immunity and non-envelope-specific T cell responses also can contribute to protection against SFTSV infection. Furthermore, we found that this DNA vaccine induced a strong neutralizing antibody and SFTSV-specific T cell response in monkeys, which was comparable with that observed in SFTS patients. This study provides important insights into the development of an effective vaccine, as well as corresponding immune parameters, to control SFTSV infection.

S5-2

Negative regulator of IFN signaling and IFN evasion of virus

Jong-Soo Lee

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Upon virus invasion, viral pathogen-associated molecular patterns (vPAMPs) are recognized by host pattern recognition receptors (PRRs) to activate antiviral innate immunity. The efficacy of this recognition system is crucial for triggering innate host defenses, which then stimulate more specific adaptive immune responses against the virus. Sensing of viral PAMPs leads to the activation of a signal cascade that ultimately result in the production of pro-inflammatory cytokines and Interferons (IFNs). Secreted IFNs then signals through its specific receptor and induce the expression of hundreds of interferon stimulated genes (ISGs) that together mediate viral clearance and restrict viral spread. Although antiviral signaling generated from the RLRs is necessary to limit the spread of viral infection, attenuation of antiviral signaling is also essential for prevention of excessive production of IFNs and pro-inflammatory cytokines, which could cause deleterious effects on the host. Consequently, host cells have developed several strategies that tightly regulate antiviral signaling for virus clearance and the maintenance of host immune homeostasis. However, viruses have evolved several strategies to counteract/evade host immune reactions. Here, we will discuss about novel host regulator which can control innate immune responses against virus infection and the immune evasion mechanism of specific FMD viral protein.

** The National Research Foundation of Korea (Grant No. 2018M3A9H4079660, 2019R1A2C2008283)

S5-3

Epidemiology of severe fever with thrombocytopenia syndrome virus

Keun Hwa Lee

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Topic 1. Severe Fever with Thrombocytopenia Syndrome Virus in Ticks and SFTS Incidence in Humans, South Korea: Most SFTSV infections occur through *Haemaphysalis longicornis* tick. During 2016-2018, we collected 3,193 ticks from rural areas in South Korea to investigate the prevalence of severe fever with thrombocytopenia syndrome virus (SFTSV). We detected SFTSV in ticks at an infection rate (IR) of 11.1%. We noted increases in the human IR associated with the monthly SFTSV IR in ticks (*Emerg Infect Dis*. 2020, 26 (9):2292-94).

Topic 2. Family Cluster Analysis of SFTSV infection in Korea: SFTSV infection can also occur between family members, and nosocomial transmission of SFTSV is also possible through close contact with a patient (*Am J Trop Med Hyg*. 2016, 95(6):1351-1357, *Zoonoses and Public Health.* 2018, DOI: 10.1111/zph.12481, and *Open Forum Infect Dis.* 2019, 6(5):ofz210. doi: 10.1093/ofid/ofz210. eCollection).

Topic 3. Confirmation of both SFTS V and *O. tsutsugamushi* co-infection in patient: To determine prevalence of SFTS in South Korea, we examined serum samples from patients with fever and insect bite history in endemic areas of scrub typhus, is an acute febrile illness caused by *Orientia tsutsugamushi*, a bacterium transmitted to humans through chigger mite bites. Prevalence of this syndrome among patients suspected of having scrub typhus was high (23.0%, 17/74), suggesting possible co-infection and we also confirmed that a patient was mixed infected with SFTSV and two genotypes of *O. tsutsugamushi* (*Emerg Infect Dis*. 2016, 22(11): 1992-95 and *Am. J. Trop. Med. Hyg.* 2018 99(2):287-90).

Topic 4. Endemic Severe Fever with Thrombocytopenia Syndrome, South East Asia: Severe fever with thrombocytopenia syndrome (SFTS) has been identified in China, South Korea, and Japan since 2009. We found retrospective evidence of SFTS virus (SFTSV) infection in Vietnam and Myanmar, which suggests that SFTSV infections also occur in South East Asia, which is not known to be an SFTS endemic country (*Emerg Infect Dis.* 2019, 25 (5):1029-1031 and *Emerg Infect Dis.* 2020, 26 (8):1878-81).

Topic 5. SFTSV transmission and Migratory Birds Routes among Asia: *Haemaphysalis longicornis* acts as a transmission host between animals and humans and SFTSV is circulating between China,

South Korea and Japan. However, it is not known if a genetic connection exists between the viruses in these regions and, if so, how SFTSV is transmitted across China, South Korea, and Japan. We hypothesize that the SFTSV in South Korea share common phylogenetic origins with samples from China and Japan. Further, we postulate that migratory birds, well-known carriers of the tick *H. longicornis*, are a potential source of SFTSV transmission across countries (*Am J Trop Med Hyg.* 2015, 93:468-74).

Symposium VI

Neurological disorders and brain injury

일시: 2020. 12. 3. (목) 13:20–14:50

S6-1

The pathological functions of LRRK2 in brain injury

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Mutations in the *Leucine-rich repeat kinase 2* (*LRRK2*) gene are common genetic risk factors for both familial and sporadic parkinson's disease (PD). Pathogenic mutations in LRRK2 have been shown to induce changes in its activity, and abnormal increase in LRRK2 kinase activity is thought to contribute to neuronal toxicity and PD pathology. Furthermore, LRRK2 has been suggested to be associated with multiple human diseases and pathologies. However, little is known about the underlying molecular mechanism by which endogenous, wild-type LRRK2 is regulated. Recently, we show that brain injury induces a robust expression of endogenous LRRK2 and suggest a role of LRRK2 after injury. We found that various *in vitro* and *in vivo* models of brain injury markedly enhanced LRRK2 expression in neurons and also increased the level of hypoxia-inducible factor (HIF)-1a and HIF-1a-dependent transcriptional induction of *LRRK2* exacerbated neuronal cell death following injury. Furthermore, application of brain-permeable specific inhibitor of LRRK2, substantially prevented brain tissue damage, cell death, and inflammatory response and alleviated motor and cognitive defects induced by controlled cortical impact injury. Together, these results suggest HIF-1a-LRRK2 axis as a potential therapeutic target for brain injury.

S6-2

Conditional mouse model of Parkinson's disease refined for preclinical application

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Dysfunctional E3 ligase parkin due to mutations or modifications is responsible for brain pathogenesis in both familial and sporadic forms of Parkinson's disease (PD). Clinically relevant studies in parkin-related PD pathogenesis have been largely hampered by the lack of revealing PD mouse models. For instance, *parkin null* mice failed to develop robust loss of dopaminergic neurodegeneration and Lewy-like inclusions both of which are characteristic key pathologic features of PD. To overcome this issue in *parkin knockout* approach, we adopted transgenic approach expressing a pathogenic parkin substrate, ZNF746 to exaggerate parkin downstream signaling pathway. As a robust disease causing factor, ZNF746 accumulation is associated with PD pathogenesis and mitochondrial dysfunction. Here we developed *conditional transgenic mice* (*TetP-ZNF746*) in which ZNF746 expression can be controlled temporally and spatially. *TetP-ZNF746* responder mice were mated with dopaminergic specific or pan-neuronal driver mice to simulate different pathological stages of PD. In this talk, I would like to share our characterization of these novel and revealing PD mouse models and their practical application for preclinical evaluation of well-known therapeutic approaches.

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S6-3

Deciphering the neural epitranscriptome using mouse and human brain organoid models

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Proper development of the nervous system is critical for its function, and deficits in neural development have been implicated in many brain disorders. A precise and predictable developmental schedule requires highly coordinated transcriptional cascades that orchestrate the dynamics of mammalian cortical neurogenesis. Recent discoveries of widespread mRNA chemical modifications raise the question of whether this mechanism plays post-transcriptional regulatory role in cortical neurogenesis. N6-methyladenosine (m^6A), installed by the Mettl3/Mettl14 methyltransferase complex, is the most prevalent internal mRNA modification. However, the function of m^6A methylation in mammalian brain development is largely unknown. Here we used the *Mettl14* conditional knockout mouse as a model to examine m6A function in embryonic cortical neurogenesis in vivo. *Mettl14* deletion in the embryonic mouse brain resulted in diminished m^6A content, altered cell cycle progression of radial glial cells, and impaired temporal progression of the cortical development. To gain insight into the potential molecular mechanism underlying m^6A dependent regulation, we performed m^6A-seq from mouse developing forebrain and identified high confident m^6A peaks on gene transcripts related to transcription factors, cell cycle and neuron differentiation. In addition, using m^6A-seq datasets from mouse forebrain and human forebrain organoids, we revealed conserved and unique m^6A mRNA methylation landscapes of mouse and human cortical neurogenesis. Together, our results reveal critical epitranscriptomic control of mammalian cortical neurogenesis and novel insight into mechanisms underlying this highly coordinated developmental program.

Student Presentation I

일시: 2020. 12. 4. (금) 09:30–11:30

SP1-1

Linalool has neuroprotective effects on suppressing ROS production and inflammation of Linalool in Aβ42-induced *Drosophila* model of Alzheimer's disease

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Terpenes are vital metabolites and known to be beneficial in the treatment of various diseases. Previously, our group screened terpenes that increased the survival of the Alzheimer's disease (AD) model flies and identified linalool as a neuroprotective terpene. Linalool is a monoterpene and is known to have anti-inflammatory and neuroprotective properties. Although several studies have shown the beneficial effect of linalool in AD animal models, the mechanisms underlying the beneficial effect of linalool on AD are yet to be elucidated. In the present study, we showed that linalool intake increased the survival of the AD model flies in a dose-dependent manner. Linalool also decreases Aβ-induced apoptosis in eye discs as well as the larval brain. Moreover, linalool intake was found to reduce neurodegeneration in the brain of adult AD model flies. However, linalool did not affect the total amount of Aβ42 protein or Aβ42 aggregation. Rather, linalool decreased Aβ-induced ROS levels, and inflammatory response in the brains of AD model flies. Taken together, our data suggest that linalool exerts its beneficial effects on AD by reducing Aβ 42-induced oxidative stress and inflammation.

▶ **Keywords:** Alzheimer's disease, *Drosophila*, Inflammation, Linalool, Terpene

SP1-2

Characterization of Alzheimer's disease-associated genes using *Drosophila* model

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Alzheimer's disease (AD) is a multifactorial disease, with which more than 40 genes have been associated thus far. However, it is believed that many AD-associated genes have not yet been discovered. Here, we identified novel AD-associated genes from multiple resampled genome-wide associated study (GWAS) in Korean population followed by functional genomic screening with *Drosophila* AD model. Among the potential AD-associated genes selected by GWAS, 539 genes were screened to find genes that are functionally related with AD using RNAi system. As a result, 112 genes were found to be genetic modifiers of *Drosophila* AD models. Gene ontology analysis revealed that 33 genes out of 112 are involved in endocytosis. The function of 4 endocytic genes (*garnet, shibire, EndoA,* and *CG9951*) were further analyzed. The knockdown of these genes increased Aβ42 accumulation and exacerbated Aβ42-induced neuronal damage in the brain of Aβ42-expressing fly. In conclusion, our results suggest that the down-regulation of molecular components of endocytic machinery is important pathological mechanism underlying AD, and that endocytosis is the major cellular pathway related with AD in Korean population.

SP1-3

Newly recorded sea star *Henricia oculata* (Asteroidea: Spinulosida: Echinasteridae), in the East Sea, Korea

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Henricia specimens were collected using fishing nets from the East Sea of Korea. The specimens were identified as *Henricia oculata* Pennant, 1777, belonging to the family Echinasteridae of the order *Spinulosida*. This species can be distinguished from other *Henricia* species by broad arms (R/r = 4-4.1), rough skin, thick arm base, three to nine minute, delicate abactinal spines, and inferomarginal plates reniform in shape. This species superficially resembles *H. pachyderma* in its body size and wide papular areas, but differs mainly by the number of papulae and abactinal spines, and the shape and arrangement of inferomarginal plates. In comparison with other *Henricia* species bearing broad arms, our morphological analysis showed that it differed from *H. perforata* in the shape of abactinal spines (*H. oculata*: conical; *H. perforata*: slender), the shape of inferomarginal plates (*H. oculata*: reniform; *H. perforata*: transversely elongated), and the arrangement of the series of inferomarginal plates (*H. oculata*: compact; *H. perforata*: loose). To date, two genera of Echinasteridae, *Aleutihenricia* and *Henricia*, with a total of 13 species, have been reported in Korea. The morphological characteristics of *H. oculata* are described, and photographs are provided.

SP1-4

Effect of Th2 differentiation control through formation of skin lipid barrier on *Coptidis Rhizoma*, *Glycyrrhiza uralensis* and and fermameted *Glycine max* extract

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This study is conducted to evaluate Th2 skewed condition control through skin lipid barrier formation from the treatment using *Coptidis Rhizoma, Glycyrrhiza uralensis* and fermameted *Glycine max* extract. The 6-week-old Balb/c mice were divided into 4 groups: Control group (Ctrl), lipid barrier eliminate treatment group (LBE), *Coptidis Rhizoma*, *Glycyrrhiza uralensis* and fermameted *Glycine max* extract feeding treatment after lipid barrier elimination group (3HbT), dexamethasone feeding treatment after lipid barrier elimination group (DEXT). After 3 days, differences in skin condition, improvement of skin lipid barrier, and control of Th2 skewed condition of each group were observed. Pathologic skin damage and tissue changes were less in the 3HrT than in the LBE and DEXT, and Transepidermal water loss (TEWL) and pH were also significantly decreased ($p < 0.05$). The filaggrin intensity and positive response also increased significantly in the 3HrT ($p < 0.05$). Kallikrein-related peptidase (KLK) 7, Protease activated receptor (PAR)-2, Thymic stromal lymphopoietin (TSLP), Interleukin (IL)-4, and the products of the Th2 differentiation process also showed a significant decrease compared to the LBE and DEXT (all $p < 0.05$). The *Coptidis Rhizoma, Glycyrrhiza uralensis* and fermameted *Glycine max* extract causes skin barrier recovery and function recovery through the formation of skin lipid barrier. This leads to the conclusion that *Coptidis Rhizoma, Glycyrrhiza uralensis* and fermameted *Glycine max* extract can control Th2 differentiation through the formation of skin lipid barrier.

** This work supported by Semyung University's University Innovation Support Project in 2020.

SP1-5

Study of amyloid-β-induced fragmentation of lamin A and B

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Amyloid-β (Aβ) is a peptide implicated in Alzheimer's disease. The peptide leads to specific fragmentation of lamin proteins, independently of caspase-6. In the current study, we explored whether Aβ-induced caspase-6 activation can induce the enzyme-dependent lamin fragmentation, because caspase-6 is responsible for the fragmentation process in other damage-induced apoptosis. The formation of lamin A and B fragments in cells was not induced by caspase-6, even though robust activation of caspase-6 was detected in cells treated twice for 2 h and >10 h with A β42. Purified caspase-6, however, could remove the lamin A fragment detected in nuclei isolated from Aβ-treated cells (ANU), whereas it failed to generate the expected fragment of lamin B. Caspase-6-mediated fragmentation of lamin B was achieved in ANU treated with alkaline phosphatase and in nuclei isolated from cells treated with Aβ42 in the presence of a Cdk5 inhibitor. These implies that inhibitory phosphorylation prevented the fragmentation of lamin B in Aβ -treated cells.

SP1-6

TTF-1 action in leptin-induced development of hypothalamic neurons

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The hypothalamus is a brain region necessary for many instinctive behaviors and physiological functions that require complex neural circuits primarily formed during the postnatal period. Various factors influence hypothalamic development and play roles in formation of neural circuits. Among them, leptin functions as a key signal that promotes axon outgrowth from the arcuate nucleus during a discrete developmental period. Leptin deficient *ob/ob* mice show phenotypic abnormalites of neural circuit formation. However, the underlying detailed mechanisms are unknown. Thyroid transcription factor-1 (TTF-1), also known as NKX2.1, is critical for morphogenesis of the hypothalamus and is involved in the leptin-regulated energy homeostasis in the rodent hypothalamus. In this study, we investigated whether TTF-1 is involved in the leptin-induced neural development of hypothalamus. First, we found that TTF-1 expression was highly increased during postnatal day 0-15. To study in detail, we generated mice (ObRb-TTF-1 KO) lacking TTF-1 expression selectively in cells expressing leptin receptors (ObRb). ObRb-TTF-1 KO mice showed increases in ObRb- immunopositive cells and agouti-related peptide nerve terminals in the paraventricular nucleus (PVN), but decreased number of alpha-melanocyte -stimulating hormone terminals in PVN. The expression levels of Sonic hedge hog and SIX3, which are well known genes related to neural development, were changed through the regulation of TTF-1 expression. These results suggest that hypothalamic TTF-1 is important in the leptin-induced neuronal development in the hypothalamus.

SP1-7

Stress-induced NEDDylation promotes cytosolic protein aggregation through HDAC6 in a p62-dependent manner

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Stress-coupled NEDDylation potentially regulates the aggregation of nuclear proteins, which could protect the nuclear ubiquitin-proteasome system from proteotoxic stress. However, it remains unclear how NEDDylation controls protein-aggregation responses to diverse stress conditions. Here, we identified HDAC6 as a direct NEDD8-binding partner that regulates the formation of aggresome-like bodies (ALBs) containing NEDDylated cytosolic protein aggregates during ubiquitin stress. HDAC6 colocalizes with stress-induced ALBs, and HDAC6 inhibition suppresses ALBs formation, but not stress-induced NEDDylation, suggesting that HDAC6 could carry NEDDylated-proteins to generate ALBs. Then, we monitored the ALBs-associated proteostasis network and found that p62 directly controls ALBs formation as an acceptor of NEDDylated cytosolic aggregates. Interestingly, we also observed that ALBs are highly condensed in cells treated with chloroquine, inhibits autophagic flux, indicating ALBs rely on autophagy pathway. Collectively, our data suggest that NEDD8, HDAC6, and p62, involve in the management of proteotoxic stress by forming cytosolic ALBs coupled to aggresome-autophagy flux.

SP1-8

CITESDB: A centralized portal for accessing detailed information on endangered species of wild fauna and flora

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CITESDB, developed by Korea Research Institute of Bioscience and Biotechnology (KRIBB), is a centralized portal for accessing key information on CITES species. CITES (the Convention on International Trade in Endangered Species of Wild Fauna and Flora) is an international agreement between governments to protect endangered species of wild fauna and flora. Widespread information nowadays about the endangered status of many prominent species should make the need for collecting and integrating their related information. Therefore, CITESDB contains detailed information on all species that are listed in the appendices of CITES, as well as other species included in the main species information resources, such as GBIF, NCBI taxonomy, and Korean taxonomic list. CITESDB allows users to search for the detailed information about species by querying scientific names, common names, or Korean names. Moreover, CITESDB provides statistics about species-related information and CITES trade data, and open API for accessing and exchanging the detailed information of CITES species through the internet.

SP1-9

CNS-specific expression pattern of *rnf126* in zebrafish embryos

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An E3 ligase containing RING finger, RNF126 interacts with PDK1, p21 and Ku80 in the ubiquitin proteasome system. RNF126 with Bag6 promotes anoikis resistance in cancer cells by targeting PDK1 for ubiquitin-mediated degradation. RNF126 degrades mislocalized proteins and plays critical role in DNA repair mechanism. Various molecular functions of RNF126 have been reported while its biological functions remain to be investigated in vertebrate embryogenesis. We analyzed spatiotemporal distribution of *rnf126* transcripts in zebrafish embryogenesis. Whole mount in situ hybridization using *rnf126* specific probe found *rnf126* transcripts in 1 cell and sphere stage as well as the zygotic transcripts in the primordium of brain region at bud stage. *rnf126* transcripts became restricted to the telencephalon, midbrain, and hindbrain at 18 hpf and further to the telencephalon, optic tectum, MHB, cerebellum, and rhombomere at 24 hpf. Current studies on molecular network governing expression of *rnf126* is to provide developmental mechanism underlying how Rnf126 contributes to zebrafish embryogenesis.

▶ **Keywords:** *rnf126*, ubiquitin proteasome system, optic tectum, cerebellum, rhombomere

SP1-10

Fine-tuning UDSMProt model for anti-CRISPR prediction

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UDSMProt is a universal deep sequence model pretrained on unlabeled proteins of Swiss-Prot, and can be fine-tuned for a specific prediction tasks in various fields. Here, I suggest the use of UDSMProt model for predicting anti-CRISPR protein from the amino acid sequence. Anti-CRISPR embraces a group of proteins that inhibit CRISPR-Cas system of the prokaryotic immune system. Recently, anti-CRISPR has emerged as a natural inhibitor of CRISPR-Cas system, which enables the post-translational regulation of CRISPR-Cas systems for various applications. Although experimental techniques for the discovery of anti-CRISPR have been developed, computational prediction can provide cost-effective screening strategy. However, the lack of labeled anti-CRISPR data and their low sequence similarity render the algorithm development challenging. In this study, I build an anti-CRISPR protein predictor by fine-tuning the pretrained model for anti-CRISPR data set. The performance is evaluated for an independent data set by using various metrics, in comparison with conventional predictors. While the conventional predictors use additional feature computations and pre-filtering steps, the present approach just requires protein sequence.

SP1-11

trim46 is associated with the zebrafish neurogenesis via Foxa2

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As an initial attempt to study biological functions of Trim46 in vertebrate embryogenesis, spatiotemporal expression patterns of *trim46* were examined in zebrafish embryos. *trim46* was expressed both maternally and zygotically, and the transcripts were localized in the eyes and throughout the brain region, predominantly in the midbrain-hindbrain boundary (MHB) and hindbrain at 24 hpf. Bioinformatic studies found that the promoter regions of *trim46* contain *cis*-acting elements binding to Foxa2. Cyclopamine, an inhibitor of SHH, a transcriptional regulator of *foxa2*, was treated to zebrafish embryos at 4 hpf through 24 hpf to repress the transcription of *foxa2*. It caused not only the severe defects of midbrain patterning but also significant reduction in the transcripts level of *foxa2*, *trim46*, and *shha* at 24 hpf. It is thus conceivable that Trim46 contributes to development of midbrain and MHB in response to Shh signaling via Foxa2.

SP1-12

Development of a tetracycline regulatable conditional mouse model of Parkinson's disease expressing parkin substrate, ZNF746

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Development of a revealing animal model of Parkinson's disease (PD) is imperative to understanding of PD pathogenesis and also to the evaluation of potential PD treatments. However, previously reported PD genetic models including parkin null mice are largely not sufficient for studying PD mainly due to the lack of substantial loss of dopaminergic neurons. Parkin interacting substrate, ZNF746 also known as PARIS, is a transcriptional repressor that regulates the expression of peroxisome proliferator-activated receptor gamma, coactivator 1a (PGC-1a), a master coregulator of mitochondria biogenesis and antioxidant defense. To study *in vivo* roles of ZNF746 accumulation and develop revealing mouse model of PD, we constructed chronic PD mouse models that can express PARIS under pharmacological control of tetracycline regulatable promoter (TetP-PARIS responder mice). This model was designed to express PARIS only in dopamine neuron using the dopamine neuron specific promoters. As a chronic model of PARIS expression, TetP-PARIS mice were mated with dopaminergic neuron specific driver mice, and PARIS expression was induced for 2 months starting at 3 weeks of age. With 2 month expression of PARIS in dopamine neurons, TH-positive neurons progressively degenerated in the substantia nigra, and the loss of dopaminergic nerve terminal in the striatum was evident. Consistent with nigrostriatal dopaminergic degeneration, this conditional PARIS transgenic mice displayed behavioral motor abnormalities at about 3 months of age. Interestingly, behavior deficits of this mouse model were rescued with levodopa/carbidopa treatment. Moreover, nilotinib treatment showed a protective effect on both dopaminergic neuron loss and behavior abnormalities. Studies using this PARIS expressing chronic mouse model are expected to provide a better understanding of the pathogenesis of PD and could be used to develop potential therapeutic agents.

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SP1-13

Poly (ADP-ribose)-dependent Ubiquitination of Heterochromatin protein 1 alpha (HP1α) by RNF4 E3 ligase suggests a functional role for homologous recombination repair

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The DNA repair pathway underlying DNA damage response (DDR) is the most imperative process involving diverse cellular repair machinery. DNA repair machinery is tightly regulated by various types of Post-translational modifications (PTMs), including phosphorylation, methylation, SUMOylation, ubiquitination and PolyADP-ribosylation (PARylation). Among these, functional crosstalk between Poly(ADP-ribose)(pADPr), metabolite of Poly(ADP-ribose) polymerase 1 (PARP1) activated by DNA damage, and ubiquitination to control DDR remains unclear. Thus, to determine that the functional roles of ubiquitin E3 ligases coupled Poly(ADP-ribose) signaling on DDR and characterize the DNA repair mechanism controlled by pADPr molecule, we screened for pADPr-coupled substrates of RNF4 move to DNA lesions using 17K protein microarray and *in vivo* assay systems such as BioID, micro-irradiation . We identified 2 pADPr-dependent substrates of RNF4, connected to DDR. Here, HP1α is ubiquitinated by RNF4 and localized to DNA lesions in a presence of RNF4. We also found that HP1α is move to DNA lesions in a pADPr-dependent manner. Next, to investigate the sites of ubiquitination of HP1α by RNF4, we used mass spectrometry and we found that lysine 91, lysine 102 of HP1α was ubiquitinated by RNF4. Interestingly, HP1α K91.102 ubiquitination is critical for DNA binding. And Ubiquitination of HP1α is important for DNA repair via homologous recombination (HR). These data suggest that crosstalk with ubi- and PARylation is important for HP1α localization and HR repair pathway.

Student Presentation II

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SP2-1

Transcriptomic analysis of the pathogenesis of Parkinson's disease by FAF1 in A53T mouse model

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To define details of molecular networks associated with pathogenesis of Parkinson's disease (PD) by FAF1, FAF1 was ectopically expressed in the substantia nigra pars compacta (SNpc) of in a PD mouse model, A53T at 2, 4, 6, and 8 months after birth. The SNpc expressing FAF1 for 2 weeks was isolated for purification of total RNAs. Total RNAs were subjected to next generation sequencing, which was analyzed by bioinformatic tools for genes regulated along the PD pathogenesis. Among the significantly up- and down-regulated DEGs. DEG13 containing Kelch and F-box associated domains at the central was selected. As an initial attempt to investigate its function, spatiotemporal expressions of zebrafish *DEG13* were examined, indicating that *DEG13* transcripts at bud stage and are found predominantly in the floor plate of the neural tube. Overexpression of *DEG13* enhanced expression of *dkk1b* at 10 hpf as well as *shha*, a marker of the dopaminergic progenitors in the hypothalamus at 16.5 hpf. To examine the consequences of *DEG13* knockdown in developing DA neurons, spatiotemporal expression patterns of the markers of immature and mature DA neurons were visualized using WISH analysis. Transcript levels of DA neuron markers were reduced in the ventral diencephalic region as well as in the neural crest of the midbrain at 18 hpf. These results suggest that *DEG13* contributes to the neurogenesis of DA neurons in zebrafish embryos.

▶ **Keywords:** Parkinson's disease (PD), Fas-associated factor 1 (FAF1), SNpc (Substantia nigra pars compacta), NGS (Next Generation Sequencing), Dopaminergic (DA) neurons

SP2-2

Formation of amyloid β oligomeric forms enhanced or reduced its cytotoxicity

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Amyloid β (Aβ) is a main pathogen of Alzheimer's disease. In the current study we explored the underlying mechanisms that facilitate reducing and enhancing effects of exogenous proteins on cytotoxicity of Aβ. An *Escherichia coli* chaperonin DnaK was chosen as a tool, because it is easily available and functionally stable. The chaperonin reduced or enhanced Ab cytotoxicity depending on its concentration: cytotoxicity was enhanced when the molar ratio of DnaK to Aβ42 at 20 mM Aβ42 was 0.01-0.5, while reduced cytotoxicity was observed at higher ratios (>1) at 1 mM Aβ42. The amounts of oligomeric Aβ42 species accumulated concomitantly increased with enhanced cytotoxicity, whereas the oligomers appeared to form complexes with DnaK in conditions of reduced cytotoxicity. Thus, we suggest that the difference in cytotoxicity was due to variations in the toxic oligomeric Aβ species. DnaK is a useful tool for the study of the Ab ultrastructure formation and toxicity of Aβ peptide.

SP2-3

전통발효 식품으로부터 분리한 항균활성을 가진 유산균의 바이오필름 특성

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식품의 생산 가공 단계에서 오염된 장비 및 시설은 음식물로의 교차 위험의 원인이 될수 있다. 이를 예방하고자 항균물질을 분비하고, 바이오필름을 형성하는 유산균을 활용하고자 한다. 따라서 식품의 주요 식중독균인 *B. cereus*, *Staphylococcus aureus*, *Salmonella enteritidis*, *Listeria monocytogenes*, *Escherichia coli* O157:H7에 대하여 항균활성이 강한 5종의 유산균(*Leuconostoc lemsenteroides* 1균주, *Leu. lactis* 1균주, *lactobacillus sakei* 2균주, *L. curvatus* 1균주)을 분리하여 이들의 바이오필름 형성능과 환경스트레스에 대한 저항성을 확인하였다. 분리된 5종의 유산균은 스테인리스표면, 25℃에서 높은 바이오필름을 형성하였다. 또한 저온스트레스 평가에서 5℃, 15℃에서 각각 평균 72%, 86%의 높은 생존율을 보여주었다.

SP2-4

Metagenomic analysis of the DNA viral communities in fermented food kimchi

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It is currently estimated that the number of viruses outnumber live cells in most environments. However, the studies on environmental viruses have been limited due to difficulties in culturing viruses, lack of a universal marker gene and sparse reference data. Recently, culture and marker gene-independent metagenomic approach enabled researchers to explore the community structure and diversity of viruses in various natural ecosystems. Most of environmental viruses are identified as viruses infecting bacteria which are considered major drivers of bacterial communities. The ecology of virome studies have been studied actively in ocean and human gut, however ecological role and impact of bacteriophages on microbial populations were poorly understood in fermented foods. Because fermented foods that is frequently consumed human diet are a representative environment made by microorganism. We investigated three types of starter and non-starter Kimchi to determine the community structre and diversity of viral communities using the enrichment of virus-like particles and shotgun metagenomics. Most of identified viral families were double-stranded DNA viruses infecting prokaryotes, particularly bacteria (termed bacteriophages). These communities were dominated by bacteriophages belonging to the viral order *Caudovirales* (i.e.,*Herelleviridae*, *Myoviridae*, *Podoviridae*, and *Siphoviridae*). In starter Kimchi the composition of viral families were more diverse and proportion of unclassified was larger than non-starter Kimchi. We believe that our observations contribute to the expansion of microbial diversity for fermented vegetable foods.

SP2-5

The role of commensal microbes on the longevity effect of dietary restriction

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Dietary restriction (DR) is the most well-known intervention to retard aging and to extend the lifespan in diverse organisms. Recently, commensal bacteria resided in the digestive tracts have been reported to affect the host lifespan and its composition is changed by environmental factors such as diet. However, the relationship of commensal microbes and the longevity effect of DR are not illustrated yet. To test whether the longevity effect of DR is related with commensal microbes, we generated axenic flies and measured the lifespan under the various concentration of yeast, the protein source of flies' diet. We observed that the longevity effect of DR was diminished by the removing of commensal microbes and that insulin/IGF-1 signaling (IIS) is reduced by axenic culture as similar with DR. Interestingly, the decline of lifespan and IIS induced by axenic culture were partially rescued by re-association of *Acetobacter*, indicating that *Acetobacter* have a role in the longevity effect of DR. Our results showing the relationship of commensal microbes and longevity effect of DR will provide fundamental knowledge to understand the underlying mechanisms of lifespan extension by DR.

▶ **Keywords:** Dietary restriction, commensal microbe, longevity, host-microbe interaction, *Drosophila melanogaster*

SP2-6

Odontogenic demineralized dentin matrix powder based bio-ink without compromise between biofunctionality and printability for 3D bioprinted dental constructs

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Currently, there has been a demand for the development of a bio-ink suitable for regenerative dentistry. However, the existing bio-inks have a limitation in that tissue regeneration ability must be sacrificed for excellent printability. Therefore, in this study, a demineralized dentin matrix powder (DDMp) based bioink was developed without compromise between 3D printability and dental regeneration ability. As the concentration of DDMp in cell laden bioinks increases, the bioink showed improved z-axis printability , while high cell viability(>95%) and continuous proliferation(> 7 day). Furthermore, mineralization of DPSC enhanced due to upregulated odontogenic differentiation. Finally, a centimeter scale 3D dental construct for dental regeneration was fabricated utilizing this bioink. These results showed that it is possible to construct a 3D regenerative dental construct with high shape fidelity and regeneration ability for dental regeneration using 3D bioprinting and tooth derivatives.

▶ **Keywords:** dentin derived matrix powder, 3D bioprinting, odontogenic bioink, dental regeneration

SP2-7

USP39, a new poly (ADP-ribose)-binding deubiquitinase, drives non-homologous end-joining repair by liquid demixing

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Reciprocal crosstalk between poly(ADP-ribose) (PAR), produced by PAR polymerase 1 (PARP1), and DNA repair machinery has came to light as a key regulatory mechanism of the DNA damage response (DDR). However, there is yet no firm evidence of how PAR precisely controls the DDR. To elucidate this relationship, we identified six deubiquitinating enzymes (Dubs) associated with PAR-coupled DDR. Among the six Dubs, the functional role of USP39, an inactive Dub involved with the spliceosome assembly, was characterized. USP39 rapidly localizes to DNA lesions in a PAR-dependent fashion where it regulates non-homologous end-joining (NHEJ) via its tripartite RG motif located in the N-terminus comprising 46 amino acids (N46). It is already reported that proteins containing RG motif are crucial for liquid demixing, which is contribute to modulation of the DDR. In addition to, we found that USP39 acts as a molecular trigger for liquid demixing in a PAR-coupled N46-dependent manner. Also, USP39 directly interacts with the XRCC4/LIG4 complex during NHEJ via its ZF domain. In parallel, USP39-mediated spliceosome complex controls homologous recombination (HR) repair in a PAR-independent fashion. These findings provide mechanistic insights into how PAR-chains exactly control DNA repair processes in the DDR.

SP2-8

Imaging of astrocyte-to-neuron conversion using aptamers

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Direct conversion of astrocytes into neuronal cells has emerged as a promising treatment for neurodegenerative diseases. However, a reliable method for tracing direct conversion remains challenging. Herein, we present a fluorescence probed trimer of astrocyte-specific aptamer and its use for monitoring astrocyte-to-neuron conversion in the state of living cells. Through 17 rounds of SELEX with primary rat astrocytes as a target and rat neuron cells as a negative counterpart, the most frequent sequence Ast17-30 had selected and improved as a trimer form (denoted Tri-tAst17-30), which has showed increased binding affinity with high target specificity. Significantly, unlike classical immunohistochemical imaging via cell fixation, this aptamer enabled live astrocyte-targeted imaging, which consequently led to the simultaneous monitoring of astrocyte-to-neuron conversion. These findings suggest that this approach will facilitate the study to uncover direct lineage conversion of astrocytes into neuronal cells as well as the application for astrocyte-specific gene/drug delivery.

▶ **Keywords:** Cell-SELEX, Astrocyte-to-Neuron Conversion, Aptamer, live cell staining

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SP2-9

발효식품으로부터 박테리오신 유전자를 보유한 바실러스균의 스크리닝 및 동정

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박테리오신은 미생물로부터 생산되는 천연무독성 방부제로 바실러스에서 많이 생산된다. 우리는 전통발효식품(젓갈, 김치, 장아찌, 장류)에서 *Listeria monocytogenes*와 *Bacillus cereus*에 대하여 모두 항균활성을 가진 바실러스균 10균주를 분리하였다. 16S rRNA sequence를 이용한 동정 결과 *Bacillus amyloliquefaciens* 1균주, *Bacillus subtilis* 5균주, *Bacillus tequilensis* 3균주, *Bacillus velezensis* 1균주로 나타났다. 항균력 시험결과를 바탕으로 분리된 10주의 Bacillus 균주들이 알려져 있는 26종류의 bacteriocin 유전자를 보유하고 있는지 탐색하기위해 PCR분석을 하였다. 그 결과 *B. tequilensis* M194-4 균주는 Subtilisin, Subtilosin, Mersacidin, Mycosubtilin, Bacilysin BacD Ericin, Fengycin, Sublancin, Surfactin등 가장 많은 9개의 항균물질 유전자를 보유하고 있었다.

SP2-10

Probiotic *Lactobacillus reuteri* extends the lifespan of *Drosophila melanogaster* through a mechanism dependent on dSir2 and insulin/IGF-1 signaling

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The term probiotic refers to bacteria that provide a beneficial effect to the host. In particular, lactic acid bacteria, which excrete lactic acid as their main fermentation product, are well-known representative probiotics. *Lactobacillus reuteri* is one such lactic acid bacteria isolated from human breast milk. Although *L. reuteri* has both anti-microbial and anti-inflammatory activities that have occasionally been linked to increased lifespan, there are no reports on the effect of *L. reuteri* on longevity in an animal model. To test this, we used a freeze-dried *L. reuteri* powder manufactured by Wedea Inc. in South Korea. We investigated the anti-aging effects of *L. reuteri* including lifespan and physiology, in *Drosophila melanogaster*. We measured the lifespan of flies supplemented with *L. reuteri* at 0, 50, 100, or 250 μg/mL and found that *L. reuteri* significantly increased the mean lifespan of fruit flies, especially at 100 μg/mL. This longevity effect of *L. reuteri* was not accompanied by reductions in reproductive output, food intake, or locomotor activity, indicating that increased lifespan caused by *L. reuteri* is a direct effect of the bacteria, and not an artefact caused by changes in reproduction, feeding, or locomotor activity. Flies treated long-term with *L. reuteri* showed reduced body weight compared to controls. Interestingly, *L. reuteri* supplementation did not extend the lifespan of flies on low-nutrient diet but did induce the forkhead box-O transcription factor activation, which is one of the important proteins having roles in metabolism, cellular proliferation, stress resistance and probably lifespan, suggesting that *L. reuteri* can be used as a probiotics with anti-aging effects.

▶ **Keywords:** Probiotics, *Lactobacillus reuteri*, *Drosophila melanogaster*, Lifespan, Anti-aging

SP2-11

Intein-mediated protein cyclization for improved intracellular delivery into cancer cells

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Protein delivery into cells is a potentially therapeutic tool in cancer, but its achievement is a big challenge due to membrane impermeability and reduced activity of proteins during the delivered process. Here we report an improved intracellular delivery method of proteins into cancer cells, which is based on the intra-cyclization of cell-penetrating proteins and receptor-binding proteins. As a model protein, we used an enhanced green fluorescent protein (EGFP) fused with two types of peptides: a cell-penetrating peptide (tetra-arginine; R_4) or an integrin-binding peptide (arginylglycylaspartic acid; RGD). The cyclization of peptide-conjugated EGFP (pep-EGFP) was achieved using a split *Npu* DnaE intein-mediated self-splicing process, in which the C-terminal (I_C) part of intein was fused to the N-terminus of pep-EGFP, and N-terminal (I_N) part was fused to C-terminus of pep-EGFP (i.e., I_C-Pep-EGFP-I_N). Compared with linear proteins (R_4-EGFP or RGD-EGFP), cyclized proteins (cycR_4-EGFP or cycRGD-EGFP) exhibited enhanced intracellular efficiencies in the analyses of confocal imaging and fluorescence-activated cell sorting in HeLa, HT-1080 and HEK-293T cells. Conversely, control proteins (EGFP) without peptides were not intracellularly delivered into cells, regardless the cyclization. Although the intracellular delivery mechanism was dependent on peptide sequences, time-lapse stability of cyclized fusion proteins in cells was also improved compared with that of linear fusion proteins. These findings suggest that the cyclization of peptide-conjugated proteins is effective for intracellular delivery and will be useful as a protein delivery platform.

▶ **Keywords:** protein cyclization, protein delivery, intein, cell-penetrating, integrin, RGD

SP2-12

The control of bakanae disease caused by *Fusarium fujikuroi* based on the interaction of plant-derived *Burkholderia* species with *F. fujikuroi*

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The bakanae disease of rice caused by *Fusarium fujikuroi*, which produced Gibberellic Acids as major virulence factor, is characterized by hyper-elongation of seedlings. The typical symptoms of bakanae disease are abnormal elongation including tall, lanky tilers, pale green flag leaves, dried-up leaves and infertile panicles. The bakanae disease is the most notorious seed-brone diseases and widespread problems affecting production of rice in the rice-growing countries. The most common management for preventing this disease is treatment of the seeds with hot water or fungicide. Hot water immersion method is ineffective on severely infected rice seed, because it is difficult to reach the pericarp or rice seeds. The application of fungicides is also ineffective for destroying the spores of this fungal pathogen. Also, the control of the bakanae disease has been difficult due to rapidly developing fungicide resistance in the fungi. Therefore, with an environmental-friendly approach capable of controlling the bakanae disease with microorganisms is effective in controlling the bakanae disease. In this study, identification of the interaction between *F. fujikuroi* and microorganisms using pathogenic and non-pathogenic *Burkholderia* species was confirmed by *in vitro* assay, and it has been confirmed in *in vivo* assay with rice plants that the bakanae disease was controlled by its interaction.

▶ **Keywords:** *Burkholderia* sp. KJ006, *Fusarium fujikuroi*, Bakanae disease

SP2-13

Self-assembled hyaluronic acid nanoparticles protect against osteoarthritic development by targeting CD44

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Although osteoarthritis (OA) is the most prevalent degenerative joint disease, there is no effective disease-modifying therapy. Here, an empty self-assembled hyaluronic acid nanoparticle (HA-NP) is evaluated as a potential therapeutic agent for OA treatment. In mouse primary articular chondrocytes, HA-NPs block the receptor-mediated cellular uptake of low-molecular-weight HA, and the cellular uptake of HA-NPs increases by ectopic expression of CD44, using an adenoviral delivery system (Ad-*CD44*). In addition to its long-term colloidal stability, HA-NP shows *in vitro* resistance to digestion with hyaluronidase and *in vivo* long-term retention ability in knee joint, compared with high-molecular-weight HAs. CD44 expression increases in the damaged articular cartilage of human patients and mice with OA. Ad-*CD44* infection and IL-1β treatment induces *in vitro* phenotypes of OA by enhancing catabolic factor expression in primary articular chondrocytes, and HA-NP attenuates these effects by inhibiting NF-κB activation. Accordingly, both *CD44* deficiency and intra-articular injection of HA-NP protect joint cartilage against OA development in the OA mouse model. Collectively, our results identify an empty HA-NP as a potential therapeutic agent targeting CD44 for OA treatment, and the CD44-NF-κB-catabolic gene axis as an underlying mechanism of destructive cartilage disorders.

SP2-14

The roles of LRRK2 in excitotoxicity-and oxygen and glucose deprivation-induced neuronal toxicity

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Parkinson`s disease (PD) is the most common movement disorders in the elderly population, accompanied with cardinal neuropathological features, such as progressive loss of dopaminergic neuron in substantia nigra pars compacta and the presence of proteineous inclusion bodies, known as Lewy bodies. Although the etiology of PD is not clear yet, genetic variants in multiple gens are considered as risk factors in PD initiation and progression. Mutations in leucine rich-repeat kinase 2 (LRRK2) is the most commonly found in both familial and sporadic PD. LRRK2 is a large size protein and contains multiple domains, such as GTPase and kinase functional domains and various protein-protein interaction domains. Currently, the variation of its kinase activity in various pathogenic mutations is suggested as pathogenic mechanisms in PD. However, familial PD cases are relative rare, less than 10% of all PD cases and the disease penetrance is incomplete and various in LRRK2 associated PD. Therefore, it has been suggested that combination of genetic and environmental factors modulates the occurrence and progression of diseases. Therefore, here, we investigated whether environmental factor (excitotoxicity and oxygen-glucose deprivation (OGD)) has effect on the LRRK2-linked brain pathologies, such as neuronal cell toxicity. So, in depth, we observed that excitotoxicity and OGD induced the significant increase of LRRK2 expression, and then LRRK2 expression and its activity are associated with neuronal cell toxicity by excitotoxicity and OGD.

포스터발표

포스터 발표 목록

P01 **The control of bakanae disease caused by *Fusarium fujikuroi* based on the interaction of plant-derived *Burkholderia* species with *F. fujikuroi***

Seongeom Jeong[p], Jeong Yuna, Jieun Kim, Sarang Chun, and Young-Su Seo[c]
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P02 **Effects of different leaf-fruit ratios on tree growth and chlorophyll fluorescence of 'Gamnuri' persimmon**

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Sweet Persimmon Research Institute, Gyeongsangnam-do Agricultural Research and Extension Services

P03 **The conformational diversity mimicking and statistical analysis enable drug discovery targeting the disorder-to-order transition regions**

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P04 **MEL cell-derived allograft mouse model for cancer research**

Min Young Kim[1], Sungwoo Choi[p,1], Seol Eui Lee[1], Ji sook Kim[1,2], Seung Han Son[1], Young Soo Lim[1], Bang-Jin Kim[3], Buom-Yong Ruy[3], Vladimir N. Uversky[4,5], Young Jin Lee[1], and Chul Geun Kim[c,1,6]
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P05 **CP2c protein degradation occurs via SUMOylation-mediated 20S proteasome pathway for cell cycle progression**

Seung Han Son[p,1], Young Jin Lee[2], Min Young Kim[1], Hyeon Cheol Jin[1], Ho Chul Kang[1], June Ho Shin[1], Jae Kyu Yi[1], Sungwoo Choi[1], Sangwon Lee[1], Mi-Ae Park[1], Ji Hyung Chae[1], Chan-Gil Kim[3], Vladimir N. Uversky[4,5], and Chul Geun Kim[c,1,6]

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P06 **Structural and molecular insights of the interface important for CP2c complex formation**

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P07 **MMTR/Dmap1 is involved in the lineage commitment of early embryonic stem cells through crosstalk with the PcG proteins**

Young Jin Lee[c,1], Seung Han Son[p,1], Chang Su Lim[1], Min Young Kim[1], Si Woo Lee[1], Sangwon Lee[1], Jinseon Jeon[1], Dae Hyun Ha[1], Na Rae Jung[1], Su Youne Han[1,2], Byung-Rok Do[2], Insung Na[1], Vladimir N. Uversky[3,4], and Chul Geun Kim[c,1,5]

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P08 **Anticancer effects of agents targeting disorder-to-order transition region at MBD2-p66α interaction**

Seunghan Son[p,1], Insung Na[1], Min Young Kim[1], Young Su Lim[1], Ji Sook Kim[1], Sungwoo Choi[1], Kiseok Jang[3], Yu Chen[4], Arjan van der Vaart[5], Vladimir N. Uversky[c,4], and Chul Geun Kim[c,1,2]

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P09 **A selected peptide inhibiting CP2c specifically induces cancer cell-specific synthetic lethality**

Seung Han Son[p,1], Min Young Kim[1], Ji Sook Kim[1], Seol Eui Lee[1], Young Soo Lim[1], Eonju Oh[2], Sungwoo Choi[1], Sangwon Lee[1], Min-Sung Jung[3], Eun Jung Baek[4], Jaemin Jeong[3], Dongho Choi[3], Hee-Seok Kweon[5], Ji-Yun Lee[6], Kiseok Jang[7], Chae-Ok Yun[2], Su-Jae Lee[1], Dongsun Park[8], Chan Gil Kim[9], Uversky N. Vladimir[10], and Chul Geun Kim[c,1,11]
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P10 **Gold nanoparticle-assisted SELEX for rapid discovery of small molecule-binding aptamers**

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P11 **Study on the increase of polyphenol content and bacterial growth of lactic acid bacteria using *Asparagus officinalis* extract**

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P12 **Changes in volatile compounds in Korea chili by cooking methods**

Yong-Su Ji[p], Se-Young Kwun, and Eun-Hee Park[c]
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P13 **Analysis of non-volatile compounds in radish by GC-TOF/MS and relation to cooking methods**

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P14 **Elevation of ACE2 as a SARS-CoV-2 entry receptor gene expression in Alzheimer's disease**

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P15 **Potential therapeutic target of long noncoding RNAs in brain disorders**

Sung-Hyun Kim[p], Sumin Yang, Key-Hwan Lim, and Jae-Yeol Joo[c]
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P16 **Probiotic *Lactobacillus reuteri* extends the lifespan of *Drosophila melanogaster* through a mechanism dependent on dSir2 and insulin/IGF-1 signaling**

Hye-Yeon Lee[p,1], Ji-Hyeon Lee[1], Min Hyuk Kang[1], Yongseok Gye[1], Bi Rang Park[1], Min Son[1], Su-yeon Jo[2], and Kyung-Jin Min[c,1]
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P17 **Extension of *Drosophila* lifespan by Korean red ginseng through a mechanism dependent on dSir2 and insulin/IGF-1 signaling**

Shin-Hae Lee[1], Hye-Yeon Lee[p,1], Mira Yu[1], Eunbyul Yeom[2], Ji-Hyeon Lee[1], Ah Yoon[1], Kyu-Sun Lee[2,3], and Kyung-Jin Min[c,1]
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P18 **Imaging of astrocyte-to-neuron conversion using aptamers**

Eun-Song Lee[p] and Young-Pil Kim[c]
Department of Life Science, Hanyang University

P19 **The role of commensal microbes on the longevity effect of dietary restriction**

Ji-Hyeon Lee[p,1], Shin-Hae Lee[1], Ah Yoon[1], Hye-Yeon Lee[1], Eunbyul Yeom[2], Yong-Jin An[4], Kyu-Sun Lee[2,3], Sunghyouk Park[4], and Kyung-Jin Min[c,1]
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P20 **The role of commensal microbes on the effect of metformin in *Drosophila***

Ji-Hyeon Lee[p], Hye-Yeon Lee, and Kyung-Jin Min[c]
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P21 **Role of commensal microbes in the γ-ray irradiation-induced physiological changes in *Drosophila melanogaster***

Hwa-Jin Lee[1], Shin-Hae Lee[1], Ji-Hyeon Lee[p,1], Yongjoong Kim[2], Ki Moon Seong[2], Young Woo Jin[2], and Kyung-Jin Min[c,1]
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P22 **Metagenomic analysis of the DNA viral communities in fermented food kimchi**

Jae Yon Chang[p] and Min-Soo Kim[c]
Department of Microbiology & Molecular Biology, Chungnam National University

P23 **전통발효 식품으로부터 분리한 항균활성을 가진 유산균의 바이오필름 특성**
김종희[d], 이은선, 김부민, 함준상, 오미화
국립축산과학원

P24 **발효식품으로부터 박테리오신 유전자를 보유한 바실러스균의 스크리닝 및 동정**
김종희[d], 이은선, 김부민, 함준상, 오미화
국립축산과학원

P25 **Optimization of fermentation conditions and anti-inflammatory activities of extract from fermentation of onion**
Heami Sung
Jeonnam Bioindustry Foundation, Food Research Center

P26 **Odontogenic demineralized dentin matrix powder based bio-ink without compromise between biofunctionality and printability for 3D bioprinted dental constructs**
Jonghyeuk Han[p], Wonwoo Jeong, Minkyung Kim, and Hyun-Wook Kang[c]
School of life sciences, Ulsan National Institute of Science and Technology

P27 **Study of amyloid-β-induced fragmentation of lamin A and B**
Il-Seon Park
Department of Cellular and Molecular Medicine, Chosun University

P28 **Reciprocal roles of SIRT1 and SIRT1-associating protein SAP10 on the regulation of androgen receptor activity**
In Sun Baek[p], Ji Hyun Lee, Si Eun Kim, and Eun-Joo Kim[c]
Department of Molecular Biology, Dankook University

P29 **TTF-1 action in leptin-induced development of hypothalamic neurons**
Dasol Kang[p] and Byung Ju Lee[c]
Department of Biological Sciences, University of Ulsan

P30 **Morphological change of hypothalamic microglia by energy state**
Tae Hwan Lee[p,1], Jae Geun Kim[2], and Byung Ju Lee[c,1]
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P31 **Enzyme-accelerated fluorescence signal enhancement for targeted cancer cell imaging**
Hea-Jin Kim[p], Yeon-Ju Lee, Mi-So Kim, and Young-Pil Kim[c]
Department of Life Science, Hanyang University

P32 **Materials development and production using silkworms**
Jong Woo Park[d], Jeong Won Hong, Chan Young Jeong, Su-Bae Kim, Sang Kuk Kang, Seong-Wan Kim, You-Yong Jo, Hae Yong Kweon, and Kee Young Kim
Sericultural and Apicultural Materials Division, National Institute of Agricultural Science

P33 **Cloning and characterization of maize (*Zea mays*) nitrilase to study its defensive roles**
DaeHyeon Gwak[p], JooHyeon Lee, MiJeong Lee, MinJeong Cho, Woong June Park, and Chian Kwon[c]
Department of Molecular Biology, Dankook University

P34 **SIRT1 associating protein SAP8 represses RA-induced neuronal differentiation in P19 cells**
Jin-Hong Yang[p], Ji-Hyun Lee, Si-Eun Kim, and Eun-Joo Kim[c]
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P35 **Stress-induced NEDDylation promotes cytosolic protein aggregation through HDAC6 in a p62-dependent manner**
Soyeon Kim[p], Mira Kwon, Yiseul Hwang, Junghyun Yoon, Sangwook Park, and Ho Chul Kang[c]
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P36 **Anti-oxidant, digestive enzyme inhibitory, and anti-inflammatory effect of fermented oak *Lentinus edodes* extracts**
Jun-Hui Choi[p], Se-Eun Park, Hyo-Jeong Lee, Seung Kim, and Ki-Man Kim[c]
Department of Food Science and Biotechnology, Gwangju University

P37 **The iron binding capacity and anti-inflammatory effect of the mixed extract derived from plant sources**
Se-Eun Park[p], Jun-Hui Choi, Hyo-Jeong Lee, Ki-Man Kim, and Seung Kim[c]
Department of Food Science and Biotechnology, Gwangju University

P38 **USP39, a new poly (ADP-ribose)-binding deubiquitinase, drives non-homologous end-joining repair by liquid demixing**
Junghyun Yoon[p], Yiseul Hwang[p], Soyeon Kim, Sangwook Park, and Ho Chul Kang[c]
Department of Physiology, Ajou University School of Medicine

P39 **Acid류의 체강 주입에 따른 누에 혈림프 항산화능 증강 효과 구명**
김수배[d], 김성완, 강상국, 박종우, 홍정원, 권해용, 김기영
국립농업과학원 농업생물부 잠사양봉소재과

P40 **Improved alcohol dehydrogenase production in transgenic *Escherichia coli* expressing heat shock protein**
Minhye Kim, Eunju Im[p], and Yeh-Jin Ahn[c]
Department of Biotechnology, Sangmyung University

P41 **Insulin production in transformed *E. coli* expressing plant heat shock protein**

Bomin Jang, Eunju Im[p], and Yeh-Jin Ahn[c]
Department of Biotechnology, Sangmyung University

P42 **Antioxidant and anti-inflammatory activities of water extract of *Filipendula glaberrima* Nakai**

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P43 **Antioxidant properties of ethanol extract of *Centella asiatica***

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P44 **The mechanisms of oncolytic immunotherapy and novel cancer therapeutic approach**

Seung-Hak Lee[p,1], Seungyeop Han[2], Jisu Hong[3], and Seha Kim[c,2]
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P45 **β-Cyclodextrin inhibits monocytic adhesion to endothelial cells through nitric oxide-mediated depletion of cell adhesion molecules**

Sujeong Jang[p], Jeongwon Byun, Yebum Chun, Jeongheon Lee, and Heonyong Park[c]
Department of Molecular Biology & Institute of Nanosensor and Biotechnology, Dankook University

P46 **Lysyl-tRNA synthetase is secreted through enhanced autophagy and calcium in endothelial cells**

Yerim Oh[p], Heonyong Park, and Youngsik Seo[c]
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P47 **Transcriptomic analysis of the pathogenesis of Parkinson's disease by FAF1 in A53T mouse model**

Jangham Jung[p], Boksuk Kim, Eunhee Kim, and Myungchull Rhee[c]
Department of Bioscience & Biotechnology, Graduate School, BK21 Plus Program, Chungnam National University

P48 **Generation of alveolar macrophages from human induced pluripotent stem cells**

Seri Choi[p,1,2], Won Keun Oh[2], and Eun-Mi Kim[c,1]
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[2]Korea Bioactive Natural Material Bank, Research Institute of Pharmaceutical Sciences, College of Pharmacy, Seoul National University

P49 **Establishment of ES cell-derived lung organoids for human 3D lung fibrosis model *in vitro***

YeongSoo Choi[p,1,2] , Eun-Mi Kim[1], and Ki-Kwang Kim[c,2]
[1]Department of Predictive Toxicology, Korea Institute of Toxicology
[2]Functional Genomics Laboratory, Chungnam National University

P50 **Development of a tetracycline regulatable conditional mouse model of Parkinson's disease expressing parkin substrate, ZNF746**

Hyojung Kim[p] and Yunjong Lee[c]
Department of Pharmacology, Sungkyunkwan University School of Medicine

P51 **Poly (ADP-ribose)-dependent Ubiquitination of Heterochromatin protein 1 alpha (HP1α) by RNF4 E3 ligase suggests a functional role for homologous recombination repair**

Sangwook Park[p], Soyeon Kim, Junghyun Yoon, Yiseul Hwang, and Ho Chul Kang[c]
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P52 ***trim46* is associated with the zebrafish neurogenesis via Foxa2**

Jaehun Kim[p] and Myungchull Rhee[c]
Laboratory of Neurodevelopmental Genetics, Department of Biological Sciences, College of Biological Sciences & Biotechnology, Chungnam National University

P53 **CNS-specific expression pattern of *rnf126* in zebrafish embryos**

JiHun Baek[p] and Myungchull Rhee[c]
Neurodevelopmental Genetics Laboratory, Department of Biological Sciences, College of Biological Sciences and Biotechnology, Chungnam National University

P54 **Fine-tuning UDSMProt model for anti-CRISPR prediction**

Chan-Seok Jeong
Center for Supercomputing Applications, Korea Institute of Science and Technology Information

P55 **Hemogenic endothelium from aorta gonad mesonephros in murine at embryonic 10.5 days and completion of the definitive hematopoiesis**

Soo-Been Jeon[p,1] Jieun Kim[2], Hyebin Koh[2], Jong-Hee Lee[3], and Ji Yoon Lee[c,1]
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P56 **Development of a tetracycline regulatable conditional mouse model of Parkinson's disease expressing amyloid-like protein aggregate**

Heejeong Kim[p] and Yunjong Lee[c]
Department of Pharmacology, Sungkyunkwan University School of Medicine

P57 **The roles of LRRK2 in excitotoxicity-and oxygen and glucose deprivation-induced neuronal toxicity**

Tae-Young Kim[p], You-Jung Kang, and ByoungDae Lee[c]
Department of Neuroscience, Graduate School, Kyung Hee University

P58 **Epigenetic Analysis of a CMT2D Family with phenotypic heterogeneity**

Da Eun Nam[1], Hong Ki Kim[1], Ye Won Sim[1], Byung-Ok Choi[c,2], and Ki Wha Chung[d1]
[1]Department of Biological Sciences, Kongju National University
[2]Department of Neurology, Samsung Medical Center, Sungkyunkwan University School of Medicine

P59 **Determining parental origin of *de novo* mutation in Korean CMT patiens**

Ah Jin Lee[1], Byung-Ok Choi[c,2], and Ki Wha Chung[d,1]
[1]Department of Biological Sciences, Kongju National University
[2]Department of Neurology, Samsung Medical Center, Sungkyunkwan University School of Medicine

P60 **A Nonaka myopathy patient with compound heterozygous variants of *GNE***

Si On Lim[1], Hye Ri Park[1], Yu Jin Choi[1],Byung-Ok Choi[c,2], and Ki Wha Chung[d,1]
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[2]Department of Neurology, Samsung Medical Center, Sungkyunkwan University School of Medicine

P61 **CITESDB: A centralized portal for accessing detailed information on endangered species of wild fauna and flora**

Se-Joo Kim, Won-Kyung Lee, Jinhyuk Lee, Seung-Woo Baek, and Bo Kyeng Hou[d]
Genome Editing Research Center, Korea Research Institute of Bioscience and Biotechnology

P62 **Effects of *Allium senescens* L. extract on sorafenib resistant HepG2 cells**

Sohyeon Park[p,1], Yoonjin Park[2], Sumin Lee[5], Boyong Kim[c,2,3,4], Seung Gwan Lee[c,2]
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[3]Life Together
[4]Mitosbio
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P63 **A subset of EGFR mutation serves as key biomarkers for EGFR-targeted therapy in colorectal adenocarcinoma**

Sujin Kim[p] and Jeonghee Cho[c]
Department of Nanobiomedical Science, Dankook University

P64 **Formation of amyloid β oligomeric forms enhanced or reduced its cytotoxicity**

Il-Seon Park
Department of Cellular and Molecular Medicine, Chosun University

P65 **Effect of Th2 differentiation control through formation of skin lipid barrier on *Coptidis Rhizoma*, *Glycyrrhiza uralensis* and and fermameted *Glycine max* extract**

Seong Eun Kim[p], Doo Ho Hwang, and Sang Hyun Ahn[c]
Department of Anatomy, College of Korean Medicine, Semyung University

P66 **Mitogen-Inducing factor 6 (Mig6) functions as a tumor suppressor by modulating EGFR signaling cascade**

Daseul Cho[p], Hyunjin Kim, and Jeonghee Cho[c]
Department of Nanobiomedical Science, Dankook University

P67 **Investigating the effects of altering gravity on PVD neuron dendrite development in *C. elegans* : From hypergravity to space microgravity**

Je-Hyun Moon[p], Alcantara Alfredo Jr, and Jin Il Lee[c]
Division of Biological Science and Technology, Yonsei University

P68 **FMRF-like peptide regulates a *C. elegans* putative maternal behavior in 3D**

Tong Young Lee[p,1], Kyoung-hye Yoon[2], and Jin Il Lee[c,1]
[1]Division of Biological Science and Technology, College of Science and Technology, Yonsei University
[2]Department of Physiology, Wonju College of Medicine, Yonsei University

P69 ***Alternaria alternata* 진균에 의한 느릅나무 신병해 잎반점병(leaf spot disease) 및 약제 선별 보고**

노형진[p], 김예은, 김성환[c]
단국대학교 자연과학대학 미생물학과 및 생물다양성연구소

P70 **Newly recorded sea star *Henricia oculata* (Asteroidea: Spinulosida: Echinasteridae), in the East Sea, Korea**

Michael Dadole Ubagan[p,1,2], Taekjun Lee[2], and Sook Shin[c,1,2]
[1]Department of Animal Biotechnology & Resource, Sahmyook University
[2]Marine Biological Resource Institute, Sahmyook University

P71 **New record of the unstalked crinoid *Tropiometra macrodiscus* (Crinoidea: Comatulida: Tropiometridae) from Korea Strait**

Philjae Kim[p,1,2], Tackjun Lee[1], and Sook Shin[c,1,3]
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P72 **Influence of simulated microgravity in the intestinal immunity of the Nematode *Caenorhabditis elegans***

Alfredo Jr. Alcantara[p] and Jin Il Lee[c]
Division of Biological Science and Technology, Yonsei University Mirae Campus

P73 **Biodiversity of the agriculture ecosystems of Goesan-gun district in South Korea**

Yan Sun[p,1], Bon-Jin Ku[1], Eun-Woo Baek[1], Cheol Choi[1], Byung-Gyu Sog[1], Seung-Min Lee[1], Yun-Mo Ku[2], Tae-Yeon Kim[2] and Myung-Jin Moon[c,1]
[1]Department of Biological Sciences, Dankook University
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P74 **Comparative biodiversity between organic and conventional agricultural ecosystems of Korea**

Yan Sun[p,1], Hoon Kim[1], Tae-Yeon Kim[2], and Myung-Jin Moon[c,1]
[1]Department of Biological Sciences, Dankook University
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P75 **Structural characteristics of the sponge scaffold from dragline silks in the golden orb-web spider, *Nephila clavata***

Yan Sun[p], Bon-Jin Ku, and Myung-Jin Moon[c]
Department of Biological Sciences, Dankook University

P76 **Microstructure of sponge scaffolds from eggsac silks in the golden orb-web spider, *Nephila clavata***

Yan Sun[p], Bon-Jin Ku, and Myung-Jin Moon[c]
Department of Biological Sciences, Dankook University

P77 **Size selective fabrication of silk sphere scaffolds from the major ampullate silk glands in the golden orb web spider, *Nephila clavata***

Seung-Min Lee[p] and Myung-Jin Moon[c]
Department of Biological Sciences, Dankook University

P78 **Morphological analysis of orb-web decoration (stabilimentum) of the garden spider, *Argiope bruennichi***

Seung-Min Lee[p] and Myung-Jin Moon[c]
Department of Biological Sciences, Dankook University

P79 **Microstructures of tubular scaffolds from various silk glands of the golden orb-web spider, *Nephila clavata***

Bon-Jin Ku[p], Yan Sun, and Myung-Jin Moon[c]
Department of Biological Sciences, Dankook University

P80 **Visualizing a type of brain cells with a small fluorescent molecule**

Young-ran Hwang[p] and Beomsue Kom[c]
Neural Circuit Research Group, Korea Brain Research Institute

P81 **Self-assembled hyaluronic acid nanoparticles protect against osteoarthritic development by targeting CD44**

Juhwan Yoon[p,1], Li-Jung Kang[2], Siyoung Yang[2], and Wook Kim[c,1]
[1]Department of Molecular Science & Technology, Ajou University
[2]Department of Pharmacology, Ajou University School of Medicine

P82 **Expression and bioinformatic analyses of MicroRNAs in hamster lung infected by SARS-CoV-2**

Woo Ryung Kim[p,1,2,†], Eun Gyung Park[1,2,†], Kyung-Won Kang[3], Sang-Myeong Lee[3], Bumseok Kim[4], and Heui-Soo Kim[c,2,5]
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P83 **Expression and Bioinformatic Analyses of miR-887-3p in *Pan troglodytes***

Woo Ryung Kim[p,1,2], Hiroo Imai[3], and Heui-SooKim[c,2,4]
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P84 **Molecular characterization of MicroRNA-21-5p and MicroRNA-221-3p in *FOXP2***

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P85 **Molecular characterization of SINE derived MicroRNA-422a in *ARID5B***

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P86 **Expression analyses of ol-miR-140-3p and target gene, *KIF5A* in olive flounder infected with *Streptococcus parauberis***

Eun Gyung Park[p,1,2], Woo Ryung Kim[1,2], and Heui-Soo Kim[c,2,3]
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P87 **Expression analysis of pol-miR-15b-5p in *Paralichthys olivaceus* infected by VHSV**

Yun Ju Lee[p,1], Woo Hyeon Bae[1], Du Hyeong Lee[2], Eun Gyung Park[3,4], Woo Ryung Kim[3,4], and Heui-Soo Kim[c,1,4]
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P88 **T790M gatekeeper mutation emerges via *de novo* at the early stages of erlotinib treatment in PC9 non-small cell lung cancer cells**

Sujin Kim[p,1,2], Angela Park[1], and Jeonghee Cho[c,1,2]
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[2]BK21 PLUS NBM Global Research Center of Regenerative Medicine, Dankook University

P89 **Whole transcriptome analysis identifies TNS4 as a key effector of cetuximab and a regulator of the oncogenic activity of KRAS mutant colorectal cancer cell lines**

Sujin Kim[p,1], Nayoung Kim[1], Keunsoo Kang[2], Wonkyung Kim[2], Jonghwa Won[3], and Jeonghee Cho[c,1]
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P90 **Autophosphorylation in C-terminal domain is not required for oncogenic transformation by lung-cancer derived EGFR mutants**

Jeonghee Cho[c,1,2,3,†], Sujin Kim[p,1], Jinyan Du[2], and Matthew Meyerson[2,3,4,5,†]
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[2]Department of Medical Oncology, Dana-Farber Cancer Institute
[3]Center for Cancer Genome Discovery, Dana-Farber Cancer Institute
[4]The Broad Institute of MIT and Harvard, Cambridge
[5]Department of Pathology, Harvard Medical School

P91 **Systematic screening of EGFR C-terminal intragenic deletion mutation in cancer patient samples by establishing a Nanostring technology-based platform**

Daseul Cho[p] and Jeonghee Cho[c]
Department of Nanobiomedical Science, Dankook University

P92 **Characterization of Alzheimer's disease-associated genes using *Drosophila* model**

Seokhui Jang[p], Byoungyun Choi, Chaejin Lim, Chunyu Yuan, Changmin Shin, and Kyoung Sang Cho[c]
Department of Biological Sciences, Konkuk University

P93 **Viral infection induces the upregulation of MHC-1 expression in infected cancer cells**

Sang Hoon Kim and Yong Woo Jung[d]
Korea University

P94 **Liver-selective gamma-secretase inhibition ameliorates diet-induced hepatic steatosis, dyslipidemia and atherosclerosis**

Young Hoon Jung[p,1,2], Yelin Jeong[1,2], Mincheol Shin[1,2], Sang Bae Lee[3], and KyeongJin Kim[c,1,2]
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[3]Division of Life Sciences, Jeonbuk National University

P95 **Oncogenic EGFR mutations as genomic biomarkers for cetuximab and panitumumab response in colorectal adenocarcinoma**

Nayoung Kim, Daseul Cho[p], Hyunjin Kim, Sujin Kim, Young-je Cha, Heidi Greulich, Adam Bass, Hyun-Soo Cho, and Jeonghee Cho[c]
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P96 **Linalool has neuroprotective effects on suppressing ROS production and inflammation of Linalool in Aβ42-induced *Drosophila* model of Alzheimer's disease**

Myeongcheol Shin[p] and Kyoung Sang Cho[c]
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P97 **Amyotrophic lateral sclerosis-related mutant SOD1 aggregates impair mitophagy by sequestering the autophagy receptor optineurin**

Yeong Jin Tak[p,1], Ju-Hwang Park[1], Hyangshuk Rhim[2,3], and Seongman kang[c,1]
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[2]Department of Biomedicine and Health Sciences, College of Medicine, The Catholic University of Korea
[3]Department of Medical Life Sciences, College of Medicine, The Catholic University of Korea

P98 **Metformin has potential as a cancer immunotherapy adjuvant**

Minji Choi[p,1], Jisoo Shin[1], Jooyoon Chung[1], and Jong-ho Cha[c,1,2]
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[2]Department of Biomedical Sciences, College of Medicine, Inha University

P99 **Functional analysis of lauric acid hydroxylation in human cytochrome P450 4A11 C347A, C347S, C375A, C375S**

Sung-gyu Lee[p], Vitchan Kim, Rowoon Lee, Sang-A Lee, and Donghak Kim[c]
Department of Biological Sciences, Konkuk University

P100 **Functional characterization of *Drosophila melanogaster* cytochromes P450, 6A2 and 6A8**

Sang-A Lee[p] , Vitchan Kim, Sung-Gyu Lee, Rowoon Lee, and Donghak Kim[c]
Department of Biological Sciences, Konkuk University

P101 **Dynamics of primary cilia regulates Schwann cell myelination in a state of chronic inflammation**

Hui Su Jeong[p] and Ji Eun Lee[c]
Department of Health Sciences & Technology, Samsung Advanced Institute for Health Sciences & Technology, Sungkyunkwan University

P102 **ADSSL1-mediated AMPK activation is essential for ciliogenesis to induce myoblast differentiation**

So Yeon Won[p] and Ji Eun Lee[c]
Department of Health Sciences and Technology, Samsung Advanced Institute for Health Sciences & Technology (SAIHST), Sungkyunkwan University

P103 **XAF1 directly antagonizes GRP78 to drive ER stress-induced apoptosis through the assembly of a ZNF313-mediated destruction complex**

Kyung-Woo Lee[p], Jieun Ahn, Woo-Kyung Chung, and Sung-Gil Chi[c]
Department of Life Sciences, Korea University

P104 **Study on the structure and mechanism of Severe acute respiratory syndrome coronavirus 2, (COVID19)**

Yongdae Kwon[p] and Linwoo Kang[c]
Department of Biological Sciences, Konkuk University

P105 **Cyclic peptide: promising drug molecule**
Dogyeong Kim[p], Diem-Quynh Nguyen, and Lin-Woo Kang[c]
Department of Biological Sciences, Konkuk University

P106 **Dihydrofolate Reductase (DHFR) Enzyme Kinetics and Structural Study in *Pseudomonas aeruginosa, Acinetobacter baumannii* and *Xanthomonas Oryzae***
Yeong-Jin Yun[p,1], Eunju Im[2], Yeh-Jin Ahn[2], and Lin-Woo kang[c,1]
[1]Department of Biological Sciences, Konkuk University
[2]Department of Life Science, Sangmyung University

P107 **Expression, purification, crystallization of UDP-3-O-(R-3-hydroxymyristoyl)-N-acetylglucosamine deacetylase (LpxC) from multidrug resistant bacteria and *Xanthomonas oryzae* pv. *oryzae***
Sangjun Han[p,1], Eunju Im[2], Yeh-jin Ahn[2], and Lin-Woo Kang[c,1]
[1]Department of Biological Sciences, Konkuk University
[2]Department of Life Science, Sangmyung University

P108 **Functional analysis of paclitaxel 6α-hydroxylation and arachidonic acid epoxidation in human CYP2C8**
Rowoon Lee[p], Vitchan Kim, Sung-Gyu Lee, Sang-A Lee, and Donghak Kim[c]
Department of Biological Sciences, Konkuk University

P109 **Downregulation of proteasome subunits in muscles enhances longevity in *Drosophila***
Youngjae Park[p], Myeongcheol Shin, and Kyoung Sang Cho[c]
Department of Biological Sciences, Konkuk University

P110 **Stress exposure causes distinctive changes in both behaviors and the intrinsic properties of the medial prefrontal cortex in male and female mice**
Woonhee Kim[p] and ChiHye Chung[c]
Department of Biological Sciences, Konkuk University

P111 **Establishing a better female-specific animal model of depression**
Woonhee Kim, Sejong Oh[p], and ChiHye Chung[c]
Department of Biological Sciences, Konkuk University

P112 **Protein kinase C mediates neuropeptide Y-induced reduction in inhibitory neurotransmission in the lateral habenula**
Myunghyun Cheon[p], Hoyong Park, and ChiHye Chung[c]
Department of Biological Sciences Konkuk University

P113 **Apolipoprotein D reduces neuronal damages and disease-like phenotypes in a *Drosophila* model of Alzheimer's disease**
Changmin Shin[p], Soojin Lee, and Kyoung Sang Cho[c]
Department of Biological Sciences, Konkuk University

P114 **Structure and mechanism study of 3-chymotrypsin-like protease of severe acute respiratory syndrome coronavirus 2**

Yeseul Kim[p] and Lin-Woo Kang[c]
Department of Biological Sciences, Konkuk University

P115 **Expression, crystallization and X-ray crystallographic, HPLC analysis of cystathionine ɣ-synthase (XometB) from *Xanthomonas oryzae* pv. *oryzae***

Su Min Kim[p] and Lin Woo Kang[c]
Department of Biological Sciences, Konkuk University

P116 **NORE1A induces a feedback termination of TNF signaling by antagonizing TNFR1 through ITCH-mediated destruction complex**

Seung-Hun Jang[p], Hyun-Jung Ahn, Min-Goo Lee, and Sung-Gil Chi[c]
Department of Life Sciences, Korea University

P117 **FOXO1 mediated FAF1 expression is essential for the host to prevent *T. gondii* infection**

Fei Fei Gao[p], Yeon Jae Lee, Seul Gi Jang, In-Wook Choi, Young-Ha Lee, Jae-Min Yuk, and Guang-Ho Cha[c]
Department of Infection Biology and Department of Medical Science, Chungnam National University School of Medicine

P118 **A comprehensive analysis of gorilla-specific full-length LINE-1 retrotransposons**

Soyeon Jeon[p,1], Wooseok Lee[2], and Kyudong Han[c,2,3]
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P119 **Development of an effective quantification method for human fecal microbe by comparing NGS-based metagenome profiling data**

Jinuk Jeong[p,1], Seyoung Mun[1,4], Yunseok Oh[2], Kyeonguei Yun[3], Yongju Ahn[3], and Kyudong Han[c,2,4]
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P120 **Whole-exome sequencing reveals rare genetic variations in Ovarian Granulosa Cell Tumor**

Seungyeon Kim[p,1], Seyoung Mun[1,2], Yongsik Kwak[2], Song-Yi Choi[3], and Kyudong Han[c,2,4]
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[3]Department of Pathology, School of Medicine, Chungnam National University
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P121 **Establishment of BiTE antibody platform and functional study of CD3ε / CD19 Bispecific BiTE antibody secreted from *Pichia pastoris***
Seung Hyeon Lee[p], Boram Kim, Kyung Min Kim, Kyu Tae Byun, and Chan Gil Kim[c]
Department of Biotechnology, Konkuk University

P122 **Anticancer peptide with anti-microbial effect against multidrug-resistant bacteria**
Kyung Min Kim[p], Boram Kim, Seung Hyeon Lee, Kyu Tae Byun, and Chan Gil Kim[c]
Department of Biotechnology, Konkuk University

P123 **XAF1 directly antagonizes ERa through the assembly of a BRCA1-mediated destruction complex to direct apoptotic switch of estrogen function**
Ji-Sun Lim[p], Sung-Chan Jang, Ji-Hye Yoon, Min-Goo Lee, and Sung-Gil Chi[c]
Department of Life Sciences, Korea University

P124 **VitaminD antagonize *Toxoplasma gondii* growth by reducing host Programmed cell death protein 5 (PDCD5) in ARPE-19 cells**
Yeon-Jae Lee[p], Seul-Gi Jang, Fei-Fei Gao, In-Wook Choi, He-Kyoung Kim, Jae-Yul Kwon, Jae-Min Yuk, and Guang-Ho Cha[c]
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P125 **Anti-parasite effect of 4-Hydroxyacetophenoneis mediated by regulation of HIF-1α and Akt**
Seul-Gi Jang[p], Yeon-Jae Lee, Fei-Fei Gao, In-WookChoi, He-KyoungKim, Jae-Yul Kwon, Jae-Min Yuk, Young-Ha Lee, and Guang-Ho Cha[c]
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P126 **Depolymerization of filamentous actin by LRRK2 negatively regulates actin dynamics of microglia**
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P127 **Structural insights into CYP107G1 from Rapamycin-Producing *Streptomyces rapamycinicus***
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P128 **MicroRNA 34a-AXL axis regulates vasculogenic mimicry formation in breast cancer cells**
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P129 **Hypoxia-inducible factor 2α is a novel inhibitor of chondrocyte maturation**
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P130 **Cbfβ is an anabolic regulator for blocking osteoarthritis progression during aging**
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P131 **TDAG51 is a negative regulator of PPARg-mediated adipocyte differentiation**
Sumi Kim[p,#], Nari Lee[p,#], Eui-Soon Park, Hyeongseok Yun, Tae-Uk Ha, Hyoeun Jeon, Jiyeon Yu, Seunga Choi, Bongjin Shin, Jungeun Yu, and Jaerang Rho[c]
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P132 **GJA1 depletion causes ciliary defects and abnormal laterality**
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P133 **Study on the functions of ERAD pathway in cartilage formation**
Hyo Jung Sim[p,1], Chanmi Cho[2], Ha Eun Kim[1], Siyoung Yang[2], and Tae Joo Park[c,1]
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P135 **Developmental studies and head regeneration of *Perionyx excavatus***
Jeesoo Yi[p,1], Yun Seon Bae[1], Jung Kim[2], Hae Youn Lee[c,1], and Sung Jin Cho[c,1]
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P136 **Accumulation of mitochondrial *RPPH1* RNA is associated with cellular senescence**
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[3]Department of Anatomy and Neurobiology, College of Medicine, Kyung Hee University

P134 **Structure and mechanism study of Npu intein for protein splicing**

Hyunjae Park[p] and Lin-Woo Kang[c]
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P138 ***In vivo* evaluation of scaffolds compatible for colonoid engraftments onto injured mouse colon epithelium**

KyungJin Lee[p,2,4], JooHyun Jee[p,1,2], Sang Yun Jeong[1,2], Han Kyung Kim[1,2], Seon Young Choi[1,2], Sukin Jeong[1,2], Joongwoon Lee[1,2], Ji Su Ko[1,2], Mi Sun Kim[1,2], Min-Soo Kwon[2,3], and Jongman Yoo[c,1,2]
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P139 **Deficiency of early growth response-1 (EGR1) cause irregular decidual reaction during implantation**

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P140 **Reproductive characteristics of a new animal model for study of prion protein: Establishment of replaced bank vole Prnp knock-in (Prnp$^{hr(bvprnp\text{-}I109)cdpr2}$) mice**

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P141 **Characteristics of replaced bank vole Prnp knock-in mouse in embryo development and fertility**

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P142 **A study on the cryopreservation method and container development for stability of primary cells**

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P143 **RBM47-regulated alternative splicing of TJP1 promotes cell migration during epithelial-to-mesenchymal transition**

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P144 **Dual-mode detection of miRNA based on graphene oxide**

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P145 **Development of zebrafish lexA-inducible Ab-SPOP system**

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P146 **I-pesticide causes microcephaly in zebrafish development**

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P147 **Assessment of the neurodevelopmental toxicity of D synthetic compound using zebrafish**

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P01

The control of bakanae disease caused by *Fusarium fujikuroi* based on the interaction of plant-derived *Burkholderia* species with *F. fujikuroi*

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The bakanae disease of rice caused by *Fusarium fujikuroi*, which produced Gibberellic Acids as major virulence factor, is characterized by hyper-elongation of seedlings. The typical symptoms of bakanae disease are abnormal elongation including tall, lanky tilers, pale green flag leaves, dried-up leaves and infertile panicles. The bakanae disease is the most notorious seed-brone diseases and widespread problems affecting production of rice in the rice-growing countries. The most common management for preventing this disease is treatment of the seeds with hot water or fungicide. Hot water immersion method is ineffective on severely infected rice seed, because it is difficult to reach the pericarp or rice seeds. The application of fungicides is also ineffective for destroying the spores of this fungal pathogen. Also, the control of the bakanae disease has been difficult due to rapidly developing fungicide resistance in the fungi. Therefore, with an environmental-friendly approach capable of controlling the bakanae disease with microorganisms is effective in controlling the bakanae disease. In this study, identification of the interaction between *F. fujikuroi* and microorganisms using pathogenic and non-pathogenic *Burkholderia* species was confirmed by *in vitro* assay, and it has been confirmed in *in vivo* assay with rice plants that the bakanae disease was controlled by its interaction.

▶ **Keywords:** *Burkholderia* sp. KJ006, *Fusarium fujikuroi*, Bakanae disease

P02

Effects of different leaf-fruit ratios on tree growth and chlorophyll fluorescence of 'Gamnuri' persimmon

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'Gamnuri' persimmon has high yielding ability and its fruit weight averages over 300 g. However, the high productivity can result in poor fruit quality and weak tree vigor, causing alternate bearing. The purpose of this study was to determine the effects of different leaf-fruit ratios on the tree growth and chlorophyll fluorescence for suggesting an optimum fruiting level of 'Gamnuri'. Four-year-old young trees were used in this study. The flower buds were thinned to leave 1 to 3 buds per bearing shoot before blooming in May and their leaf-fruit ratios were adjusted to 10(high crop-load), 15, and 20 (low crop-load) by fruit thinning in late June after the end of physiological fruit drop. The main measurements were conducted for collecting the responses of tree growth and chlorophyll fluorescence. The values of Fm / Fo for the plant stress and Fv / Fm for the photosynthetic efficiency decreased as leaf-fruit ratio decreased, the minimum values were found at leaf-fruit ratio 10. This means that excessive fruiting could cause increasing plants stress and reducing photosynthetic efficiency. These results suggested the optimal leaf-fruit ratio should be adjusted to higher than leaf-fruit ratio 10 in relation to healthy tree growth and fruit quality.

P03

The conformational diversity mimicking and statistical analysis enable drug discovery targeting the disorder-to-order transition regions

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Intrinsically disordered proteins (IDP) make up a highly dynamic conformational ensembles of diverse forms. Since the majority of virtual screening has the problem of focusing only on the rigid structures of protein, understanding the structural properties of IDPs and its application as a breakthrough enables unconstrained drug discovery. We segmented the target disorder-to-order transition region into a series of overlapping 20-amino-acid-long peptides and predicted the folded structure that mimics structural heterogeneity. Next, we applied our new molecular docking function that can successfully distinguished known compounds and their corresponding binding regions. In particular, through this method, we verified that Myc proto-oncogene protein inhibitor, 10058-F4, can be specifically distinguished from others of the chemical compound libraries. We also studied whether the differences between the two previously discovered MBD2 inhibitors (ABA and APC) when binding to the target protein could be distinguished through this method. Therefore, our new drug discovery method can efficiently discriminate compounds for expanded virtual screening toward IDPs.

▶ **Keywords:** Disorder-to-order transition, computer-aided drug discovery, protein-protein interaction inhibitor, conformational diversity mimicking, peptide docking

P04

MEL cell-derived allograft mouse model for cancer research

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Murine erythroleukemia (MEL) cells are often employed as a model to dissect mechanisms of erythropoiesis and erythroleukemia *in vitro*. A MEL cell derived allograft model resulting in splenomegaly was established to develop a diagnostic model for isolation/quantification of metastatic cells, anti-cancer drug screening, and evaluation of the tumorigenic or metastatic potentials of molecules *in vivo*. In this animal model, circulating MEL cells from the blood stream were successfully isolated and quantified with an additional *in vitro* cultivation step. In terms of the molecular-pathological analysis, we were able to successfully evaluate the functional discrimination between Mbd2 and p66α from NuRD complex in erythroid differentiation, and tumorigenic potential of allograft model. In addition, we showed that the number of circulating MEL cells in drug-treated mice was dose-dependently decreased. Our data demonstrate that the newly established allograft model is useful to dissect erythroleukemia pathologies and non-invasively provides valuable means for isolation of metastatic cells, screening of anti-cancer drugs, and evaluation of the tumorigenic potentials.

▶ **Keywords:** circulating tumor cells, erythroleukemia, allograft, liquid biopsy, cancer treatment

P05

CP2c protein degradation occurs via SUMOylation-mediated 20S proteasome pathway for cell cycle progression

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CP2c is one of CP2 family transcription factors and relies on interactions with various partner proteins to regulate expression of target genes as a transcriptional activator or repressor. Previously, we identified Small Ubiquitin-like Modifier 1 (SUMO1) as CP2c-interacting proteins by a yeast two-hybrid screening, and here we addressed the question of whether SUMOylation is another way to endow CP2c with regulatory versatility. CP2c directly interacted to SUMO1, E2 enzyme UBE2I, or E3 enzyme PIAS1 *in vitro* and *in vivo*. Interestingly only SUMO1 reduced the protein level and transcriptional activity of CP2c. C-terminal Glycine residue of SUMO1 requires for binding to regions of CP2c (39-134 aa and 306-415 aa). In addition, degradation of SUMOylated CP2c occurs ubiquitin-independently via the 20S proteasomal pathway, and precisely timed degradation of CP2c is required to ensure accurate progression of cell cycle. This study presents the first experimental evidence for SUMO-PSME3-mediated 20S proteasome machinery function to the target protein degradation whereby SUMO-1 directly binds to the target CP2c protein in cell cycle progression.

▶ **Keywords:** Protein degradation, SUMO1, SUMOylation, Transcription factor CP2c, PSME3, 20S proteasome

P06

Structural and molecular insights of the interface important for CP2c complex formation

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CP2c is one of CP2c family transcription factors and relies on interaction with various partmer proteins to regulate expression of target genes. Two kinds of CP2c transcription factor complexes, homotetrameric CP2c complex (tCP2c) and heterohexameric complex (CBP) containing CP2c, CP2b, and PIAS1, binds and regulate for normal and neoplastic gene regulation. However, nature of these complexes for the discrimination of DNA binding sequences or their complex structures were not known in detail. Here, we uncovered differential binding modes of these complexes to specific target DNA and identified the protein-protein interaction interface commonly important for these complexes using various molecular biological, structural and biochemical analyses. Importantly, we found that a peptide consisted of six amino acids (NYPQRP) eliminates DNA binding ability of both CP2c complexes by inhibiting complex formation *in vitro* and *in vivo*. Our study provides more precise features of the two CP2c complexes and may serve as a paradigm for developing a CP2c complex targeting inhibitor for anticancer therapeutics.

▶ **Keywords:** transcription factor CP2c, CP2c complexes, DNA binding modes, protein-protein interaction domain, peptide 5-2, DSP crosslinking, mass spectrometry, erythroid differentiation

P07

MMTR/Dmap1 is involved in the lineage commitment of early embryonic stem cells through crosstalk with the PcG proteins

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Epigenetic modification including histone modification, nucleosome remodelling, chromatin (un)folding, and remodelling is a significant transcriptional regulation mechanism. By these epigenetic modifications, transcription factors and their regulators are recruited to the regulatory region of target genes and regulate expression. The Mat1-mediated transcriptional repressor (MMTR)/DNA methyltransferase 1-associated protein (Dmap1) is a transcription corepressor involved in chromatin remodelling, cell cycle regulation, DNA repair, and tumour suppression. The Tip60-p400 complex proteins, including MMTR/Dmap1, interact with the Myc in embryonic stem cells (ESCs). These proteins interplay with the stem cell-related proteome networks and regulate gene expressions. Here, we show that MMTR/Dmap1, along with other Tip60-p400 complex proteins, bind the promoters of differentiation commitment genes and control their expression during differentiation in mouse ESCs. Furthermore, we propose a novel mechanism of MMTR/Dmap1 control histone mark bivalency and transcriptional poising of commitment genes in early stage lineage commitment of mouse ESCs by crosstalk with the polycomb group proteins.

▶ **Keywords:** MMTR/Dmap1, Tip-p400 complex, polycomb repressive complexes (PRCs), bivalency, embryonic stem cells

P08

Anticancer effects of agents targeting disorder-to-order transition region at MBD2-p66α interaction

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Targeting intrinsically disordered protein regions (IDRs) that are typically involved in promiscuous protein-protein interactions (PPIs) for drug development is a fascinating but challenging task. MBD2-p66α interaction was involved in the disorder-to-order transitions in both regions, critically mediating the integrated epigenetic function of the NuRD complex. We previously screened two chemicals targeting the MBD2-p66α interaction (ABA and APC) using a novel platform. In this study, we demonstrated that ABA evokes a potent anti-leukemia effect. Molecular mechanism behind the efficacy was positive correlation with p66α/MBD2 ratio among leukemia cell lines with respect to interplay between NuRD and CP2c complex. ABA treated mouse erythroleukemia (MEL) cells undergoes apoptosis, cell cycle alteration, and aneuploidy. Through MEL cell allograft model study, we successfully evaluated anti-leukemia efficacy of ABA without side effect. Finally, we revealed that patients with high p66α/MBD2 ratio shows poor prognosis in several cancer types. Thus, we strongly suggest ABA could be a recommendable cure for patients with high p66α/MBD2 ratio.

▶ **Keywords:** Intrinsically disordered protein regions, MBD2, p66α, myeloid leukemia, anticancer effect

P09

A selected peptide inhibiting CP2c specifically induces cancer cell-specific synthetic lethality

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Oncogene CP2c is expressed predominantly in almost all cancers and associated with poor prognosis. We identified inhibitory peptide (ACP52) that interfere with transcriptional complex formation by attaching to the important protein-protein interaction region of CP2c. We also showed that ACP52 linking with a cell penetrating peptide induces synthetic lethality in various cancer cells. Through comprehensive molecular and cellular studies, we elucidate the existence of an unexpected transcription-independent synthetic pathway leading to cancer cell specific G2/M cell cycle arrest and apoptosis. Mechanistically, the liberated CP2c triggers DNA damage responses at the transcription- and replication-coupled regions by inhibiting TDP2. In addition, the liberated CP2c degrades YY1. Both activities rewire global cancer signals regardless of p53 status.

Importantly, ACP52 functions in a wide range of cancers except for the case expressing MDM2 cleaved by CASP2. We confirmed pharmacological synergy between ACP52 and CASP2 inhibitor in these ACP52-resistant cases. In this study, the CP2c deregulation strategy provides an opportunity to develop pan-anticancer drug without adverse effects.

▶ **Keywords:** transcription factor CP2c, pan-anticancer drug ACP52, G2/M cell cycle arrest, apoptosis, YY1/MDM2/p53, TDP2-mediated DNA damage response

P10

Gold nanoparticle-assisted SELEX for rapid discovery of small molecule-binding aptamers

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While DNA aptamers have emerged as an artificial bioreceptor, there is a limitation in monitoring the selection process of aptamer libraries during systematic evolution of ligands by exponential enrichment (SELEX). Herein, we report a gold nanoparticle-assisted SELEX (GNP-SELEX) for the rapid discovery of small hormone-specific ssDNA aptamers. This GNP-SELEX allowed for rapid determination of target-specific aptamer library enrichment with neither target modification nor post-SELEX monitoring process. The visual monitoring was accomplished by salt-induced color change of GNP solution in combination with aptamers and target molecules. With targeting two hormones (brassinolide; BL and bisphenol A; BPA) as a model, we identified ssDNA aptamers with high selectivity and binding affinity. The rational design of selected aptamers by three-dimensional molecular simulation increased their ability to detect BL or BPA in real samples as bioreceptors. We suggest that this self-monitoring SELEX platform will promote the discovery of ssDNA aptamers against diverse small molecules in a rapid and simple way.

P11

Study on the increase of polyphenol content and bacterial growth of lactic acid bacteria using *Asparagus officinalis* extract

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프로바이오틱스는 널리 알려진 바와 같이 설사 질환의 예방과 치료, 전신 감염의 예방, 염증성 장 질환의 관리, 면역 조절, 알레르기 예방 및 치료, 항암효과, 콜레스테롤 혈증 치료, 유당불내증 완화와 같은 건강상의 이점을 가지고 있다. 본 연구는 다양한 종류의 아스파라거스 추출물을 사용하여 항산화 프로바이오틱스의 대량 배양 및 항산화 활성능의 향상을 목적으로 한다. 대량 배양 조건 시험에 대한 연구 결과 아스파라거스 추출 용매에 따른 차이는 있으나 La2, La3, La4, Le1, Le2, Le3, Le4에서 대조군보다 더 많은 증식을 보였다. 또한, 총폴리페놀함량 측정을 통한 항산화 활성 시험의 결과, La1, La3, La4, Le2, Le3에서 폴리페놀함량이 대조군보다 증가하는 것을 확인하였다. 이러한 결과는 추출물 첨가에 의한 프로바이오틱스의 대량 배양 및 항산화 활성뿐만 아니라 다른 생리 활성에도 효과적일 것으로 보인다.

P12

Changes in volatile compounds in Korea chili by cooking methods

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This study presents an analysis that aims to identify volatile compounds of Korea chili by six cooking methods, such as drying, frying, steaming, boiling, roasting, and crushing. A total of 1,332 compounds were detected by GC-TOF/MS, profile of volatile compounds was compared using multivariate Analysis of Principal Components (PCA). A results of PCA unveiled variations in the levels of 2-furanmethanol, oxolan-2-one, furan-2-carbaldehyde and 2-mehoxy-4-vinylphenol between cooking methods. The volatile compounds of control and baking chili showed a different component distribution, and boiling, drying, roasting, and steaming chili showed similar component distribution.

▶ **Keywords:** Korea chili, GC-TOF/MS, Volatiles compounds, Characterization

P13

Analysis of non-volatile compounds in radish by GC-TOF/MS and relation to cooking methods

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This study characterizes the non-volatile compounds profile of radish by cooking methods such as drying, frying, steaming, boiling, roasting, and crushing. Non-volatile compounds were determined by Gas Chromatography Time-of-Flight Mass Spectrometry(GC-TOF/MS). Data showed that a total of 764 compounds were detected and profile of non-volatile compounds was compared using multivariate Analysis of Principal Components (PCA). Our findings in PCA results that L-isoleucine, L-aspartic acid, α-D-glucopyranoside were all detected and L-threonine, D-fructopyranose, D-fructose, D-galactose, butanoic acid were indicated significant difference. The non-volatile compound data revealed that cooking methods was also affected in the radish metabolomics profile.

▶ **Keywords:** Radish, GC/MS, Non-volatiles compounds, Characterization

P14

Elevation of ACE2 as a SARS-CoV-2 entry receptor gene expression in Alzheimer's disease

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Previously, a recent study by Liu and colleagues, published in the Journal of Infection, described the mortality of elderly patients with Covid-19 compared to young and middle-age patients. In addition, the SARS-CoV-2 pandemic that showed high mortality in older adults who have chronic comorbidities such as chronic obstructive pulmonary disease (COPD). Considering the high mortality rate and pandemic status of COVID-19, development of effective therapeutics is an urgent issue that requires the identification of quality pathogen. Genomic characterization recently revealed that angiotensin-converting enzyme 2 (ACE2) is a SARS-CoV-2 binding protein for cell entry, and control of ACE2 is a potential therapeutic target to reduce SARS-CoV-2 transmission. Here, we report on genetic risk factors for transmission of SARSCoV-2 in AD patients using GWAS. Emerging analyses may link these findings to prevention or therapeutics for SARS-CoV2. We found that expression of the Ace2 gene, which codes for a SARSCov-2-binding protein, was increased in AD patient brain. Interestingly, ACE inhibitors have recently been suggested as treatments for NDs. Thus, there needed for studies of genomic expression of Ace2 gene in elderly COVID-19 patients. Our results will allow researchers to decrease the mortality rate and prevent new SARSCoV-2 infections.

P15

Potential therapeutic target of long noncoding RNAs in brain disorders

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Non-coding regions for protein translation on DNA are constantly regarded as genomic junk area historically. Considering 2% of the human genome encodes for proteins, the change of definition for a gene transcript has been demanded. The emerging studies using high-throughput screening such as genome-wide analysis have unveiled the importance of biological function of non-coding region. Recent discoveries have revealed that there are approximately 170,000 long noncoding RNAs (lncRNAs) encoded in mammalian cells. For therapeutic strategy, oligonucleotide therapy using an antisense oligonucleotide (ASO) that is synthesized single strand possibly regulate various mechanisms in consequence by binding to complementary targets such as mRNA, miRNA. The drug potential of ASO against lncRNA in Angelman syndrome (AS) was suggested. Patients with genetic defects in AS present with malfunctioning nervous system features, caused by a maternally inherited defect in *UBE3A*, a gene that encodes for E3 ubiquitin ligase. The roles of lncRNAs is unique in the sense that, after the initial step of transcription which regulates many types of gene expression, subsequent steps mediate several brain diseases therapeutic practices on diseases by targeting RNA Therefore, lncRNA targeted studies would discover new targets for efficient and effective drug development for treatment of various brain diseases.

P16

Probiotic *Lactobacillus reuteri* extends the lifespan of *Drosophila melanogaster* through a mechanism dependent on dSir2 and insulin/IGF-1 signaling

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The term probiotic refers to bacteria that provide a beneficial effect to the host. In particular, lactic acid bacteria, which excrete lactic acid as their main fermentation product, are well-known representative probiotics. *Lactobacillus reuteri* is one such lactic acid bacteria isolated from human breast milk. Although *L. reuteri* has both anti-microbial and anti-inflammatory activities that have occasionally been linked to increased lifespan, there are no reports on the effect of *L. reuteri* on longevity in an animal model. To test this, we used a freeze-dried *L. reuteri* powder manufactured by Wedea Inc. in South Korea. We investigated the anti-aging effects of *L. reuteri* including lifespan and physiology, in *Drosophila melanogaster*. We measured the lifespan of flies supplemented with *L. reuteri* at 0, 50, 100, or 250 μg/mL and found that *L. reuteri* significantly increased the mean lifespan of fruit flies, especially at 100 μg/mL. This longevity effect of *L. reuteri* was not accompanied by reductions in reproductive output, food intake, or locomotor activity, indicating that increased lifespan caused by *L. reuteri* is a direct effect of the bacteria, and not an artefact caused by changes in reproduction, feeding, or locomotor activity. Flies treated long-term with *L. reuteri* showed reduced body weight compared to controls. Interestingly, *L. reuteri* supplementation did not extend the lifespan of flies on low-nutrient diet but did induce the forkhead box-O transcription factor activation, which is one of the important proteins having roles in metabolism, cellular proliferation, stress resistance and probably lifespan, suggesting that *L. reuteri* can be used as a probiotics with anti-aging effects.

▶ **Keywords:** Probiotics, *Lactobacillus reuteri*, *Drosophila melanogaster*, Lifespan, Anti-aging

P17

Extension of *Drosophila* lifespan by Korean red ginseng through a mechanism dependent on dSir2 and insulin/IGF-1 signaling

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Many studies have indicated that Korean red ginseng (KRG) has anti-inflammatory and anti-oxidative effects, thereby inducing many health benefits in humans. Studies into the longevity effects of KRG are limited and have provided contradictory results, and the molecular mechanism of lifespan extension by KRG is not elucidated yet. Herein, the longevity effect of KRG was investigated in *Drosophila melanogaster* by feeding KRG extracts, and the molecular mechanism of lifespan extension was elucidated by using longevity-related mutant flies. KRG extended the lifespan of *Drosophila* when administrated at 10 and 25 μg/mL, and the longevity benefit of KRG was not due to reduced feeding, reproduction, and/or climbing ability in fruit flies, indicating that the longevity benefit of KRG is a direct effect of KRG, not of a secondary artifact. Diet supplementation with KRG increased the lifespan of flies on a full-fed diet but not of those on a restricted diet, and the longevity effect of KRG was diminished by the mutation of *dSir2*, a deacetylase known to mediate the benefits of dietary restriction. Similarly, the longevity effect of KRG was mediated by the reduction of insulin/IGF-1 signaling. In conclusion, KRG extends the lifespan of *Drosophila* through Sir2 and insulin/IGF-1 signaling and has potential as an anti-aging dietary-restriction mimetic and prolongevity supplement.

▶ **Keywords:** Korean Red Ginseng, Lifespan, *Drosophila melanogaster*, Sir2, insulin/IGF-1 signaling

P18

Imaging of astrocyte-to-neuron conversion using aptamers

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Direct conversion of astrocytes into neuronal cells has emerged as a promising treatment for neurodegenerative diseases. However, a reliable method for tracing direct conversion remains challenging. Herein, we present a fluorescence probed trimer of astrocyte-specific aptamer and its use for monitoring astrocyte-to-neuron conversion in the state of living cells. Through 17 rounds of SELEX with primary rat astrocytes as a target and rat neuron cells as a negative counterpart, the most frequent sequence Ast17-30 had selected and improved as a trimer form (denoted Tri-tAst17-30), which has showed increased binding affinity with high target specificity. Significantly, unlike classical immunohistochemical imaging via cell fixation, this aptamer enabled live astrocyte-targeted imaging, which consequently led to the simultaneous monitoring of astrocyte-to-neuron conversion. These findings suggest that this approach will facilitate the study to uncover direct lineage conversion of astrocytes into neuronal cells as well as the application for astrocyte-specific gene/drug delivery.

▶ **Keywords:** Cell-SELEX, Astrocyte-to-Neuron Conversion, Aptamer, live cell staining

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P19

The role of commensal microbes on the longevity effect of dietary restriction

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Dietary restriction (DR) is the most well-known intervention to retard aging and to extend the lifespan in diverse organisms. Recently, commensal bacteria resided in the digestive tracts have been reported to affect the host lifespan and its composition is changed by environmental factors such as diet. However, the relationship of commensal microbes and the longevity effect of DR are not illustrated yet. To test whether the longevity effect of DR is related with commensal microbes, we generated axenic flies and measured the lifespan under the various concentration of yeast, the protein source of flies' diet. We observed that the longevity effect of DR was diminished by the removing of commensal microbes and that insulin/IGF-1 signaling (IIS) is reduced by axenic culture as similar with DR. Interestingly, the decline of lifespan and IIS induced by axenic culture were partially rescued by re-association of *Acetobacter*, indicating that *Acetobacter* have a role in the longevity effect of DR. Our results showing the relationship of commensal microbes and longevity effect of DR will provide fundamental knowledge to understand the underlying mechanisms of lifespan extension by DR.

▶ **Keywords:** Dietary restriction, commensal microbe, longevity, host-microbe interaction, *Drosophila melanogaster*

P20

The role of commensal microbes on the effect of metformin in *Drosophila*

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Metformin has been commonly used in the treatment of type 2 diabetes because it has many beneficial effects such as good safety profile, efficacy, and comparatively reduced cost. Nevertheless, treatment with metformin is often associated with gastrointestinal side-effects and reduced quality of life of patients. Some researches demonstrated that metformin causes the imbalance of intestinal fluid homeostasis. Since it is well known that the alteration of intestinal microbes is related to gastrointestinal dysfunction, we hypothesized that the gastrointestinal side-effects of metformin may be related with the change of commensal microbial flora in the gut. To prove our hypothesis, we used the fruit fly, *Drosophila melanogaster*, which is one of the excellent model organisms in the host-microbe study. Similar to the results in human subjects, the incidence ratio of fly with an intestinal barrier dysfunction was increased under 25 mM of metformin. Since it is known that the fly with intestinal barrier dysfunction has a shorten lifespan, we measured the lifespan of fly fed the metformin and observed that supplementation of metformin decreased the lifespan of flies. To test whether the effect of metformin on the intestinal barrier and lifespan of fly was related with the commensal microbe, we investigated the lifespan of axenic fly and the microbial flora alteration in fly with supplementation of metformin. Interestingly, the reduced lifespan of fly by supplementation of metformin slightly recovered by removal of commensal microbes, indicating that the presence of commensal microbes is involved in the effect of metformin on fly lifespan. Also, supplementation of the 25 mM metformin increased the total microbial load in a fly, especially *Lactobacillus*, one of the main phyla in the fly's gut. In the case of *Acetobacter*, another main phylum in the fly's gut, the number of bacteria was rather decreased by supplementation of 25 mM metformin. To investigate whether that *Lactobacillus* performs a key role in the side-effects of metformin on lifespan, we measured the lifespan of axenic fly inoculated with *Acetobacter* or *Lactobacillus* under the supplementation of metformin. Interestingly, the median lifespan of fly inoculated with *Lactobacillus* showed a similar trend to that of conventionally reared fly, indicating that *Lactobacillus* is related with the side-effects by metformin, but not that of fly inoculated with *Acetobacter*. Our results will provide the fundamental knowledge to address the side-effects of taking metformin.

▶ **Keywords:** metformin, commensal microbe, lifespan, intestinal dysfunction, host-microbe interaction, *Drosophila melanogaster*

P21

Role of commensal microbes in the γ-ray irradiation-induced physiological changes in *Drosophila melanogaster*

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Ionizing radiation induces biological/physiological changes and affects the commensal microbes, but few studies have examined the relationship between the physiological changes induced by irradiation and commensal microbes. This study investigated the role of commensal microbes in the γ-ray irradiation-induced physiological changes in Drosophila melanogaster. The bacterial load was increased in the 5 Gy irradiated flies, but irradiation decreased the number of operational taxonomic units. The mean lifespan of conventional flies showed no significant change by irradiation, whereas that of axenic flies was negatively correlated with the radiation dose. γ-Ray irradiation did not change the number of eggs in conventional flies, but the number was increased in axenic flies. Locomotion of conventional flies was decreased after 5 Gy radiation exposure, whereas no significant change in locomotion activity was detected in axenic flies after irradiation. γ-Ray irradiation increased the generation of reactive oxygen species both in conventional and axenic flies, but the increase was higher in axenic flies. Similarly, the amounts of mitochondria were increased in irradiated axenic flies, but not in conventional flies. These results suggest that axenic flies are more sensitive in their mitochondrial responses to radiation than conventional flies, and increased sensitivity leads to a reduced lifespan and other physiological changes in axenic flies.

▶ **Keywords:** γ-ray irradiation, commensal microbes, lifespan, fecundity, locomotion, mitochondria, reactive oxygen species (ROS), *Drosophila melanogaster*

P22

Metagenomic analysis of the DNA viral communities in fermented food kimchi

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It is currently estimated that the number of viruses outnumber live cells in most environments. However, the studies on environmental viruses have been limited due to difficulties in culturing viruses, lack of a universal marker gene and sparse reference data. Recently, culture and marker gene-independent metagenomic approach enabled researchers to explore the community structure and diversity of viruses in various natural ecosystems. Most of environmental viruses are identified as viruses infecting bacteria which are considered major drivers of bacterial communities. The ecology of virome studies have been studied actively in ocean and human gut, however ecological role and impact of bacteriophages on microbial populations were poorly understood in fermented foods. Because fermented foods that is frequently consumed human diet are a representative environment made by microorganism. We investigated three types of starter and non-starter Kimchi to determine the community structre and diversity of viral communities using the enrichment of virus-like particles and shotgun metagenomics. Most of identified viral families were double-stranded DNA viruses infecting prokaryotes, particularly bacteria (termed bacteriophages). These communities were dominated by bacteriophages belonging to the viral order *Caudovirales* (i.e.,*Herelleviridae*, *Myoviridae*, *Podoviridae*, and *Siphoviridae*). In starter Kimchi the composition of viral families were more diverse and proportion of unclassified was larger than non-starter Kimchi. We believe that our observations contribute to the expansion of microbial diversity for fermented vegetable foods.

P23

전통발효 식품으로부터 분리한 항균활성을 가진 유산균의 바이오필름 특성

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식품의 생산 가공 단계에서 오염된 장비 및 시설은 음식물로의 교차 위험의 원인이 될수 있다. 이를 예방하고자 항균물질을 분비하고, 바이오필름을 형성하는 유산균을 활용하고자 한다. 따라서 식품의 주요 식중독균인 *B. cereus*, *Staphylococcus aureus*, *Salmonella enteritidis*, *Listeria monocytogenes*, *Escherichia coli* O157:H7에 대하여 항균활성이 강한 5종의 유산균(*Leuconostoc lemsenteroides* 1균주, *Leu. lactis* 1균주, *lactobacillus sakei* 2균주, *L. curvatus* 1균주)을 분리하여 이들의 바이오필름 형성능과 환경스트레스에 대한 저항성을 확인하였다. 분리된 5종의 유산균은 스테인리스표면, 25℃에서 높은 바이오필름을 형성하였다. 또한 저온스트레스 평가에서 5℃, 15℃에서 각각 평균 72%, 86%의 높은 생존율을 보여주었다.

P24

발효식품으로부터 박테리오신 유전자를 보유한 바실러스균의 스크리닝 및 동정

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박테리오신은 미생물로부터 생산되는 천연무독성 방부제로 바실러스에서 많이 생산된다. 우리는 전통발효식품(젓갈, 김치, 장아찌, 장류)에서 *Listeria monocytogenes*와 *Bacillus cereus*에 대하여 모두 항균활성을 가진 바실러스균 10균주를 분리하였다. 16S rRNA sequence를 이용한 동정 결과 *Bacillus amyloliquefaciens* 1균주, *Bacillus subtilis* 5균주, *Bacillus tequilensis* 3균주, *Bacillus velezensis* 1균주로 나타났다. 항균력 시험결과를 바탕으로 분리된 10주의 Bacillus 균주들이 알려져 있는 26종류의 bacteriocin 유전자를 보유하고 있는지 탐색하기위해 PCR분석을 하였다. 그 결과 *B. tequilensis* M194-4 균주는 Subtilisin, Subtilosin, Mersacidin, Mycosubtilin, Bacilysin BacD Ericin, Fengycin, Sublancin, Surfactin등 가장 많은 9개의 항균물질 유전자를 보유하고 있었다.

P25

Optimization of fermentation conditions and anti-inflammatory activities of extract from fermentation of onion

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This purpose of this study was to determine the optimization of fermentation conditions and anti-inflammatory activities from onion. The yield, lactic acid bacteria count, contents of quercetin and anti-inflammatory activities of oninon extract (OE) were investigated with water addition ratio, temperatures, and times. The results indicate that the optimum water addition ratio, temperature, and time were water addition level of 2 times, 90°C, and 3 h, respectively. The extraction yield of OE was 6%. The contents of quercetin in OE were increased after fermentation by lactic acid bacteria when analyzed by high performance liquid chromatography. In order to effectively anti-inflammatory agents, we examined the inhibitory effects on the production of lipopolysaccharide (LPS)-induced NO in RAW 264.7 cells. Among the fermentation conditions, OE (2 times water, 90°C, and 3 h) showed the highest NO inhibition effect. Finally, the water addition ratio, temperature and time were selected as water, 90°C and 3 hour, respectively. Consequently, the fermentation conditions for onion were optimized and statistically confirmed.

P26

Odontogenic demineralized dentin matrix powder based bio-ink without compromise between biofunctionality and printability for 3D bioprinted dental constructs

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Currently, there has been a demand for the development of a bio-ink suitable for regenerative dentistry. However, the existing bio-inks have a limitation in that tissue regeneration ability must be sacrificed for excellent printability. Therefore, in this study, a demineralized dentin matrix powder (DDMp) based bioink was developed without compromise between 3D printability and dental regeneration ability. As the concentration of DDMp in cell laden bioinks increases, the bioink showed improved z-axis printability , while high cell viability(>95%) and continuous proliferation(> 7 day). Furthermore, mineralization of DPSC enhanced due to upregulated odontogenic differentiation. Finally, a centimeter scale 3D dental construct for dental regeneration was fabricated utilizing this bioink. These results showed that it is possible to construct a 3D regenerative dental construct with high shape fidelity and regeneration ability for dental regeneration using 3D bioprinting and tooth derivatives.

▶ **Keywords:** dentin derived matrix powder, 3D bioprinting, odontogenic bioink, dental regeneration

P27

Study of amyloid-β-induced fragmentation of lamin A and B

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Amyloid-β (Aβ) is a peptide implicated in Alzheimer's disease. The peptide leads to specific fragmentation of lamin proteins, independently of caspase-6. In the current study, we explored whether Aβ-induced caspase-6 activation can induce the enzyme-dependent lamin fragmentation, because caspase-6 is responsible for the fragmentation process in other damage-induced apoptosis. The formation of lamin A and B fragments in cells was not induced by caspase-6, even though robust activation of caspase-6 was detected in cells treated twice for 2 h and >10 h with A β42. Purified caspase-6, however, could remove the lamin A fragment detected in nuclei isolated from Aβ-treated cells (ANU), whereas it failed to generate the expected fragment of lamin B. Caspase-6-mediated fragmentation of lamin B was achieved in ANU treated with alkaline phosphatase and in nuclei isolated from cells treated with Aβ42 in the presence of a Cdk5 inhibitor. These implies that inhibitory phosphorylation prevented the fragmentation of lamin B in Aβ -treated cells.

P28

Reciprocal roles of SIRT1 and SIRT1-associating protein SAP10 on the regulation of androgen receptor activity

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Androgen receptor (AR) plays a pivotal role in the progression and development of prostate cancer. In previous study, we identified novel SIRT1 associating protein 10 (SAP10). He we found that SAP10 increased the transcriptional activity of androgen receptor (AR), which was repressed by the functional mutants of SAP10 using transcription assay. In addition, SIRT1 inhibited SAP10-mediated AR transcriptional activity. Moreover, both SAP10 inhibitor and SIRT1 activator suppressed cell growth in LNCaP and LNCaP LN3 prostate cancer cells by cell viability assay. These data suggest that reciprocal roles of SIRT1 and SAP10 on the regulation of AR activity, and provides the possibility of prostate cancer treatment. This possibility is currently being investigated.

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P29

TTF-1 action in leptin-induced development of hypothalamic neurons

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The hypothalamus is a brain region necessary for many instinctive behaviors and physiological functions that require complex neural circuits primarily formed during the postnatal period. Various factors influence hypothalamic development and play roles in formation of neural circuits. Among them, leptin functions as a key signal that promotes axon outgrowth from the arcuate nucleus during a discrete developmental period. Leptin deficient *ob/ob* mice show phenotypic abnormalites of neural circuit formation. However, the underlying detailed mechanisms are unknown. Thyroid transcription factor-1 (TTF-1), also known as NKX2.1, is critical for morphogenesis of the hypothalamus and is involved in the leptin-regulated energy homeostasis in the rodent hypothalamus. In this study, we investigated whether TTF-1 is involved in the leptin-induced neural development of hypothalamus. First, we found that TTF-1 expression was highly increased during postnatal day 0-15. To study in detail, we generated mice (ObRb-TTF-1 KO) lacking TTF-1 expression selectively in cells expressing leptin receptors (ObRb). ObRb-TTF-1 KO mice showed increases in ObRb- immunopositive cells and agouti-related peptide nerve terminals in the paraventricular nucleus (PVN), but decreased number of alpha-melanocyte -stimulating hormone terminals in PVN. The expression levels of Sonic hedge hog and SIX3, which are well known genes related to neural development, were changed through the regulation of TTF-1 expression. These results suggest that hypothalamic TTF-1 is important in the leptin-induced neuronal development in the hypothalamus.

P30

Morphological change of hypothalamic microglia by energy state

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The hypothalamus regulates energy homeostasis by receiving and integrating many peripheral signals and neuronal inputs. Recently, many studies have reported role of glial cells in feeding and energy balance. However, detailed function of microglia in the hypothalamic control of energy metabolism is largely unknown. Here, we show that morphological change of microglia in the hypothalamus is associated with change of body energy state. We first identified change in microglial morphology in the hypothalamus after 24 h fasting. Interestingly, immunohistochemical analysis showed that microglial cell number, dendrite length, branch points and terminal points were decreased in the hypothalamic arcuate nucleus by fasting compared to normally fed mice. However, these changes were recovered by 4 h refeeding. These results suggest that change in microglial morphology according to body energy state reflects action of microglia on the regulation of energy homeostasis probably through interacting with neurons in the hypothalamus.

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Enzyme-accelerated fluorescence signal enhancement for targeted cancer cell imaging

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Imaging cancer cells is essential for cancer diagnosis. However, limited sensitivity in fluorescence imaging by bioprobe at the low-abundance target is one of the remaining task to resolve. Here we report ligand-assisted enzyme-accelerated signal enhancement (LA-EASE) imaging of cancer cells using aptamers or peptides via polydopamine (PDA) deposition. It is achieved by sequential reaction between target, biotinylated ligand, neutravidin conjugated HRP followed by fast PDA accumulation and amino quantum dot (QD) combined to PDA. We assessed the enhanced imaging using aptamer and peptide that has affinity to membrane proteins of PC-3 and MCF-7 cells respectively. As a result, LA-EASE method exhibited approximately 100-fold improved sensitivity than traditional fluorescent imaging using dye-labeled bioprobes. we expect that this approach can be universal imaging platform with high sensitivity.

P32

Materials development and production using silkworms

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Bombyx mori is traditionally an economically important lepidopteran insect for silk production. Biotechnology for producing substances in silkworms, there are transgenesis, virus expression system, and gene scissors. We have developed a transgenic technique and conducted research for producing fluorescent silk and various substances. In addition, research is being conducted to produce animal medicine materials and functional proteins in silkworm using insect viruses. We are conducting research to apply the gene scissors technology, which has recently been in the spotlight, to silkworms. It is thought that the use of gene scissors technology can induce a variety of mutations compared to traditional breeding, as well as freedom from the regulation of LMO, which is pointed out in the transgenesis. As a result, a variety of genetic engineering techniques are used to use silkworms.

P33

Cloning and characterization of maize (*Zea mays*) nitrilase to study its defensive roles

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Auxin is involved in not only plant growth regulation, but also defense responses. One of the auxin biosynthetic enzymes nitrilase (EC 3.5.5.1) have dual functions in auxin biosynthesis and defense against nitrile toxicity. Up to date the function of nitrilase have been studied mainly in terms of auxin biosynthesis, and the study on its defensive roles in plants is scarce. However, detoxification by nitrilase and its induction by diverse stress stimulation have been documented. To further study the function of nitrilase in plants, we are currently carrying out the cloning of the maize nitrilase. We will briefly present the current status of our work and discuss about more possibilities to explore the defensive roles of maize nitirilases.

** Student participants (D.G., J.L., M.L., M.C.) in this work were supported by the 2020 University Innovation Support Project to Dankook University.

P34

SIRT1 associating protein SAP8 represses RA-induced neuronal differentiation in P19 cells

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SIRT1 is an NAD-dependent deacetylase that involved in cell survival, metabolism, senescence and differentiation. In previous study, we identified novel SIRT1 associating protein 8 (SAP8). Here we found that SAP8 interacts with histone H2B by immunoprecipitation (IP). In addition, the intrinsic transcriptional repression activity of SAP8 was revealed by luciferase reporter assay. For further analysis of SAP8 function, we generated a P19 stable cell with SAP8 knock down. The depletion of SAP8 suppressed RA-induced neuronal differentiation of P19 cells. These data suggest that SAP8 regulates RA-induced neuronal differentiation of P19 cells by transcriptional repression and that H2B may be involved. This possibility is currently being investigated.

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P35

Stress-induced NEDDylation promotes cytosolic protein aggregation through HDAC6 in a p62-dependent manner

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Stress-coupled NEDDylation potentially regulates the aggregation of nuclear proteins, which could protect the nuclear ubiquitin-proteasome system from proteotoxic stress. However, it remains unclear how NEDDylation controls protein-aggregation responses to diverse stress conditions. Here, we identified HDAC6 as a direct NEDD8-binding partner that regulates the formation of aggresome-like bodies (ALBs) containing NEDDylated cytosolic protein aggregates during ubiquitin stress. HDAC6 colocalizes with stress-induced ALBs, and HDAC6 inhibition suppresses ALBs formation, but not stress-induced NEDDylation, suggesting that HDAC6 could carry NEDDylated-proteins to generate ALBs. Then, we monitored the ALBs-associated proteostasis network and found that p62 directly controls ALBs formation as an acceptor of NEDDylated cytosolic aggregates. Interestingly, we also observed that ALBs are highly condensed in cells treated with chloroquine, inhibits autophagic flux, indicating ALBs rely on autophagy pathway. Collectively, our data suggest that NEDD8, HDAC6, and p62, involve in the management of proteotoxic stress by forming cytosolic ALBs coupled to aggresome-autophagy flux.

P36

Anti-oxidant, digestive enzyme inhibitory, and anti-inflammatory effect of fermented oak *Lentinus edodes* extracts

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This study samples fermented extracts developed using oak *L. edodes* mushrooms and four kinds of vegetable lactobacillus (*Pediococcus pentosaceus, Lactobacillus plantarum, Lactobacillus acidophilus, Lactobacillus fermentum*), and carries out various physiological activities assay and analysis to evaluate the efficacy of fermentants and to develop fermented food materials. We investigated the anti-oxidant and anti-inflammatory effects of fermented oak *L. edodes* extracts by DPPH and hydroxyl radical scavenging activity assay, polyphenol and flavonoid content analysis, α-amylase, α-glucosidase, lipase assays, MTT assay, NO assay, ELISA. The extract reduced the radical levels and has 45.8-76.2 mg/g of polyphenols, and 0.07-0.14 mg/g of flavonoids. The extract treatment decreased digestive enzymatic activities including α-amylase, α-glucosidase, and lipase by 11-44 %. The extract also inhibited the secretion of inflammatory cytokines, such as IL-1β, TNF-α, PGE2, IL-4. These results show that fermented oak *L. edodes* extract may have beneficial effects for nutrient absorption control and improvement of immune function.

▶ **Keywords:** Oak *Lentinus edodes*, Anti-oxidant, Digestive enzyme inhibitory, Anti-inflammatory

** This research was supported by “Development of export strategic vegetable table sauces using fermented oak mushroom product for Southeast Asian (2020)” from Korea Forest Service (Korea Forestry Promotion Institute), Republic of Korea.

P37

The iron binding capacity and anti-inflammatory effect of the mixed extract derived from plant sources

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We investigated iron content from plant-derived extracts and developed new iron materials using iron, which is an inorganic material of natural materials, and studied iron-related functionality of this material. This study samples the mixed extract derived from plant sources using two plant sources extracts, and performed several assays related total iron binding capacity and inflammation. We investigated the anti-oxidant, iron binding capacity, and anti-inflammatory effects of the mixed extract derived from plant sources by Fe^{2+}-chelating activity assay, total iron binding capacity assay, MTT, and NO assays. The mixed extract inhibited Fe^{2+}-ferrozine complex response, and total iron binding capacity. The mixed extract suppressed the level of NO. These results reveal that the mixed extract derived from plant sources may have has the potential to serve as a functional food related to iron metabolism and inflammation.

▶ **Keywords:** Plant sources, Iron binding capacity, Anti-inflammatory, Anti-oxidant

** This research was supported by Ministry of SMEs and Startups (MSS), Republic of Korea (2020).

P38

USP39, a new poly (ADP-ribose)-binding deubiquitinase, drives non-homologous end-joining repair by liquid demixing

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Reciprocal crosstalk between poly(ADP-ribose) (PAR), produced by PAR polymerase 1 (PARP1), and DNA repair machinery has came to light as a key regulatory mechanism of the DNA damage response (DDR). However, there is yet no firm evidence of how PAR precisely controls the DDR. To elucidate this relationship, we identified six deubiquitinating enzymes (Dubs) associated with PAR-coupled DDR. Among the six Dubs, the functional role of USP39, an inactive Dub involved with the spliceosome assembly, was characterized. USP39 rapidly localizes to DNA lesions in a PAR-dependent fashion where it regulates non-homologous end-joining (NHEJ) via its tripartite RG motif located in the N-terminus comprising 46 amino acids (N46). It is already reported that proteins containing RG motif are crucial for liquid demixing, which is contribute to modulation of the DDR. In addition to, we found that USP39 acts as a molecular trigger for liquid demixing in a PAR-coupled N46-dependent manner. Also, USP39 directly interacts with the XRCC4/LIG4 complex during NHEJ via its ZF domain. In parallel, USP39-mediated spliceosome complex controls homologous recombination (HR) repair in a PAR-independent fashion. These findings provide mechanistic insights into how PAR-chains exactly control DNA repair processes in the DDR.

P39

Acid류의 체강 주입에 따른 누에 혈림프 항산화능 증강 효과 구명

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체내에 흡수된 산소 중 대부분은 에너지 대사를 통해 이용된 후 배출되지만 소량의 산소는 불완전환원으로 전자를 흡수하고 활성산소가 되어 노화의 주요 요인으로 간주되고 있다. 이에 활성산소를 제거하는 항산화 관련 연구가 관심을 받고 있다. 이 연구에서는 누에에 신기능성을 부가하기 위하여, 항산화능을 증강 시킬 수 있는 물질 Acid류에서 선발하고, 이를 주사접종을 통한 체강 주입 후 누에 사멸률을 측정 하였다. 누에 혈림프에서 DPPH assay를 통해 항산화효과를 측정한 결과, Caffeic acid가 가장 높은 항산화능 증강효과를 갖는 것을 확인하였고, 적정농고 구명결과, 1000ppm/PBS(mL)에서 가장 높은 항산화능 증강 효과 있다는 것을 확인하였다. 또한 시간에 따른 누에의 항산화능 증강 효과를 검증한 결과 6시간에서 무처리 대비 약 1.5배가 증가하는 것을 확인 할 수 있었다. 이러한 결과를 통해 누에 혈림프에서 항산화능을 증가 시킬 수 있으며 이를 이용하여 새로운 건강기능효과를 부여 할 수 있을 것으로 사료 된다.

P40

Improved alcohol dehydrogenase production in transgenic *Escherichia coli* expressing heat shock protein

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Escherichia coli (*E. coli*) is the most favorable host to produce a variety of recombinant proteins, and genome engineering can further improve its productivity. In this study, transgenic cell lines were developed by inserting carrot heat shock protein 70 gene (*Daucus carota* L. Hsp70) into *E. coli*. *DcHsp70* gene was attached to the Lipoprotein (*Lpp*) promoter and FRT (Flippase recombination target) cassette by overlap PCR. The resulting Lpp promoter - *DcHsp70* - FRT construct was inserted into the *yddE (*pseudogene*)* site in the *E. coli* genome by lambda Red-mediated homologous recombination. Under stress conditions (high temperature, high pH, and sodium acetate treatment), the transgenic cell lines showed higher growth rates than the control cell line. For the recombinant protein expression, the *alcohol dehydrogenase* (ADH) gene from *Geobacillus stearothermophilus* in the 6His-tagged pET11a expression vector was inserted into the transgenic *E. coli*. Recombinant 6His-ADH was expressed by isopropyl β-D-1-thiogalactopyranoside treatment, and the amount of recombinant protein expressed in the transformed cell line was 11 times higher than that of the control cell line. Our results showed that heterologous expression of DcHsp70 can increase growth rates and recombinant protein production in *E. coli*.

P41

Insulin production in transformed *E. coli* expressing plant heat shock protein

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Insulin is an important hormone that regulate metabolism. In this study, we developed a transgenic *Escherichia coli* through genome engineering to produce recombinant human insulin. Transgenic *E. coli* was developed by inserting carrot heat shock protein 70 into the *yddE* (pseudogene) site of the *E. coli* genome. Then, proinsulin, A chain and B chain portions of insulin were inserted into the PVFT2S expression vector containing the 6His tag and GST tag. Recombinant insulin was induced by isopropyl β-D-1-thiogalactopyranoside treatment, and the 6xHis-GST tagged insulin was purified using Ni-affinity chromatography. In this study, transgenic *E. coli* expressing DcHsp70 showed higher cell viability and growth rate than wild type and control cell lines. In addition, insulin A and B chains are expressed higher in transgenic *E. coli* expressing DcHsp70 than in the control cell line. Therefore, the plant heat shock protein 70 inserted into *E. coli* helps to improve the production of recombinant proteins and cell survive. Therefore, molecular chaperones such as heat shock proteins can be usefully used in the field of biotechnology to produce recombinant proteins.

P42

Antioxidant and anti-inflammatory activities of water extract of *Filipendula glaberrima* Nakai

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Filipendula glaberrima Nakai is perennial specialty plant that grows deep in the mountains in Korea. In this study, we measured antioxidant and anti-inflammatory activities using of water extract of *Filipendula glaberrima* Nakai. The ABTS, DPPH, total polyphenol and FRAP were measured to investigate of antioxidant activities. The ABTS and DPPH assays are methods of measuring free radical elimination activity. Total phenol content is a method measuring the amount of polyphenol. FRAP is a method based on the fact that antioxidants have a reducing force (Fe^{3+}toFe^{2+}). To investigate of anti-inflammatory activity, lipopolysaccharide (LPS) was used in RAW 264.7 macrophage cells to induce inflammation. Then, nitric oxide (NO) and IL-6 were measured. As a result, the extract showed antioxidant activity in a dose-dependent manner, in all experiments. Also, the extract significantly inhibited inflammatory mediators (NO, IL-6). In conclusion, the water extract of *Filipendula glaberrima* Nakai has antioxidant and anti-inflammatory activities and can be used as a substance of functional foods.

▶ **Keywords:** *Filipendula glaberrima* Nakai, antioxidant, anti-inflammation

P43

Antioxidant properties of ethanol extract of *Centella asiatica*

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Centella asiatica is a perennial plant commonly found in the mountains and fields in Korea. In this experiment, we measured antioxidant capacity of *C. asiatica*. The 70% ethanol extract of *C. asiatica* was prepared, and four assays were performed. The ABTS assay and DPPH assay are methods of measuring free radical scavenging ability. Also, total polyphenol content was measured, because polyphenol acts as an antioxidant in the human body. Finally, the FRAP assay was performed. FRAP assay is a method of measuring the ability to reduce Fe^{3+} to Fe^{2+}, because most antioxidants have reducing power. As a result, in all experiments, antioxidant efficacy was shown in a concentration-dependent manner. In conclusion, the ethanol extract of *C. asiatica* has antioxidant power and further research is needed to identify of active substances.

▶ **Keywords:** *Centella asiatica*, ABTS, DPPH, Polyphenol, FRAP

P44

The mechanisms of oncolytic immunotherapy and novel cancer therapeutic approach

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Oncolytic virus (OV) is a novel therapeutic agent against several types of cancer including aggressive and/or recurrent cancer. Cancer hallmarks provide a beneficial environment to OVs to easily and specifically infect tumor cells. The infection of OV induces oncolysis of the tumor cells and stimulates host anti-viral immune response and it allows to re-burst anti-tumor immune response in the tumor microenvironment. OV, as an immunotherapeutic agent, can be used with general cancer chemotherapeutics, immune checkpoint inhibitors to enhance efficacy in cancer treatment. Also, such engineered OVs role as viral vectors to deliver desired genetic materials to the tumor cells can assist immunotherapy as well. In this review, we will introduce the mechanisms of oncolytic immunotherapy and novel therapeutic approaches against cancer. This review will provide novel insights into therapeutic agents and cancer therapy.

P45

β-Cyclodextrin inhibits monocytic adhesion to endothelial cells through nitric oxide-mediated depletion of cell adhesion molecules

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Cyclodextrins (CDs) are used as drug delivery agents. In this study, we examined whether CDs have an inflammatory effect on endothelial cells. First, we found that β-CD promoted cell proliferation in bovine aortic endothelial cells and elevated nitric oxide (NO) production through dephosphorylation of threonine-495 (T-495) in endothelial nitric oxide synthetase (eNOS). Dephosphorylation of T-495 is known to activate eNOS. Phosphorylation of T-495 was found to be catalyzed by protein kinase Cε(PKCε). We then found that β-CD inhibits binding of PKCε to diacylglycerol (DAG) via formation of a β-CD-DAG complex, indicating that β-CD inactivates PKCε. Furthermore, β-CD controls activation of PKCε by reducing the recruitment of PKCε into the plasma membrane. Finally, β-CD inhibits expression of intercellular and vascular cell adhesion molecule-1 by increasing NO via control of PKCε/eNOS and suppression of THP-1 cell adhesion to endothelial cells. These findings imply that β-CD plays an important role in anti-inflammatory processes.

P46

Lysyl-tRNA synthetase is secreted through enhanced autophagy and calcium in endothelial cells

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Lysyl-tRNA synthetase (KRS), one of the aminoacyl-tRNA synthetases, was recently determined to be secreted as a pro-inflammatory agent. In cancer cell, KRS is known to be secreted through the exosome. However, it is not known how KRS is secreted in the vascular endothelial cells. In this study, we found that KRS is highly expressed in the vessels exposed to oscillatory shear stress, a pro-atherogenic factor. In contrast, KRS expression appeared to be down-regulated in the vessels exposed to laminar shear stress (LSS), an anti-atherogenic factor. Then, we investigated whether and how KRS is secreted in the KRS-overexpressed endothelial cells. Interestingly, serum starvation, calcium ionphore and autophagy inducers enhance KRS secretion. These data indicate that autophagy is associated with KRS secretion in endothelial cells. Moreover, extracellular KRS is shown to suppress various LSS-stimulated signaling pathways, including ERK, Akt, and eNOS, suggesting that KRS has pro-atherogenic activity. In comparison, extracellular KRS induces cell proliferation in vascular smooth muscle cells. Together, we suggest that KRS secreted via autophagy acts as an atherogenic autocrine/paracrine.

P47

Transcriptomic analysis of the pathogenesis of Parkinson's disease by FAF1 in A53T mouse model

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To define details of molecular networks associated with pathogenesis of Parkinson's disease (PD) by FAF1, FAF1 was ectopically expressed in the substantia nigra pars compacta (SNpc) of in a PD mouse model, A53T at 2, 4, 6, and 8 months after birth. The SNpc expressing FAF1 for 2 weeks was isolated for purification of total RNAs. Total RNAs were subjected to next generation sequencing, which was analyzed by bioinformatic tools for genes regulated along the PD pathogenesis. Among the significantly up- and down-regulated DEGs. DEG13 containing Kelch and F-box associated domains at the central was selected. As an initial attempt to investigate its function, spatiotemporal expressions of zebrafish *DEG13* were examined, indicating that *DEG13* transcripts at bud stage and are found predominantly in the floor plate of the neural tube. Overexpression of *DEG13* enhanced expression of *dkk1b* at 10 hpf as well as *shha*, a marker of the dopaminergic progenitors in the hypothalamus at 16.5 hpf. To examine the consequences of *DEG13* knockdown in developing DA neurons, spatiotemporal expression patterns of the markers of immature and mature DA neurons were visualized using WISH analysis. Transcript levels of DA neuron markers were reduced in the ventral diencephalic region as well as in the neural crest of the midbrain at 18 hpf. These results suggest that *DEG13* contributes to the neurogenesis of DA neurons in zebrafish embryos.

▶ **Keywords:** Parkinson's disease (PD), Fas-associated factor 1 (FAF1), SNpc (Substantia nigra pars compacta), NGS (Next Generation Sequencing), Dopaminergic (DA) neurons

P48

Generation of alveolar macrophages from human induced pluripotent stem cells

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Alveolar macrophages (AMϕs), tissue-resident macrophages in the alveoli, play critical a role in the innate immune response against viruses, pathogenic microbes, inhaled toxic chemicals, and particular matters. Using human AMϕs for pulmonary toxicity test is huddled due to limited sources of AMϕs. Recent studies have reported that AMϕs are originated from yolk-sac or fetal liver and not from circulating bone marrow derived-monocytes. Here, we differentiated human iPS cells into AMϕ-like cells using a unique differentiation strategy. hiPSC-derived AMϕs showed macrophage-like morphology and expressed AMϕ-specific surface markers (CD206, CD68, CD11c, TREM2, HLA-DPQR, CD163, CD45, CD14, and CD169). In addition, hiPSC-derived AMϕs have M1/M2 polarizing activity and phagocytotic activity against E-coli, indicating that hiPSC-derived AMϕs are mature and functional. Altogether, these data suggest that hiPS-derived AMϕs could be a useful source for infectious disease modeling, inflammation research, developmental biology, and pulmonary toxicity test.

▶ **Keywords:** Macrophage, human pluripotency stem cell

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P49

Establishment of ES cell-derived lung organoids for human 3D lung fibrosis model *in vitro*

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특발성 폐 섬유증 (IPF)은 예후가 좋지 않은 만성 질환으로써 다양한 원인으로 상피 세포 기능 장애가 특징이며 적절한 치료법이 없다. 최근 자가조직화가 가능한 장기유사체인 줄기 세포 유래 3D 오가노이드가 보고되고 있으며 필요성 또한 증가하고 있다. 본 연구에서 in vitro. 인간 3D 폐 섬유증 모델을 확립하기 위해 매트리젤 내 배양 방법을 사용하여 인간 배아 줄기세포 (hESC) 유래 폐 오가노이드 (hLOs)를 생성하였다. hLOs는 폐아 또는 폐포낭과 같은 형태를 관찰하였고, 폐 특이적 마커를 발현하고 폐 표면활성제 단백질을 분비하는 라미널체를 생성하였다. 또한 hLO는 IPF를 유발하는 것으로 알려진 블레오마이신으로 처리되어 SMA-α, vimentin, Collagen, IL-1β, MMP7과 ICAM-1 같은 상피-간엽 전이 (EMT) 관련 유전자의 발현을 현저히 증가시켰다. 결과적으로 hLO에 대한 블레오마이신 처리가 섬유화증의 특징 중 하나인 EMT 현상을 모방한다는 것을 보여준다. 따라서 hLO는 IPF에 대한 약물 스크리닝을 위한 시험관 내 3D 인간 폐 섬유증 모델을 구축하는 데 유용한 모델이 될 수 있음을 시사한다.

P50

Development of a tetracycline regulatable conditional mouse model of Parkinson's disease expressing parkin substrate, ZNF746

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Development of a revealing animal model of Parkinson's disease (PD) is imperative to understanding of PD pathogenesis and also to the evaluation of potential PD treatments. However, previously reported PD genetic models including parkin null mice are largely not sufficient for studying PD mainly due to the lack of substantial loss of dopaminergic neurons. Parkin interacting substrate, ZNF746 also known as PARIS, is a transcriptional repressor that regulates the expression of peroxisome proliferator-activated receptor gamma, coactivator 1a (PGC-1a), a master coregulator of mitochondria biogenesis and antioxidant defense. To study *in vivo* roles of ZNF746 accumulation and develop revealing mouse model of PD, we constructed chronic PD mouse models that can express PARIS under pharmacological control of tetracycline regulatable promoter (TetP-PARIS responder mice). This model was designed to express PARIS only in dopamine neuron using the dopamine neuron specific promoters. As a chronic model of PARIS expression, TetP-PARIS mice were mated with dopaminergic neuron specific driver mice, and PARIS expression was induced for 2 months starting at 3 weeks of age. With 2 month expression of PARIS in dopamine neurons, TH-positive neurons progressively degenerated in the substantia nigra, and the loss of dopaminergic nerve terminal in the striatum was evident. Consistent with nigrostriatal dopaminergic degeneration, this conditional PARIS transgenic mice displayed behavioral motor abnormalities at about 3 months of age. Interestingly, behavior deficits of this mouse model were rescued with levodopa/carbidopa treatment. Moreover, nilotinib treatment showed a protective effect on both dopaminergic neuron loss and behavior abnormalities. Studies using this PARIS expressing chronic mouse model are expected to provide a better understanding of the pathogenesis of PD and could be used to develop potential therapeutic agents.

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P51

Poly (ADP-ribose)-dependent Ubiquitination of Heterochromatin protein 1 alpha (HP1α) by RNF4 E3 ligase suggests a functional role for homologous recombination repair

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The DNA repair pathway underlying DNA damage response (DDR) is the most imperative process involving diverse cellular repair machinery. DNA repair machinery is tightly regulated by various types of Post-translational modifications (PTMs), including phosphorylation, methylation, SUMOylation, ubiquitination and PolyADP-ribosylation (PARylation). Among these, functional crosstalk between Poly(ADP-ribose)(pADPr), metabolite of Poly(ADP-ribose) polymerase 1 (PARP1) activated by DNA damage, and ubiquitination to control DDR remains unclear. Thus, to determine that the functional roles of ubiquitin E3 ligases coupled Poly(ADP-ribose) signaling on DDR and characterize the DNA repair mechanism controlled by pADPr molecule, we screened for pADPr-coupled substrates of RNF4 move to DNA lesions using 17K protein microarray and *in vivo* assay systems such as BioID, micro-irradiation . We identified 2 pADPr-dependent substrates of RNF4, connected to DDR. Here, HP1α is ubiquitinated by RNF4 and localized to DNA lesions in a presence of RNF4. We also found that HP1α is move to DNA lesions in a pADPr-dependent manner. Next, to investigate the sites of ubiquitination of HP1α by RNF4, we used mass spectrometry and we found that lysine 91, lysine 102 of HP1α was ubiquitinated by RNF4. Interestingly, HP1α K91.102 ubiquitination is critical for DNA binding. And Ubiquitination of HP1α is important for DNA repair via homologous recombination (HR). These data suggest that crosstalk with ubi- and PARylation is important for HP1α localization and HR repair pathway.

P52

trim46 is associated with the zebrafish neurogenesis via Foxa2

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As an initial attempt to study biological functions of Trim46 in vertebrate embryogenesis, spatiotemporal expression patterns of *trim46* were examined in zebrafish embryos. *trim46* was expressed both maternally and zygotically, and the transcripts were localized in the eyes and throughout the brain region, predominantly in the midbrain-hindbrain boundary (MHB) and hindbrain at 24 hpf. Bioinformatic studies found that the promoter regions of *trim46* contain *cis*-acting elements binding to Foxa2. Cyclopamine, an inhibitor of SHH, a transcriptional regulator of *foxa2*, was treated to zebrafish embryos at 4 hpf through 24 hpf to repress the transcription of *foxa2*. It caused not only the severe defects of midbrain patterning but also significant reduction in the transcripts level of *foxa2*, *trim46*, and *shha* at 24 hpf. It is thus conceivable that Trim46 contributes to development of midbrain and MHB in response to Shh signaling via Foxa2.

P53

CNS-specific expression pattern of *rnf126* in zebrafish embryos

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An E3 ligase containing RING finger, RNF126 interacts with PDK1, p21 and Ku80 in the ubiquitin proteasome system. RNF126 with Bag6 promotes anoikis resistance in cancer cells by targeting PDK1 for ubiquitin-mediated degradation. RNF126 degrades mislocalized proteins and plays critical role in DNA repair mechanism. Various molecular functions of RNF126 have been reported while its biological functions remain to be investigated in vertebrate embryogenesis. We analyzed spatiotemporal distribution of *rnf126* transcripts in zebrafish embryogenesis. Whole mount in situ hybridization using *rnf126* specific probe found *rnf126* transcripts in 1 cell and sphere stage as well as the zygotic transcripts in the primordium of brain region at bud stage. *rnf126* transcripts became restricted to the telencephalon, midbrain, and hindbrain at 18 hpf and further to the telencephalon, optic tectum, MHB, cerebellum, and rhombomere at 24 hpf. Current studies on molecular network governing expression of *rnf126* is to provide developmental mechanism underlying how Rnf126 contributes to zebrafish embryogenesis.

▶ **Keywords:** *rnf126*, ubiquitin proteasome system, optic tectum, cerebellum, rhombomere

P54

Fine-tuning UDSMProt model for anti-CRISPR prediction

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UDSMProt is a universal deep sequence model pretrained on unlabeled proteins of Swiss-Prot, and can be fine-tuned for a specific prediction tasks in various fields. Here, I suggest the use of UDSMProt model for predicting anti-CRISPR protein from the amino acid sequence. Anti-CRISPR embraces a group of proteins that inhibit CRISPR-Cas system of the prokaryotic immune system. Recently, anti-CRISPR has emerged as a natural inhibitor of CRISPR-Cas system, which enables the post-translational regulation of CRISPR-Cas systems for various applications. Although experimental techniques for the discovery of anti-CRISPR have been developed, computational prediction can provide cost-effective screening strategy. However, the lack of labeled anti-CRISPR data and their low sequence similarity render the algorithm development challenging. In this study, I build an anti-CRISPR protein predictor by fine-tuning the pretrained model for anti-CRISPR data set. The performance is evaluated for an independent data set by using various metrics, in comparison with conventional predictors. While the conventional predictors use additional feature computations and pre-filtering steps, the present approach just requires protein sequence.

P55

Hemogenic endothelium from aorta gonad mesonephros in murine at embryonic 10.5 days and completion of the definitive hematopoiesis

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Background & Aim: In the pluripotent stem cells, the development of hematopoietic cells from mesoderm divides into 2 steps including primitive hematopoiesis which is defined by hemangioblast and definitive hematopoiesis defining by hemogenic endothelium (HE). HE is a specialized subset of endothelial cells which can differentiate into blood lineage cells in fetal embryo. Emerging data continuously suggest that HE plays an important role in generating blood lineage cells by regulation of pivotal transcription factor, but characterization with cell activity for single HE still remains unclear. In the present study, we explored that isolated HE from aorta gonad mesonephros can proliferate and further culture to generate blood lineage cells including megakaryocytes, erythrocytes, and leukocytes with functional phenotype. Next, we investigated the cell activity and the frequency of lineage cells with surface markers in differentiated blood cells. Methods: To this end, ICR mice were sacrificed at embryonic day 10.5 and their AGM were purely isolated, then individually cultured till 21 days post seeding at 96 well. To examine cell growth kinetics over long-term expansion, cumulative cell number and population doubling were tested from HE cell. H&E staining and FACS were performed to detect surface markers for HE and blood lineage cells. Results & Conclusion: HE cell was rapidly increased by optimized culture condition and was expanded with absolute speed for proliferation in erythropoiesis (population doublings, RBC, > 130-folds, leukocyte, 21-folds, Megakaryocyte, 3-folds) Immunocytochemistry data showed that pan endothelial cell marker, CD31 and CD34 were highly expressed in HE cells. Definitive hematopoiesis containing megakaryocyte and lymphocyte easily occurs within 20 days via functional HE (CD45, 89.5 ± 2.4, CD4, 11.9 ± 2.3, CD8, 8.3 ± 2.6, NK, 17.9 ± 4.8). These data suggest that fetal HE successfully generate definitive blood lineage cells. Based on this study, we

will next establish plan for media optimization to differentiate hematopoietic cells from pluripotent stem cells via definitive HE after confirmation for their functional acquirement in vivo and vitro assay.

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P56

Development of a tetracycline regulatable conditional mouse model of Parkinson's disease expressing amyloid-like protein aggregate

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Development of a revealing animal model of Parkinson's disease (PD) is imperative to understanding of PD pathogenesis and also to the evaluation of potential PD treatments. However, previously reported PD genetic models are largely not sufficient for studying PD pathogenesis mainly due to the lack of substantial and progressive loss of dopaminergic neurons and Lewy like inclusion formation. To study *in vivo* roles of amyloid like aggregate accumulation and develop revealing mouse model of PD with protein aggregation and dopaminergic neurodegeneration, we constructed acute or chronic PD mouse models that can express amyloid-like artificial b sheet conformation aggregate under pharmacological control of tetracycline regulatable promoter (*TetP-amyloid mimic*). These models were designed to express amyloid like inclusion in dopamine neurons using the dopamine neuron specific promoters. When the recombinant adenoassociated virus expressing tTA under the control of mini tyrosine hydroxylase promoter was stereotaxically injected into the substantia nigra of *TetP-amyloid mimic* mice, TH-positive neuron number was decreased and protein aggregation was observed in the substantia nigra. As a chronic model of amyloid mimic inclusion expression, *TetP-amyloid mimic* mice were mated with dopaminergic neuron specific driver mice, and amyloid mimic inclusion expression was induced for 1 months starting at 3 weeks of age. With 1-month expression of amyloid mimic aggregates in dopamine neurons, TH-positive neurons progressively degenerated in the substantia nigra, and the loss of dopaminergic nerve terminal in the striatum was evident. Consistent with nigrostriatal dopaminergic degeneration, this transgenic mice displayed behavioral motor abnormalities at about 2 months of age. These novel acute and chronic mouse models of PD are expected to provide useful tools in understanding the pathogenesis of PD and development of potential therapeutic agents targeting aberrant protein aggregation and dopaminergic neuron loss.

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P57

The roles of LRRK2 in excitotoxicity-and oxygen and glucose deprivation-induced neuronal toxicity

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Parkinson`s disease (PD) is the most common movement disorders in the elderly population, accompanied with cardinal neuropathological features, such as progressive loss of dopaminergic neuron in substantia nigra pars compacta and the presence of proteineous inclusion bodies, known as Lewy bodies. Although the etiology of PD is not clear yet, genetic variants in multiple gens are considered as risk factors in PD initiation and progression. Mutations in leucine rich-repeat kinase 2 (LRRK2) is the most commonly found in both familial and sporadic PD. LRRK2 is a large size protein and contains multiple domains, such as GTPase and kinase functional domains and various protein-protein interaction domains. Currently, the variation of its kinase activity in various pathogenic mutations is suggested as pathogenic mechanisms in PD. However, familial PD cases are relative rare, less than 10% of all PD cases and the disease penetrance is incomplete and various in LRRK2 associated PD. Therefore, it has been suggested that combination of genetic and environmental factors modulates the occurrence and progression of diseases. Therefore, here, we investigated whether environmental factor (excitotoxicity and oxygen-glucose deprivation (OGD)) has effect on the LRRK2-linked brain pathologies, such as neuronal cell toxicity. So, in depth, we observed that excitotoxicity and OGD induced the significant increase of LRRK2 expression, and then LRRK2 expression and its activity are associated with neuronal cell toxicity by excitotoxicity and OGD.

P58

Epigenetic Analysis of a CMT2D Family with phenotypic heterogeneity

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Charcot-Marie-Tooth disease type 2 (CMT2) is a type of CMT with genetic defects that disrupt the structure and function of the axons of the peripheral nerves. Although known as a clinically and genetically heterogeneous inherited neuropathy, studies on the mechanism of clinical heterogeneity remain undefined. We found a family of CMT2 types identified as *GARS* mutations (c.1007C>A, p.P336H) with phenotypic heterogeneity. This study tried to analyze the cause of phenotypic heterogeneity from an epigenetic perspective by performing DNA methylation analysis on CpG islands (GC%> 50%) of the *GARS* promoter. The methylation patten of each patient was analyzed by bisulfite-sequencing PCR for a CpG islands of the *GARS* promoter ranging from -386 to +264 relative to TSS (NM_001316772.1). As a result, a CpG site was relatively more methylated in a patient with mild symptoms. The surrounding sequence containing this site was predicted to bind transcription factor SP1. It was reported that SP1 is a zinc finger transcription factor that binds to GC-rich motifs of many promoters and can be an activator or a repressor of specific genes. This study suggests that methylation of the *GARS* promoter is likely to affect the clinical heterogeneity of the CMT2 family by inhibiting gene expression, but further research is needed.

P59

Determining parental origin of *de novo* mutation in Korean CMT patiens

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Charcot-Marie-Tooth disease (CMT) is a group of peripheral neuropathies that are genetically and clinically heterogeneous. In a previous study of *de novo* CMT1A in Koreans, we reported that the incidence of the pathogenic *de novo* mutation is gender-specific because the occurrence of *de novo* mutations is more often of paternal origin and is related to the father age. In addition, the possibility that *de novo* patients had relatively mild symptoms was suggested. Therefore, in this study, we tried to determine the *de novo* rate and analyze the gender specificity pattern in other types Korean CMT patients. As a result of analysis of 433 CMT patients, the *de novo* ratio was determined to be 38.9% (n=56). We analyzed the type of *de novo* mutation in 56 patients. Among the types of DNA mutations, transition mutations were most common in 41 cases (73.2%), and missense mutations in in amino acids mutations were most common in 49 cases (87.5%). *De novo* mutation, in particularly, occurred most frequently as a C>T mutation in the CpG sequence. As a result of the analysis on the parental origin of the mutation revealed more frequent paternal origins, as in previous studies on CMT1A. Although father age and clinical severity have not been analyzed in this study, *de novo* rate and possibility of gender-specific mechanisms of Korean. This study may be helpful by understanding and treating patients of sporadic CMT patients.

P60

A Nonaka myopathy patient with compound heterozygous variants of *GNE*

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Nonaka myopathy, also called GNE myopathy, is an autosomal recessive hereditary neuromuscular disease, characterized by distal muscle weakness, atrophy and sparing the quadriceps muscle. Recently, compound heterozygous variants in *GNE* were reported in a Taiwanese with GNE myopathy mimicking distal Hereditary Motor Neuropathy (dHMN). We report a Korean myopathy patient with symptoms similar the previously reported GNE myopathy patient. The patient's muscle magnetic resonance imaging (MRI) revealed abnormalities in proximal muscle weakness as well as distal muscle, and the result of nerve conduction studies did not show low motor nerve conduction velocities (MNCVs). To identify the causative variants in the patient, we performed whole exome sequencing in proband. We screened the variants in myopathy-associated genes. As a result, the compound heterozygous variants, c.86T>C (p.M29T) and c.1714G>C (p.V572L), in the *GNE* and a heterozygous variant, c.3269T>G (p.V1090G) in the *SYNE1* were identified. In the *GNE*, the p.V572L has already been reported as pathogenic and the p.M29T has been reported in GNE myopathy patients of Korean. Mutations in *SYNE1* have been reported to cause Emery-Dreifuss muscular dystrophy 4 (EDMD4), proximal myopathy. This study suggests that the compound heterozygous variants in *GNE* could cause Nonaka myopathy phenotype.

P61

CITESDB: A centralized portal for accessing detailed information on endangered species of wild fauna and flora

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CITESDB, developed by Korea Research Institute of Bioscience and Biotechnology (KRIBB), is a centralized portal for accessing key information on CITES species. CITES (the Convention on International Trade in Endangered Species of Wild Fauna and Flora) is an international agreement between governments to protect endangered species of wild fauna and flora. Widespread information nowadays about the endangered status of many prominent species should make the need for collecting and integrating their related information. Therefore, CITESDB contains detailed information on all species that are listed in the appendices of CITES, as well as other species included in the main species information resources, such as GBIF, NCBI taxonomy, and Korean taxonomic list. CITESDB allows users to search for the detailed information about species by querying scientific names, common names, or Korean names. Moreover, CITESDB provides statistics about species-related information and CITES trade data, and open API for accessing and exchanging the detailed information of CITES species through the internet.

P62

Effects of *Allium senescens* L. extract on sorafenib resistant HepG2 cells

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Allium senescens L. known as a perennial aromatic herb is distributed in northern Europe and Asia, especially Ulleung island in south Korea. *Allium* species have been used for food and medicine for thousands of years. Although *Allium senescens L.* is effective to blood refreshing, modulation of cholesterol levels in blood, activation of detoxification in liver, there is no research for cancer drug resistance in hepatocarcinoma. An amount of p-Coumaric acid in the extract was evaluated using UV-HPLC. Unlike protein of relevant evolutionary and lymphoid interest (PRELI) plays as various roles including suppression of apoptosis, activation of differentiation and protection for desiccation in cells, this research documented for PRELI associated with drug resistance. Efficiency of the extract for PRELI, drug transporters, autophagy and mitochondrial apoptosis were evaluated using qPCR. Consequently, the extract attenuates drug resistance of HepG2 cells through down regulation of PRELI, key protein associated with modulation of expression for the drug transporters, activation of autophagy and mitochondrial apoptosis. *Allium senescens L.* extract is a useful material to protect drug resistance and to sustain efficacy of sorafenib against liver cancer.

P63

A subset of EGFR mutation serves as key biomarkers for EGFR-targeted therapy in colorectal adenocarcinoma

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Targeting aberrant EGFR mutants is currently used as an effective clinical strategy in treating various cancer types including lung cancer. Recently, we reported that eleven colon cancer patient-derived EGFR mutants (G63R, E114K, R165Q, R222C, S492R, P596L, K708R, E709K, G719S, G724S and L858R) are oncogenic and sensitive to anti-EGFR monocloncal antibodies, cetuximab and pantitumumab in vitro and in vivo. Notably, these results suggest that a subset of EGFR mutants may also contribute to colonic tumorigenesis, providing the rationale of patient selection for EGFR-targeted therapy. In present study, we further explored the clinical relevance of our finding using colon organoid model. To this end, we introduced cDNA of previously characterized eleven EGFR mutants to colon-derived organoid by lentiviral infection and examined whether these EGFR mutants are able to transform the organoids. We found that while the growth of control normal organoid was strictly dependent on all eight essential niche factors, the organoids harboring EGFR mutants were able to grow in the presence of minimal niche factors such as Noggin, Gastrin, n-Acetylcysteine, nicotinamide and B27. These results are consistent with our previous findings and further demonstrate that a subset of EGFR mutant function as key oncogenic drivers for development of colon cancer. We propose that these EGFR mutations serve as crucial biomarkers for EGFR-directed therapy in treatment of colon cancer.

P64

Formation of amyloid β oligomeric forms enhanced or reduced its cytotoxicity

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Amyloid β (Aβ) is a main pathogen of Alzheimer's disease. In the current study we explored the underlying mechanisms that facilitate reducing and enhancing effects of exogenous proteins on cytotoxicity of Aβ. An *Escherichia coli* chaperonin DnaK was chosen as a tool, because it is easily available and functionally stable. The chaperonin reduced or enhanced Ab cytotoxicity depending on its concentration: cytotoxicity was enhanced when the molar ratio of DnaK to Aβ42 at 20 mM Aβ42 was 0.01-0.5, while reduced cytotoxicity was observed at higher ratios (>1) at 1 mM Aβ42. The amounts of oligomeric Aβ42 species accumulated concomitantly increased with enhanced cytotoxicity, whereas the oligomers appeared to form complexes with DnaK in conditions of reduced cytotoxicity. Thus, we suggest that the difference in cytotoxicity was due to variations in the toxic oligomeric Aβ species. DnaK is a useful tool for the study of the Ab ultrastructure formation and toxicity of Aβ peptide.

P65

Effect of Th2 differentiation control through formation of skin lipid barrier on *Coptidis Rhizoma*, *Glycyrrhiza uralensis* and and fermameted *Glycine max* extract

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This study is conducted to evaluate Th2 skewed condition control through skin lipid barrier formation from the treatment using *Coptidis Rhizoma, Glycyrrhiza uralensis* and fermameted *Glycine max* extract. The 6-week-old Balb/c mice were divided into 4 groups: Control group (Ctrl), lipid barrier eliminate treatment group (LBE), *Coptidis Rhizoma*, *Glycyrrhiza uralensis* and fermameted *Glycine max* extract feeding treatment after lipid barrier elimination group (3HbT), dexamethasone feeding treatment after lipid barrier elimination group (DEXT). After 3 days, differences in skin condition, improvement of skin lipid barrier, and control of Th2 skewed condition of each group were observed. Pathologic skin damage and tissue changes were less in the 3HrT than in the LBE and DEXT, and Transepidermal water loss (TEWL) and pH were also significantly decreased ($p < 0.05$). The filaggrin intensity and positive response also increased significantly in the 3HrT ($p < 0.05$). Kallikrein-related peptidase (KLK) 7, Protease activated receptor (PAR)-2, Thymic stromal lymphopoietin (TSLP), Interleukin (IL)-4, and the products of the Th2 differentiation process also showed a significant decrease compared to the LBE and DEXT (all $p < 0.05$). The *Coptidis Rhizoma, Glycyrrhiza uralensis* and fermameted *Glycine max* extract causes skin barrier recovery and function recovery through the formation of skin lipid barrier. This leads to the conclusion that *Coptidis Rhizoma, Glycyrrhiza uralensis* and fermameted *Glycine max* extract can control Th2 differentiation through the formation of skin lipid barrier.

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P66

Mitogen-Inducing factor 6 (Mig6) functions as a tumor suppressor by modulating EGFR signaling cascade

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The epidermal growth factor receptor (EGFR), a member of ErBb family, plays a crucial role in the activation of a plethora of key cellular signaling programs leading to proliferation, differentiation and survival. Consequently, its aberrant activation is closely associated with cancer pathogenesis. Different classes of genomic alterations involving EGFR identified in cancer, including lung adenocarcinoma and glioblastoma (GBM), have been shown to be responsible for altered EGFR regulation and cellular transformation. Mitogen-inducible gene 6 (Mig6), also known as RALT, is a negative feedback inhibitor of EGFR and other ErbB family members. Recently, our group has reported a novel molecular mechanism of phosphorylation-mediated feedback inhibitory role of Mig6 against EGFR activation. In addition, we showed high frequency of hemizygous focal deletion of Mig6 in *EGFR*-amplified glioma patient samples. In this study, we further investigated the biochemical and functional roles of Mig6 using GBM cell models and found that levels of Mig6 expression is closely associated with oncogenic potential in these cell lines. We also sought to explore the functional significance of Mig6 genomic alterations in tumorigenesis and found that a subset of patient-derived mutant Mig6 is not able to bind to EGFR and failed to inhibit EGFR activation. Furthermore, we showed that Mig6 effectively suppress various mutant EGFR including C-terminal deletion irrespective of autophosphorylation and asymmetric dimerization. Taken together, our results suggest that decreased activity of Mig6 may induce the aberrant activation of EGFR signaling, leading to cancer development and thus a subset of genomic alteration of Mig6 can be used as a crucial biomarker for EGFR-targeted therapy.

P67

Investigating the effects of altering gravity on PVD neuron dendrite development in *C. elegans* : From hypergravity to space microgravity

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Space flight has shown that altering gravity can affect many biological processes including muscle and bone development. However, gravity's effect on neuronal development is not clear. Previously, we showed that hypergravity affects axonal development of motor neurons. Here, we will investigate the effects of altering gravity on neuron dendrite development by observing the PVD neuron in *C.elegans* in different gravity conditions. The PVD sensory neuron develops post-embryonically, and by adulthood displays intricately organized and non-overlapping dendrites spanning the entire body length. To investigate whether PVD development is normal in altered gravity, we exposed *C. elegans* to hypergravity in a centrifuge. We identified hypergravity-induced abnormal structures are increased in whole PVD neuron. Next time we will expose *C.elegans* to simulated microgravity on a clinostat, and real microgravity aboard the International Space Station. We have conducted a space flight experiment at Kennedy Space Center in Dec 2018. Now we are planning to prepare next space flight launching in 2022.

P68

FMRF-like peptide regulates a *C. elegans* putative maternal behavior in 3D

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To investigate the biology of *C. elegans* in 3D, we designed a cultivation habitat which we term NGT-3D and NGB-3D. Growth, brood size, and lifespan in NGT-3D are comparable with a 2D standard plate. Interestingly, wild-type worms show dwelling and egg-laying behaviors in a stereotypical pattern in NGB-3D that is not observed in regular plates: the mother worms spread the bacteria, remain near the border of the bacteria and move away from the bacteria to lay their eggs. We found that an FMRF-like peptide FLP-17 and its cognate receptor EGL-6 both play a role in this egg-laying behavior. Although loss-of-function mutants of *egl-6* and *flp-17* show generally normal locomotion behavior, unlike wild-type, they do not move away from the bacteria to lay their eggs. When *flp-17* mutant mothers are cultivated in NGT-3D, we find that they have lower reproductive fitness compared to wild-type. We are investigating the relationship between fitness and FLP-17-mediated maternal behavior and investigating which environmental cue influences worms to do these behaviors.

P69

Alternaria alternata 진균에 의한 느릅나무 신병해 잎반점병(leaf spot disease) 및 약제 선별 보고

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느릅나무는 전 세계적으로 약 30~40종이 보고되어 있으며, 그 중 24종이 아시아에서 보고되었다. 한국에 널리 보급되어있는 느릅나무는 껍질, 잎, 뿌리 등이 약재로써 그 가치를 높이 평가받고 있다. 느릅나무 유묘를 재배하는 과정에서 잎에 반점이 생기는 증상을 발견하고 원인균을 분리하여 형태적, 분자생물학적 동정을 수행한 결과 진균인 *Alternaria alternata* 로 확인되었다. 코흐의 가설에 따라 이균을 느릅나무 잎에 접종한 결과 반점을 형성하였다. 형성된 병반으로부터 접종균을 다시 분리 확인함으로서 *A. alternata* 에 의한 병해임을 확인하였다. 국내외적으로 느릅나무(*Ulmus Ulmus davidiana* var. *japonica* L.) 에 *A. alternata* 에 의한 잎반병이 보고된 사실이 없는바 신병해로서 느릅나무 잎반병으로 제안하고자 한다. 이 병의 화학적 방제를 위해 4종의 살균제를 PDA 배지에 첨가 후 균사 생장 억제를 조사한 결과 플루아지남 수화제, 메트코나졸 액상수화제, 테부코나졸 첨가 배지에서 생장이 억제되었다. 느릅나무 유묘를 대상으로 포장시험을 수행한 결과 이들 3개 약제 모두 기주에 약해를 나타내지 않았으며 83% 이상의 방제효율을 보였다.

P70

Newly recorded sea star *Henricia oculata* (Asteroidea: Spinulosida: Echinasteridae), in the East Sea, Korea

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Henricia specimens were collected using fishing nets from the East Sea of Korea. The specimens were identified as *Henricia oculata* Pennant, 1777, belonging to the family Echinasteridae of the order *Spinulosida*. This species can be distinguished from other *Henricia* species by broad arms (R/r = 4-4.1), rough skin, thick arm base, three to nine minute, delicate abactinal spines, and inferomarginal plates reniform in shape. This species superficially resembles *H. pachyderma* in its body size and wide papular areas, but differs mainly by the number of papulae and abactinal spines, and the shape and arrangement of inferomarginal plates. In comparison with other *Henricia* species bearing broad arms, our morphological analysis showed that it differed from *H. perforata* in the shape of abactinal spines (*H. oculata*: conical; *H. perforata*: slender), the shape of inferomarginal plates (*H. oculata*: reniform; *H. perforata*: transversely elongated), and the arrangement of the series of inferomarginal plates (*H. oculata*: compact; *H. perforata*: loose). To date, two genera of Echinasteridae, *Aleutihenricia* and *Henricia*, with a total of 13 species, have been reported in Korea. The morphological characteristics of *H. oculata* are described, and photographs are provided.

P71

New record of the unstalked crinoid *Tropiometra macrodiscus* (Crinoidea: Comatulida: Tropiometridae) from Korea Strait

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Two crinoid specimens of genus *Tropiometra* were collected from Busan and Tongyeong by SCUBA diving on August 2010 and January 2011, respectively. These specimens were identified as *Tropiometra macrodiscus* (Hara, 1895), which belongs to the family Tropiometridae of superfamily Tropiometroidea. The genus *Tropiometra* A.H. Clark, 1907 comprised four species worldwide at present and has been not reported in Korean fauna. *T. macrodiscus* was first described by Hara, 1895 in Japan. This species can be difficult to be distinguished from *T. afra* (Hartlaub, 1890), and these two species had confusion in examination of their phylogenetic position in early stage of crinoid classification. However, it can be distinguished from *T. afra* species by having more longish stouter arms, magnificantly many cirri (XLII-XLIII), and numerous segments (32-42). We classified based on the morphological characteristics of *T. macrodiscus* and the DNA barcode, 658 bp of COI.

P72

Influence of simulated microgravity in the intestinal immunity of the Nematode *Caenorhabditis elegans*

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Astronauts during and after long-term space gravity exposure are known to have experienced altered metabolic functions and weaker immunity. However, little is known on how the body senses microgravity and how it affects immunity. In this study, we utilized *Enterobacter* labeled with td-Tomato fluorescence to investigate intestinal infection of the nematode *Caenorhabditis elegans*, under simulated microgravity. *Enterobacter* normally does not infect the intestine of *C. elegans;* however in immunocompromised *dbl-1* mutants, robust infection occurs. Our preliminary results showed that simulated microgravity induces *Enterobacter* gut colonization in *C. elegans* similar to immunocompromised mutant animals. Our study would like to investigate on how microgravity influence immune signaling pathways. Moreover, we will be sending *C. elegans* aboard the International Space Station (ISS) to verify these effects under real space gravity.

▶ **Keywords:** *C. elegans*, *Enterobacter*, Microgravity, Immunity

P73

Biodiversity of the agriculture ecosystems of Goesan-gun district in South Korea

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Agricultural ecosystem biodiversity monitoring and community variation analysis of insects were conducted from April 2020 to September 2020 in selected conventional and organic farming fields in Goesan-gun district, Chungcheongbuk-do, South Korea. A total number of 615 species in 14 orders and 140 families were identified. The numbers of species collected in the locations practicing organic farming were greater than the conventional farming both in the paddy fields (306 vs. 218 species) and the upland fields (228 vs. 171 species). Among them, Hemiptera had the most number of species, followed by Diptera, Coleoptera, Hymenoptera and Araneae. We calculated various index values of biodiversity (diversity index H', richness index R, evenness index J', dominance index D, and similarity index QS) based on quantitative measurements of species and individuals collected over three years of field monitoring. Variations in biodiversity index values in different agricultural systems show that the positive effect of organic farming is to produce more biodiversity than conventional farming systems. When compared to other index results reported in Korea, Japan and China, the richness index was higher and other index values were at similar levels.

▶ **Keywords:** agriculture, biodiversity, ecosystem, Goesan, insect

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P74

Comparative biodiversity between organic and conventional agricultural ecosystems of Korea

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This research demonstrates the effect of organic agriculture on biodiversity compared to conventional agriculture to determine whether organic farming benefits biodiversity. We conducted comparative analysis of insects and spiders in organic and conventional farming areas in Goesan-gun province, Chungcheongbuk-do, South Korea for 4 crop years from 2016 to 2020. We demonstrates the effect of organic agriculture on biodiversity compared to conventional agriculture to determine whether organic farming benefits biodiversity. Our bio-monitoring of both agricultural systems in selected paddy field and upland fields shows that organic agriculture supports greater biodiversity than conventional agriculture. A total number of 1,452 species in 223 families and 17 orders were identified during the monitoring period. Among them, Hemiptera had the most number of species, followed by Diptera, Hymenoptera, Coleoptera and Araneae. The number of species collected in the location practicing organic farming was higher than conventional farming in both paddy fields (761 vs. 481 species) and upland fields (631 vs. 476 species). According to the Margelef's species richness index, organic paddy field had highest RI. The highest dominance index was calculated in organic upland field, but evenness index indicates there is not domination process going on. Overall, organic fields seemed to have greater biodiversity than conventional fields.

▶ **Keywords:** biodiversity, invertebrate, agriculture, ecosystem

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P75

Structural characteristics of the sponge scaffold from dragline silks in the golden orb-web spider, *Nephila clavata*

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In recent years, various types of silk scaffolds for tissue engineering have been produced, such as sponges for cartilage, fibers for ligaments, and tubes for blood vessels. Since silk can easily produce biopolymers, silk-based scaffolds have been molded into various forms and structures suitable for the treatment of various tissue reconstruction and regeneration. In addition, silk fibroin is an universal protein biomaterial that can be used to form membranes, fibers, microspheres and porous scaffolds for various biomedical applications. The purpose of this research is to study silk scaffolds that can stimulate cartilage tissue differentiation for tissue engineering. We made a sponge-like silk scaffold with dragine silk, mainly made from the major ampullat glands of the golden orb-web spider *Nephila clavata*. Using histological tissue preparation technology and field emission scanning electron microscopy (FESEM), the fine structure characteristics of the sponge scaffold of dragline silks were observed. The average pore size of each sponge scaffold gradually decreases with the concentration of silk material. However, the sponge scaffolds extracted from the high-concentration silk solution showed increased rigidity expression and better microstructure morphology. Here, we discuss the results obtained from our research to determine the correlation between the concentration of the silk solution and the pore size of the sponge-like silk scaffold.

▶ **Keywords:** fine structure, silk, scaffold, spider, dragline, *Nephila clavata*

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P76

Microstructure of sponge scaffolds from eggsac silks in the golden orb-web spider, *Nephila clavata*

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The high mechanical properties and biodegradability of spider silk are well known. Due to its characteristics, spider silk scaffolds are considered to be important biological materials for repairing tissue damage in bone and cartilage components. We obtained various sponge-like silk scaffolds with different pore diameters by drying the eggsac silk fibroin solution. The silk fibroin solution used to make the silk scaffold is mainly extracted from the tubuliform glands of the golden orb-web spider *Nephila clavata*. In order to understand the structure and biomechanics of cartilage scaffolds, the microstructural properties of silk-based tubular structures were studied using histological tissue preparation and field emission scanning electron microscopy (FESEM). Our current study shows that in eggcase silk, the pore size reage of the sponge scaffolds was produced by controlling the concentration of the silk solution. In addition, the pore sizes of the scaffolds decreased as the concentration of eggcase protein increased. Considering the remarkable mechano-chemical properties of spider silk, the results obtained from our research could provide a new silk-based biomaterials for the engineering of tissue regeneration, particularly to repair tissue damage to bone or cartilage components.

▶ **Keywords:** microstructure, silk, sponge, scaffold, spider, eggsac, *Nephila clavata*

** **Acknowledgement:** This research was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIT) (No. 2019R1I1A3A01062105).

P77

Size selective fabrication of silk sphere scaffolds from the major ampullate silk glands in the golden orb web spider, *Nephila clavata*

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Spider silk is an alternative biomaterial resource since of mechanical and biological properties, so silk-based scaffolds have been used extensively in modern tissue engineering. Recently, silk-based microspheres provide new possibilities for drug delivery and other applications due to their biocompatibility and biodegradability. This research was initiated to produce silk scaffold with a size of microsphere suitabe for controllable drug delivery through control of content in silk materials. The silk microspheres are fabricated by HFIP on oil method, which is able to assemble spheres very high speed, distinct from the traditional method. Dragline silk, known to be secreted from major ampullate gland, and found to have mechanical properties through previous studies, was used to make silk solution by directly extracting the gland. In our present research, a final volume of 2.5 ml spider silk solution was prepared from 14 major ampullate glands, and silk spheres were produced with ranges of 2 to 60 μm by mixing 1:1 with HFIP. To establish the silk solution concentration and HFIP mixing ratio for selectively obtaining the most optimal and intended sized spheres, various concentrations of silk-HFIP solution were examined. Also fine structural analyses were performed including electron microscopical visualization.

▶ **Keywords:** microstructure, spider, silk, scaffold, microsphere, ampullate gland, *Nephila clavata*

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P78

Morphological analysis of orb-web decoration (stabilimentum) of the garden spider, *Argiope bruennichi*

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Most orb-weaving spiders in the genus *Argiope* insert silky ribbon-like structures on their web, whose ornaments are called 'stabilimentum'. The function of this web decoration is still unknown, but it has been proposed that stabilimenta could provide either attraction for prey insects or protection to the spider by extending the outline of the web to visible against predator animals. Stabilimentum in *Argiope bruennichi* is basically a zig-zag lines of silk structure that produced from the aciniform silk glands. But they are known to make disk form of decorations while juvenile. These decorative silks are constructed entirely from the silks of both posterior median spinneret (PMS) and posterior lateral spinnerets (PLS). It is known that the number of nozzles increases as the individual grows. Depending on the stage of growth, various forms of decoration are found. In addition, it was confirmed that there is a relationship between the location where decorative silk is installed on the web and the location where the spider hides. Based on our recent observations that spiders are hiding on the opposite side of where they are more likely to become prey, we could conclude that decorations can function as a concealment rather than attracting prey.

▶ **Keywords:** microstructure, silk, spider, stabilimentum, *Argiope bruennichi*

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P79

Microstructures of tubular scaffolds from various silk glands of the golden orb-web spider, *Nephila clavata*

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Currently, research to mimic natural organisms is being conducted in the medical engineering fields. According to many studies currently reported, various scaffolds are made of fibrin solutions extracted from silkworm cocoons. Therefore spider's silk is biodegradable, less toxic to the human body, and has more strong mechanical properties than silkworm's cocoon. In recent years, various types of silk scaffolds have been produced for tissue engineering, such as sponges for cartilage, fibers for ligaments, and tubes for blood vessels. Among them, tubular scaffolds are suitable for cardiovacular tissue engineering, as they are considered as potential candidate scaffolds for artificial blood vessels. In this study, we fabricated a variety of tubular silk scaffolds by a dip coating method using a silk solution in the golden orb-web spider, *Nephila clavata*. The silk solution for tubular scaffold were fabricated extracted from major ampullate glands and tubuliform glands. To understand the architecture and biomechanics of scaffolds for vascular applications, the microstructural properties of silk-based tubular structures were investigated using histologic tissue preparation and field emission scanning electron microscopy (FESEM) visualization.

▶ **Keywords:** fine structure, spider, silk gland, tubular scaffold, *Nephila clavata*

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P80

Visualizing a type of brain cells with a small fluorescent molecule

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The brain controls the physiological responses of our body and can store some information as a memory. Through the accumulation of knowledge of the brain cells, it becomes clear that the orchestration of brain cells between neurons and glia is essential for the functions of the brain. Visualizing live brain cells often require multiple types of transgenic animals labeled with fluorescence proteins, causing a challenge to apply most laboratories due to the cost and the complexity of techniques. VizBrCells lab has opened to develop a simple, rapid, and reliable methods to visualize a type of brain cells mainly using fluorescent small molecules. Through the power of diversity of brain cell types and biomolecules, we've screened promising candidates for further developing an unsung fluorescent chemical as an innovative tool for tracking live cells in the brain.

P81

Self-assembled hyaluronic acid nanoparticles protect against osteoarthritic development by targeting CD44

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Although osteoarthritis (OA) is the most prevalent degenerative joint disease, there is no effective disease-modifying therapy. Here, an empty self-assembled hyaluronic acid nanoparticle (HA-NP) is evaluated as a potential therapeutic agent for OA treatment. In mouse primary articular chondrocytes, HA-NPs block the receptor-mediated cellular uptake of low-molecular-weight HA, and the cellular uptake of HA-NPs increases by ectopic expression of CD44, using an adenoviral delivery system (Ad-*CD44*). In addition to its long-term colloidal stability, HA-NP shows *in vitro* resistance to digestion with hyaluronidase and *in vivo* long-term retention ability in knee joint, compared with high-molecular-weight HAs. CD44 expression increases in the damaged articular cartilage of human patients and mice with OA. Ad-*CD44* infection and IL-1β treatment induces *in vitro* phenotypes of OA by enhancing catabolic factor expression in primary articular chondrocytes, and HA-NP attenuates these effects by inhibiting NF-κB activation. Accordingly, both *CD44* deficiency and intra-articular injection of HA-NP protect joint cartilage against OA development in the OA mouse model. Collectively, our results identify an empty HA-NP as a potential therapeutic agent targeting CD44 for OA treatment, and the CD44-NF-κB-catabolic gene axis as an underlying mechanism of destructive cartilage disorders.

P82

Expression and bioinformatic analyses of MicroRNAs in hamster lung infected by SARS-CoV-2

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COVID-19 caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is infectious disease with multiple severe symptoms. In our research, miRNAs binding to the sequence of SARS coronavirus (SARS-CoV), MERS coronavirus (MERS-CoV), SARS-CoV-2 were identified by bioinformatic tools. Five miRNAs (hsa-miR-15a-5p, hsa- hsa-miR-15b-5p, hsa-miR-195-5p, hsa-miR-16-5p and hsa-miR-196-1-3p) commonly bind to the SARS-CoV, MERS-CoV and SARS-CoV-2. We also identified miRNAs binding to receptor proteins such as ACE2, ADAM17 and TMPRSS2 which are important for understanding of infection mechanism by SARS-CoV-2. The expression patterns of those miRNAs were examined in hamster lung samples infected by SARS-CoV-2. Five miRNAs (hsa-miR-15b-5p, hsa-miR-195-5p, hsa-miR-221-3p, hsa-miR-140-3p, hsa-miR-422a) showed different expression pattern in lung tissues of before and after infection. Especially, hsa-miR-15b-5p and hsa-miR-195-5p showed a large difference in expression, indicating that they could be the diagnostic biomarker for the SARS-CoV-2 infection.

P83

Expression and Bioinformatic Analyses of miR-887-3p in *Pan troglodytes*

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Transposable element (TE), which jumps around another region of genome, can be alternative enhancer, promotor and generate some microRNAs (miRNAs). MicroRNA is short single strand RNA (ssRNA) that is about 22 nucleotides in length. The miRNA binds to 3' untranslated and regulates the expression of target messenger RNA (mRNA). The miRNA also plays a crucial role in several biological processes at the post transcriptional level. MicroRNA-887-3p is derived from long interspersed element (LINE), which is group of non-long terminal repeat retrotransposons and account for approximately 21% of human genome. The expression patterns of miR-887-3p is analyzed in various tissue samples of chimpanzee (*Pan troglodytes*) that has considerable genetic similarities with human. MicroRNA-887-3p is highly expressed in spleen of chimpanzee. Additionally, bioinformatic analyses about miR-887-3p are also conducted by using several bioinformatic tools. For the additional study, target gene of miR-887-3p will be selected and its expression patterns in chimpanzee will be analyzed. The present study provides the better understanding about molecular biological function of miRNAs in primates.

P84

Molecular characterization of MicroRNA-21-5p and MicroRNA-221-3p in *FOXP2*

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Chimpanzee is known as *Pan troglodytes* which is included in great ape and it is one of closest living relatives of human. MicroRNAs (miRNA) are small non-coding RNAs, which play an important role in biological processes at the post-transcriptional level. By targeting mRNAs for degradation or translational suppression, miRNA is one of significant regulator for gene expression in eukaryotic organisms. Especially miR-21-5p and miR-221-3p are known to be expressed strongly in oligodendrocytes. These miRNAs were highly expressed in small intestine of chimpanzee. One of the common target gene of miR-21-5p and miR-221-3p, Forkhead box protein P2 (*FOXP2*) is well known as key regulator required for proper development of speech and language. According to several studies, *FOXP2* has connection with chemo-treatment of colon cancer. *FOXP2* is highly expressed in colon, inversely showed low expression in small intestine of chimpanzee. As a result, it is probable that miR-21-5p and miR-221-3p binds to 3' untranslated region (UTR) of *FOXP2* and regulates its expression. For the additional study, miR-21-5p and miR-221-3p will co-transfected with *FOXP2* in the level of cell. The present study will offer better consideration of various miRNAs expression analysis in chimpanzee.

P85

Molecular characterization of SINE derived MicroRNA-422a in *ARID5B*

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MicroRNA (miRNA) is a class of small non-coding RNA, regulates the expression of target messenger RNA by complementary binds to the 3' untranslated region (UTR) at the post-transcriptional level. A few of miRNAs are derived from transposable element (TE) also known as transposon, that jumps around the host genome. Especially, miR-422a is derived from one class of the TE called short interspersed element (SINE). The expression patterns of miR-422a is analyzed in various tissue samples of crab-eating monkey (*Macaca fascicularis*). miR-422a is highly expressed in both small intestine and liver and one of the target gene of miR-422a, AT-Rich Interaction Domain 5B (*ARID5B*) expressed reversely compared to miR-422a. *ARID5B* encodes a member of the AT-rich interaction domain (ARID) family of DNA binding proteins. As a results suggests, it is possible that miR-422a binds to 3'UTR of *ARID5B* and regulates its transcription level. For the further study, miR-422a will co-transfected with *ARID5B* in the level of cell. Due to a few miRNA studies conducted in crab-eating monkey, current study provides the better understanding of biological function of miRNAs in crab-eating monkey.

P86

Expression analyses of ol-miR-140-3p and target gene, *KIF5A* in olive flounder infected with *Streptococcus parauberis*

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MicroRNAs (miRNAs) are small non-coding RNAs made up of 20~24 nucleotides in length and they bind to 3' untranslated region (3' UTR) of the target gene to regulate gene expression. miRNAs are known to participate in many pathological processes. In this study, the expression of the pol-miR-140-3p was investigated in association with the infection of *Streptococcus parauberis* (*S. parauberis*), which is one of the major bacterial pathogens that cause streptococcosis in *Paralichthys olivaceus*. As a result, pol-miR-140-3p was down-regulated in brain after infected by *S. parauberis*. On the contrary, the expression of the Kinesin Family Member 5A (*KIF5A*), the target gene of pol-miR-140-3p, was increased in infected samples compare to its control. This negative interaction between the pol-miR-140-3p and *KIF5A* could suggest the possibility of pol-miR-140-3p as a biomarker on *S. parauberis* infection in *Paralichthys olivaceus*.

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Expression analysis of pol-miR-15b-5p in *Paralichthys olivaceus* infected by VHSV

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Viral hemorrhagic septicemia virus (VHSV), an OIE listed viral pathogen, is an etiological agent of contagious disease, Viral hemorrhagic septicemia, causing massive mortality in farmed olive flounder (*Paralichthys olivaceus*). Olive flounder is economically important mariculture fish cultured in several countries including South Korea, Japan, and China. MicroRNAs (miRNAs) are small non-coding RNA with 20-24 nucleotides in length. miRNAs bind to 3' untranslated region (3' UTR) of target messenger RNA (mRNA) and regulate gene expression by inducing mRNA degradation and translational repression. miRNAs play an important role in various biological functions such as cell proliferation, development and inflammation. The relative expression patterns of pol-miR-15b-5p were examined by quantitative real-time polymerase chain reaction (qRT-PCR) in olive flounder tissues infected by VHSV at 1, 3, and 7 days post-infection. Overall, pol-miR-15b-5p was down-regulated in infected individuals by VHSV compared to its control. Especially, relative expressions of pol-miR-15b-5p showed the greatest difference in stomach between control and infection samples. The present research will provide better understanding of miRNA function for viral diseases in olive flounder. For the further study, target gene analysis and cell experiment will be conducted.

▶ **Keywords:** *Paralichthys olivaceus*, miR-15b-5p, VHSV

P88

T790M gatekeeper mutation emerges via *de novo* at the early stages of erlotinib treatment in PC9 non-small cell lung cancer cells

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The emergence of the T790M gatekeeper mutation in the *Epidermal Growth Factor Receptor* (*EGFR*) gene is an important mechanism that can lead to the acquired resistance to EGFR-targeted tyrosine kinase inhibitors used in a subset of non-small cell lung cancer (NSCLC) patients harboring activating mutations. Here we investigated the paths leading to the acquisition of the T790M mutation by establishing an erlotinib resistant PC9 cell model harboring ectopically introduced *EGFR* cDNA. We detect the emergence of T790M mutation within the *EGFR* cDNA in a subset of erlotinib resistant PC9 cell models through Sanger sequencing and droplet digital PCR-based methods, confirming that T790M mutation can emerge via *de novo* events following treatment with erlotinib. In addition, we show that the *de novo* T790M bearing erlotinib resistant PC9 cells are sensitive to the 3rd generation EGFR-targeted drug, WZ4002. Furthermore, GFP-based competition cell proliferation assays reveal that PC9 cells ectopically expressing EGFR mutant become more dominantly resistant to erlotinib than parental PC9 cells by acquiring T790M mutation. Taken together, we believe that our findings expand upon the previous notion of evolutionary paths of T790M development, providing an important clue to designing a therapeutic strategy to overcome drug resistance.

▶ **Keywords:** De novo mutation, EGFR (epidermal growth factor receptor), EGFR-Targeted therapy; Erlotinib, Erlotinib-resistance, NSCLC (non-small cell lung cancer), T790M

P89

Whole transcriptome analysis identifies TNS4 as a key effector of cetuximab and a regulator of the oncogenic activity of KRAS mutant colorectal cancer cell lines

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Targeting of activated epidermal growth factor receptor (EGFR) with therapeutic anti-EGFR monoclonal antibodies (mAbs) such as cetuximab and panitumumab has been used as an effective strategy in treatment of colorectal cancer (CRC). However, its clinical efficacy occurs only in the limited number of patients. Here, we performed whole-transcriptome analysis in xenograft mouse tumors induced by *KRAS*^{G12D} mutation-bearing LS174T CRC cells following treatment with either cetuximab or PBS. By integrated analyses of differential gene expression with TCGA and CCLE public database, we identified TNS4, overexpressed in CRC patients and *KRAS* mutation-harboring CRC cell lines, significantly downregulated by cetuximab. While ablation of TNS4 expression via shRNA results in significant growth inhibition of LS174T, DLD1, WiDr, and DiFi CRC cell lines, conversely, its ectopic expression increases the oncogenic growth of these cells. Furthermore, TNS4 expression is transcriptionally regulated by MAP kinase signaling pathway. Consistent with this finding, selumetinib, a MEK1/2 inhibitor, suppressed oncogenic activity of CRC cells and this effect is more profound in combination with cetuximab. Altogether, we propose that TNS4 plays a crucial role in CRC tumorigenesis and that suppression of TNS4 would be an effective therapeutic strategy in treating a subset of cetuximab-refractory CRC patients including *KRAS* activating mutations.

▶ **Keywords:** TNS4, KRAS, EGFR, Cetuximab, Selumetinib, colon cancer

P90

Autophosphorylation in C-terminal domain is not required for oncogenic transformation by lung-cancer derived EGFR mutants

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Aberrant activation of cancer-derived mutant Epidermal Growth Factor receptor (EGFR) is closely associated with cancer pathogenesis. Here, we showed that while blocking of all 10 potential tyrosine phosphorylation within C-terminal domain of wild-type EGFR by substitution of tyrosine to phenylalanine using site-directed mutatgenesis abrogates EGF-mediated cellular transformation, lung-cancer derived L858R, exon 19 deletion and exon 20 insertion mutant EGFR retain oncogenic potential in the absence of tyrosine phosphorylation. Consistent with this finding, we found that the mutant EGFR (CYF10) lacking autophosphorylation are able to transform Ba/F3 cells without IL-3. Using luminex and immunoprecipitation analysis, we demonstrated that the key EGFR-associated proteins including Grb2 and PLC-ɣ are neither phosphorylated nor bound to CYF10 mutants in the transformed cell context. In contrast, we found that Bcar1 (pCas130) and Shc adaptor proteins are highly phosphorylated to the same levels in the cells transformed by either all mutant EGFR or their cognate CYF10 mutants. Taken together, we concluded that Bcar1and Shc proteins, but not Grb2, can be activated through an alternative mechanism independent of EGFR phosphorylation and potentially contribute to oncogenic signaling cascade of CYF10 mutant leading to cellular transformation.

P91

Systematic screening of EGFR C-terminal intragenic deletion mutation in cancer patient samples by establishing a Nanostring technology-based platform

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Various oncogenic mutations in epidermal growth factor receptor (EGFR) have been identified in several types of cancer. Recently, our group has reported an additional class of genomic alterations leading to cellular transformation identified by genomic characterization of GBM and lung cancer patient samples, which are intragenic deletion mutations occurring within exon 25-28 of EGFR gene. To further explore the significance of EGFR C-terminal intragenic deletion mutation in cancer development, first we sought to investigate the frequency of these mutations in various types of cancer patient samples. For this purpose, we aimed to develop a novel high-throughput screening method based on Nanostring nCounter technology. In brief, we designed nanostring probes specifically recognize all possible exonic junctions of mRNA transcripts within exon 25-28 region generated by aberrant RNA splicing events. Using mRNAs prepared from cell lines expressing 10 different EGFR C-terminal deletion mutants, we were able to validate specificity of all designed probes. In summary, we successfully generated a nCounter nanostring technology based systematic screening platform, which allow us qualitatively and quantitatively to identify all potential oncogenic EGFR C-terminal intragenic deletion mutations in patient mRNA samples.

P92

Characterization of Alzheimer's disease-associated genes using *Drosophila* model

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Alzheimer's disease (AD) is a multifactorial disease, with which more than 40 genes have been associated thus far. However, it is believed that many AD-associated genes have not yet been discovered. Here, we identified novel AD-associated genes from multiple resampled genome-wide associated study (GWAS) in Korean population followed by functional genomic screening with *Drosophila* AD model. Among the potential AD-associated genes selected by GWAS, 539 genes were screened to find genes that are functionally related with AD using RNAi system. As a result, 112 genes were found to be genetic modifiers of *Drosophila* AD models. Gene ontology analysis revealed that 33 genes out of 112 are involved in endocytosis. The function of 4 endocytic genes (*garnet, shibire, EndoA,* and *CG9951*) were further analyzed. The knockdown of these genes increased Aβ42 accumulation and exacerbated Aβ42-induced neuronal damage in the brain of Aβ42-expressing fly. In conclusion, our results suggest that the down-regulation of molecular components of endocytic machinery is important pathological mechanism underlying AD, and that endocytosis is the major cellular pathway related with AD in Korean population.

P93

Viral infection induces the upregulation of MHC-1 expression in infected cancer cells

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Cancer cells can evade immune system by the downregulation of major histocompatibility complex-1 (MHC-1) molecules and upregulation of immunosuppressive ligands such as programmed death ligand 1 (PD-L1). In addition, cancer cells provide inhibitory cytokines so that the microenvironments of cancer maintain as an anti-inflammatory condition. However, it is not clear if cancer cells provide pro-inflammatory microenvironments to help clear viral infection, when they were infected with life-threatning viruses. To test this question, we infected EL-4 cells, a lymphoma cell line, with lymphocytic choriomeningitis virus (LCMV) and examined if this infection causes the phenotypic change of cancer cells. On day 7 post infection, we observed that expressions of MHC-1 and PD-L1 molecules increased, while decreased PD-1 expression was found in virus-infected cancer cells. Since the overexpression of MHC-1 molecules was found on virus-infected cells, we further examined whether virus-specific CD8 T cells can recognize the antigen presented by these cancer cells and if these CD8 T cells can mount immune response. When LCMV-specific memory T cells were cultured with virus-infected EL-4 cells, we found that these CD8 T cells were able to produce IFN-γ and TNF-α, but the levels of these proteins were lower compared to positive controls. Altogether, these data suggest that cancer cells infected with viruses presented the viral antigens to CD8 T cells so that the delivery of viral antigen to cancer would be a novel therapeutic strategy.

P94

Liver-selective gamma-secretase inhibition ameliorates diet-induced hepatic steatosis, dyslipidemia and atherosclerosis

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Hepatic gamma-secretase regulates low-density lipoprotein receptor (LDLR) cleavage and degradation, affecting clearance of plasma triglyceride (TG)-rich lipoproteins (TRLs). In this study, we investigated whether gamma-secretase inhibition modulates risk of Western (high-fat/sucrose and high-cholesterol)-type diet (WTD)-induced hepatic steatosis, dyslipidemia and atherosclerosis. We evaluated liver and plasma lipids in WTD-fed mice with hepatocyte-specific ablation of the non-redundant gamma-secretase-targeting subunit Nicastrin (L-Ncst). In parallel, we investigated the effect of liver-selective Ncst antisense oligonucleotides (ASO) on lipid metabolism and atherosclerosis in wildtype (WT) and ApoE knockout (ApoE$^{-/-}$) mice fed normal chow or WTD. WTD-fed L-Ncst and Ncst ASO-treated WT mice showed reduced total cholesterol and LDL-cholesterol (LDL-C), as well as reduced hepatic lipid content as compared to Cre- and control ASO-treated WT mice. Treatment of WTD-fed ApoE$^{-/-}$ mice with Ncst ASO markedly lowered total and LDL cholesterol, hepatic TG and attenuated atherosclerotic lesions in the aorta, as compared to control ASO-treated mice. L-Ncst and Ncst ASO similarly showed reduced plasma glucose as compared to control mice. In conclusion, inhibition of hepatic gamma-secretase reduces plasma glucose, and attenuates WTD-induced dyslipidemia, hepatic fat accumulation and atherosclerosis, suggesting potential pleiotropic application for diet-induced metabolic dysfunction.

P95

Oncogenic EGFR mutations as genomic biomarkers for cetuximab and panitumumab response in colorectal adenocarcinoma

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Somatic mutations of Epidermal Growth Factor Receptor (EGFR) occur in ~3% of colorectal cancer patients. Here, through systematic functional screening of 21 recurrent EGFR mutations selected from public datasets, we show that 11 colon cancer-derived EGFR mutants; G63R, E114K, R165Q, R222C, S492R, P596L, K708R, E709K, G719S, G724S and L858R, are oncogenic, and able to transform cells in a ligand-independent manner. We demonstrate that cellular transformation by these mutants requires receptor dimerization. Importantly, the EGF-induced and constitutive oncogenic potential of these EGFR mutants are inhibited by cetuximab or panitumumab in vivo and in vitro. Taken together, we propose that a subset of EGFR mutations can serve as genomic predictors for response to anti-EGFR antibodies and that metastatic CRC patients with such mutations may benefit from these drugs as part of the first-line therapy.

P96

Linalool has neuroprotective effects on suppressing ROS production and inflammation of Linalool in Aβ42-induced *Drosophila* model of Alzheimer's disease

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Terpenes are vital metabolites and known to be beneficial in the treatment of various diseases. Previously, our group screened terpenes that increased the survival of the Alzheimer's disease (AD) model flies and identified linalool as a neuroprotective terpene. Linalool is a monoterpene and is known to have anti-inflammatory and neuroprotective properties. Although several studies have shown the beneficial effect of linalool in AD animal models, the mechanisms underlying the beneficial effect of linalool on AD are yet to be elucidated. In the present study, we showed that linalool intake increased the survival of the AD model flies in a dose-dependent manner. Linalool also decreases Aβ-induced apoptosis in eye discs as well as the larval brain. Moreover, linalool intake was found to reduce neurodegeneration in the brain of adult AD model flies. However, linalool did not affect the total amount of Aβ42 protein or Aβ42 aggregation. Rather, linalool decreased Aβ-induced ROS levels, and inflammatory response in the brains of AD model flies. Taken together, our data suggest that linalool exerts its beneficial effects on AD by reducing Aβ 42-induced oxidative stress and inflammation.

▶ **Keywords:** Alzheimer's disease, *Drosophila*, Inflammation, Linalool, Terpene

P97

Amyotrophic lateral sclerosis-related mutant SOD1 aggregates impair mitophagy by sequestering the autophagy receptor optineurin

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Amyotrophic lateral sclerosis (ALS) is a neurodegenerative disease characterized by the progressive demise of motor neurons. One of the causes of familial ALS is the mutation of the gene encoding superoxide dismutase 1 (SOD1), which leads to abnormal protein aggregates. How SOD1 aggregation drives ALS is still poorly understood. Recently, ALS pathogenesis has been functionally implicated in mitophagy, specifically the clearance of damaged mitochondria. Here, to understand this mechanism, we investigated the relationship between the mitophagy receptor optineurin and SOD1 aggregates. We found that mutant SOD1 (mSOD1) proteins associate with and then sequester optineurin, which is required to form the mitophagosomes, to aggregates in N2a cells. Optineurin recruitment into mSOD1 aggregates resulted in a reduced mitophagy flux. Furthermore, we observed that an exogenous augmentation of optineurin alleviated the cellular cytotoxicity induced by mSOD1. Taken together, these studies demonstrate that ALS-linked mutations in SOD1 interfere with the mitophagy process through optineurin sequestration, suggesting that the accumulation of damaged mitochondria may play a crucial role in the pathophysiological mechanisms contributing to ALS.

P98

Metformin has potential as a cancer immunotherapy adjuvant

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The type 2 diabetes drug, metformin, has been reported to possess antitumor effects and maintain high cytotoxic T lymphocyte (CTL) activity, suggesting that metformin may play a role in immune surveillance. However, the functions and the detailed mechanisms of metformin related to cancer immunity are not fully understood. Here we show that metformin increases CTL activity by reducing the stability and membrane localization of programmed death ligand-1 (PD-L1), one of the key immune checkpoints in cancer immune evasion. The antitumor effect of metformin is significant in immunocompetent but not in immunodeficient mouse model. Furthermore, we discover that AMP-activated protein kinase (AMPK) activated by metformin directly phosphorylates S195 of PD-L1. S195 phosphorylation induces abnormal glycosylation of PD-L1, resulting in its ER accumulation and ER-associated degradation (ERAD). Consistently, tumor tissues from metformin-treated breast cancer patients exhibit reduced levels of PD-L1 with AMPK activation. Blocking the inhibitory signal of PD-L1 by metformin enhances CTL activity against cancer cells. Our findings identify a new regulatory mechanism of PD-L1 expression through the ERAD pathway and suggest that the combination of metformin and CTLA4 blockade has the potential to increase the efficacy of immunotherapy.

P99

Functional analysis of lauric acid hydroxylation in human cytochrome P450 4A11 C347A, C347S, C375A, C375S

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Human cytochrome P450 (P450) 4A11 is only functionally active in the 4A subfamily. P450 4A11 catalyzes the conversion of arachidonic acid to 20-hydroxyeicosatetraenoic acid (20-HETE), a bioactive mediator preventing hyperpolarization of the vascular smooth muscle and enhancing the vasoconstrictor responses. P450 4A11 has eight cysteine residues including a heme coordinate one. Mutagenesis and proteomics analysis suggested that the redox status of cysteine residues in P450 4A11 may be changed and the reducing agents can convert the oxidized cysteine residues to be functionally active. Five cysteine residues are oxidized to be sulfenic acids and two cysteine residues may participate in the disulfide bonds. In this study, P450 4A11 C347A, C347S, C375A, and C375S mutants are generated and their enzymatic functions were characterized. The recombinant enzymes of P450 4A11 wild type and mutants were expressed in *Escherichia coli*. Only P450 4A111 C347A was successfully expressed with typical P450 features. The expression level of P450 4A11 C347A was 84 nmol/liter culture. P450 4A11 wild type and C347A were purified using Ni^{2+}-NTA affinity column chromatography. The purified P450 4A11 protein exhibited the type I binding spectra with lauric acid. Lauric acid binding to CYP4A11 C347A yielded a K_d value of 13.69 μM. Catalytic activities of P450 4A11 wild type and C347A in lauric acid hydroxylation were analyzed using gas chromatograph-mass spectrometry system (GC/MS). Kinetic parameters were estimated from the fitted curves to the Michaelis-Menten equation using GraphPad Prism for nonlinear regression analysis. The purified 4A11 enzyme produced 12α -hydroxylated lauric acid as a major metabolite. Steady-state kinetic analysis of lauric acid hydroxylation showed that the catalytic efficiencies (k_{cat}/K_m) of CYP4A11 C347A was 0.00003.

▶ **Keywords:** Cytochrome P450, CYP4A11, SDM, Lauric acid, GC/MS

P100

Functional characterization of *Drosophila melanogaster* cytochromes P450, 6A2 and 6A8

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The genomic analysis of *Drosophila melanogaster* identified about 90 putative genes encoding cytochrome P450 (P450) enzymes. Among these P450s, the CYP6 family of *Drosophila melanogaster* appears to be responsible for resistance of insecticides or xenobiotic metabolism of various fatty acids. In this study, two cytochrome P450 genes *cyp6a2* and cyp6a8 were amplified and cloned into pCW expression vector. Recombinant proteins of P450 6A2 and P450 6A8 were successfully expressed in *Escherichia coli* and purified using Ni-affinity chromatography. The principle of the P450 spectral assay is that the ferrous form of the hemeprotein reacts with carbon monoxide (CO) to form a complex that particularly produces a spectrum with a wavelength maximum at ~450 nm, due to the signature cysteine thiolate axial ligand to the heme iron in these proteins. The binding of substrates to P450s, which is usually viewed as the first step in the catalytic cycle, has been studied extensively via a variety of biochemical and biophysical approaches. The many substrates may be divided into at a minimum two classes in accordance with the different spectral properties of the complexes formed Type I substrates produce a blue shift, while type II compounds show a red shift in the *Soret* region of the absorption spectra of cytochrome P450. CYP6A2 showed tight binding to monoterpene, and CYP6A8 showed tight binding to only lauric acid among fatty acids. Catalytic activity will be analyzed according to binding analysis.

▶ **Keywords:** Cytochrome p450, *Drosophila melanogaster*, CYP6A2, CYP6A8, Monoterpene

P101

Dynamics of primary cilia regulates Schwann cell myelination in a state of chronic inflammation

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In the injured PNS, immune is essential for elimination of damaged nerve debris for axonal regeneration. Aging-caused chronic inflammation disturbs the regeneration by leading to accumulation of pro-inflammatory cytokines and nerve debris that affects myelination of Schwann cells(SCs). Primary cilium, a microtubule-based organelle, has been suggested the role in the myelination. Previous studies have revealed primary cilia are essential for signal transduction to control myelination. Thus, we have hypothesized that chronic inflammation may affect the cilia-mediated signaling in SCs and subsequent axonal regeneration. To investigate the effect of chronic inflammation in cilia dynamics, we examined the primary cilia in the mouse SCs and zebrafish model after inducing inflammation with Trinitrobenzene sulfonic acid (TNBS). The data showed increased cilia and decreased myelination both in vitro and in vivo systems. Therefore, we propose that disassembly of primary cilia in SCs is involved in myelination and further axonal regeneration under chronic inflammation.

P102

ADSSL1-mediated AMPK activation is essential for ciliogenesis to induce myoblast differentiation

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In distal myopathy, a group of heterogeneous genetic diseases, mutations in adenylosuccinate synthase like 1(*ADSSL1*) have been identified. Previously, in the hind limb of mice, it was reported that expression of ADSSL1 decreases right after acute injury, whereas its expression increases when satellite cells are activated. To uncover the ADSSL1-invovled pathology, we have investigated whether ADSSL1 is required for muscle differentiation. Using mouse myoblast cell line C2C12, we performed loss of function study of ADSSL1 and found that depletion of ADSSL1 interfered muscle differentiation by downregulating regulators for muscle differentiation including myogenin and desmin. Given that ADSSL1 catalyzes conversion of IMP to AMP and AMP-activated kinase (AMPK) plays a role in ciliogenesis of human neuroblastoma cells, we examined if ADSSL1 is involved in the activation of AMPK during muscle differentiation. We found that ADSSL1 is required for AMPK activation and ciliogenesis for differentiation of C2C12 cells. Thus, our data suggest that understanding the regulatory mechanism of ciliogenesis during muscle differentiation provides ideas to treat distal myopathy.

P103

XAF1 directly antagonizes GRP78 to drive ER stress-induced apoptosis through the assembly of a ZNF313-mediated destruction complex

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Endoplasmic reticulum (ER) stress-induced, unfolded protein response (UPR)-mediated apoptosis is a protective mechanism whose failure contributes to malignant tumor progression. XAF1 is a stress-inducible, pro-apoptotic tumor suppressor. In this study, we explored the role for XAF1 in UPR signaling and ER stress-induced apoptosis. In response to ER stress, XAF1 expression is activated at the transcription level, and this activation is abolished by blockade of PERK-Nrf2, but not of IRE1a or ATF6 signaling, indicating that XAF1 is a transcription target of Nrf2 and activated by ER stress through the PERK pathway. XAF1 induction greatly enhances apoptotic response of tumor cells to ER stress while blockade of XAF1 induction reduces apoptotic sensitivity of tumor cells to ER stress. Intriguingly, XAF1 decreases the protein level of the ER stress sensor GRP78 and consequently activates UPR signaling. Mechanistically, XAF1 binds directly to GRP78 and stimulates its proteasomal degradation in an ubiquitin E3 ligase ZNF313-dependent manner. XAF1 facilitates ZNF313 interaction with GRP78 and thereby promotes ZNF313-mediated K48-mediated ubiquitination of GRP78. Unlikely wild-type XAF1, mutant XAF1 lacking GRP78- or ZNF313-binding domain shows no activity to promote ER stress-induced apoptosis. XAF1 sensitizes cells to ER stress and drives apoptotic switch of UPR function away from cell cycle arrest by directly antagonizing GRP78 through the assembly of a ZNF313-mediated destruction complex. Our study identifies first a cell-fate decisions function of XAF1 under ER stress conditions.

P104

Study on the structure and mechanism of Severe acute respiratory syndrome coronavirus 2, (COVID19)

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The problem with COVID-19 infection is becoming a problem around the world. Covid-19 virus has a high infection rate and mutation rate. So it still has a strong infection. For this reason, it is urgent to develop unique treatments and vaccines for the Covid19 virus. The nucleocapsid (N) protein of COVID-19 participates a fundamental role in the self-assembly of the virus by packing the virus genome with a helical ribonucleic capsid (RNP) and its release. The N protein is essentially composed of two structural domains between the disordered regions and dimerized through the C-terminal structural domain (CTD). The main activity of proteins is their ability to oligomerize during capsid formation by utilizing dimers as building blocks, but the structural and mechanical bases of this activity are not well known. But it has some distinct advantages over other potential COVID-19 antigens. Therefore, understanding and insights into the structure and mechanisms can contribute to the development of treatments and vaccines.

▶ **Keywords:** COVID19, N protein, SARS-CoV-2, nucleocapsid protein

P105

Cyclic peptide: promising drug molecule

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Substances currently used for drug screening and development can be largely divided into small molecule and macromolecule (biopharmaceutical). These molecules have numerous advantages, but they also have limitations according to their respective characteristics. As a result, interest in the new drug molecule, which complements their shortcomings and has only advantages, has increased, and recently peptide has been seen as a potential alternative between the two molecules. In particular, the circular form of peptide is spotlighted as a promising molecule for the development of novel drugs because of its ability to combine a wide range of target molecules. The cyclic peptide can act as an attractive scaffold in the development of new pharmaceuticals with its favorable properties such as good binding affinity, target selectivity, and low toxicity. In this study, we tried to synthesize cyclical peptides using split-intein circular ligation of peptides and proteins (SICLOPPS) technology and to check if intein splicing efficiency changes according to peptide sequence.

▶ **Keywords:** Cyclic peptide, drug molecule, pharmaceutical, SICLOPPS

P106

Dihydrofolate Reductase (DHFR) Enzyme Kinetics and Structural Study in *Pseudomonas aeruginosa, Acinetobacter baumannii* and *Xanthomonas Oryzae*

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It is necessary to develop a new mechanism of antibiotic agents due to the acceleration of the appearance of the multi-drug resistance (MDR) microorganisms. Identifying potent inhibitor of Dihydrofolate reductase, DHFR, is a prominent instance of finding new antibiotic agents. World health organization (WHO) present a catalog of 12 families of bacteria that pose the greatest threat to human health. *Acinetobacter baumannii* and *Pseudomonas aeruginosa* are in the most priority group, which means most critical to human health now. Dihydrofolate reductase (DHFR) is such a target that is indispensable for almost microorganism's survival. Tetrahydrofolate (THF) is an important factor that can retain central dogma in whole cells including bacterial cells, critical to human health. In the situation of tetrahydrofolate don't be retained appropriately in microorganisms, they can't sustain DNA, RNA, and amino-acid synthesis pathway. DHFR is an enzyme which transforms dihydrofolate to THF. Inhibition of DHFR is critical for the survival of microorganisms. Thus, DHFR is selected as our target to opposing the acceleration of multi-drug resistance appearance.

▶ **Keywords:** Multi-drug resistance (MDR), dihydrofolate reductase (DHFR), tetrahydrofolate (THF), dihydrofolate (DHF)

P107

Expression, purification, crystallization of UDP-3-O-(R-3-hydroxymyristoyl)-N-acetylglucosamine deacetylase (LpxC) from multidrug resistant bacteria and *Xanthomonas oryzae* pv. *oryzae*

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Today super-bacteria are still threatening humanity. Except for the well-trodden path to the discovery of antibacterial agents targeting peptidoglycan, DNA replication, or protein biosynthesis, the development of novel antibiotics directed against the previously unexploited targets is an urgent need for the treatment of multidrug-resistant (MDR) bacterial pathogens. One of the emerging targets in Gram-negative bacteria is the biosynthetic pathway of lipid A, typically a phosphorylated, hexa-acylated glucosamine disaccharide that makes up the outer leaflet of the outer membrane. The outer membrane of gram-negative bacteria is comprised of Lipopolysaccharide (LPS) that serves as the permeability barrier to protect the bacterium against antibiotics. As the membrane anchor of LPS, lipid A is essential for LPS assembly in the outer membrane. Since lipid A is the toxic component of LPS and is required for bacterial viability, inhibition of its biosynthesis is lethal to bacteria. One promising target is the zinc-dependent metalloamidase UDP-3-O-(R-3-hydroxymyristoyl)-N-acetylglucosamine deacetylase (LpxC), which catalyzes the committed step of lipid A (endotoxin) biosynthesis. LpxC is an essential, single-copy gene that is conserved in virtually all Gram-negative bacteria.

▶ **Keywords:** UDP-3-O-(R-3-hydroxymyristoyl)-N-acetylglucosamine deacetylase (LpxC), lipopolysaccharide (LPS), lipid A, multidrug-resistant (MDR), drug target

P108

Functional analysis of paclitaxel 6α-hydroxylation and arachidonic acid epoxidation in human CYP2C8

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Human cytochrome P450 (CYP) 2C family contains four members of gene products (*CYP2C8*, *CYP2C9*, *CYP2C18*, and *CYP2C19*). These genes are localized within a single gene locus in Chromosome 10. Of these enzymes, Cytochrome P450 2C8 (CYP2C8) is one of the principal P450 monooxygenase expressed in human liver. It is involved in the metabolism of many clinically used drugs, including anticancer, anti-inflammatory, antidiabetic, antimalarial agents. The representative xenobiotic substrate of CYP2C8 is paclitaxel. CYP2C8 is also known to metabolize physiologically important endogenous molecule such as arachidonic acid. In this study, recombinant enzymes of CYP2C8 was successfully expressed in *Escherichia coli* and purified using Ni-affinity chromatography. Its catalytic activities for paclitaxel 6α-hydroxylation and arachidonic acid epoxidation were analyzed by ultra-performance liquid chromatography-tandem mass spectrometry (UPLC-MS/MS). In reaction to paclitaxel, the purified CYP2C8 enzyme produced 6α-hydroxylated paclitaxel as a major metabolite. The steady-state kinetic analysis of paclitaxel 6α-hydroxylation determined that the k_{cat} was 1.3±0.1 min^{-1} and the K_m was 22±4.0 μM. And it metabolized arachidonic acid to epoxyeicosatrienoic acids (EETs), chiefly 11,12-EET and 14,15-EET.

▶ **Keywords:** CytochromeP450, CYP2C8, Paclitaxel, Arachidonic acid, UPLC-MS/MS

P109

Downregulation of proteasome subunits in muscles enhances longevity in *Drosophila*

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Ubiquitin-proteasome system (UPS) that keeps clearance of misfolded proteins is important to control protein homeostasis. It has been known that protein aggregation cause aging as well as neurodegeneration. However, the mechanism by which protein aggregation cause aging or neurodegeneration is not clear. Here, we conducted screening test using aged flies to assess correlation between aging and UPS. When the 310 UPS-related genes were respectively down-regulated in muscle, knockdown of a variety of UPS-related genes mostly reduced the increased levels of ubiquitinated protein aggregation at the flight muscles of the 15-day-old-flies. Interestingly, we found that most of proteasome subunit genes was selected as suppressors which reduce protein aggregation. Also, when selected proteasome subunit genes are downregulated, autophagosome, marker of autophagy activation, was activated in muscles. Furthermore, knockdown of proteasome subunits, especially proteasome catalytic subunit beta2, 5, in muscle increased lifespan of flies. Taken together, we suggested that down regulation of proteasome in muscle enhance *Drosophila* longevity via the autophagy activation manner.

▶ **Keywords:** Aging, Proteasome, Protein homeostasis, Screening, UPS

P110

Stress exposure causes distinctive changes in both behaviors and the intrinsic properties of the medial prefrontal cortex in male and female mice

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Depression is a common psychiatric disorder and the prevalence of that is known to be much higher in female than male. However, most of preclinical studies so far have been done with males, thus leaving the specific mechanisms underlying the sexual difference in depression largely unknown. Dysfunction of Medial prefrontal cortex (mPFC) has been often proposed to be accompanied with psychiatric disorders including depression. Here, we employed the female-specific depression animal model, sub-chronic variable stress (SCVS), to investigate whether the sex difference in mPFC when stressed is related with the higher prevalence of depression in female. When we analyzed the physiological properties of mPFC neurons, we found that SCVS results quite distinctive changes in females and males in subregions of the mPFC. In the infralimbic cortex (IL), males showed an increase in firing threshold even though they exhibit no depressive behaviors, whereas females showed an increase in input resistance. In the prelimbic cortex (PL), only females showed an increase excitability without altering intrinsic properties or firing threshold by SCVS. Our observations suggest that the same stress exposure leads to divergent changes in the mPFC depending on the sex, possibly mediating more severe vulnerability for depression in females.

P111

Establishing a better female-specific animal model of depression

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Women are diagnosed with major depressive disorders (or depression) more often than men are. However, the animal studies had been primarily used male mice exclusively largely due to both the complexity in considering estrous cycle and the lack of proper animal models to study gender difference in depression. Recently, sub-chronic variable stress (SCVS) that is comprised with two cycles of foot-shock, tail suspension and restraint stress per cycle for 6 days has been proposed to induce helpless behaviors in female but not in male mice. Here, we modified the previously reported SCVS paradigm to minimize the variations per trials by modifying the numbers of foot-shocks to 80 times, 100 times and 120 times so to establish better gender specific animal model of depression. The validation of animal models was done by running a series of behavioral tests including novelty suppressed feeding test (NSF), tail suspension test (TST), sucrose preference test (SPT) and forced swim test (FST). Among 4 different SCVS paradigms we tested, we found that the modified SCVS with 80 foot-shocks is the most reliable gender-specific animal model, given the overall behavioral scores. We believe our study will be instrumental for future studies of gender specificity in depression.

P112

Protein kinase C mediates neuropeptide Y-induced reduction in inhibitory neurotransmission in the lateral habenula

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Neuropeptide Y (NPY) is one of peptide neuromodulators, well known for orexigenic, anxiolytic and antidepressant effects. We previously reported that NPY decreases GABAergic transmission in the lateral habenula (LHb). In the current study, we aim to investigate the underlying signaling pathways that mediate inhibitory action of NPY in the LHb by employing whole-cell patch clamp recording with pharmacological interventions. Here, we revealed that Y1 receptors (Y1Rs) but not Y2Rs mediate NPY-induced decrease of GABAergic transmission in the LHb. Surprisingly, NPY-induced decrease of inhibitory transmission in the LHb was not dependent on adenylyl cyclase (AC)/protein kinase A (PKA)-dependent pathway as reported in other brain areas. Instead, pharmacological blockade of phospholipase C (PLC) or protein kinase C (PKC) activity abolished the decrease of GABAergic transmission by NPY in the LHb. Our findings suggest that Y1Rs in the LHb may trigger the activation of PLC/PKC-dependent pathway but not the classical AC/PKA-dependent pathway to decrease inhibitory transmission of the LHb.

P113

Apolipoprotein D reduces neuronal damages and disease-like phenotypes in a *Drosophila* model of Alzheimer's disease

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Apolipoprotein D (ApoD) is a member of the lipocalin family which is secreted from subsets of neurons and glial cells. Previously, it has been reported that the expression level of *ApoD* is strongly up-regulated in the brain of Alzheimer's disease (AD) patients, and that ApoD has a protective function against oxidative stress in several animal models. However, the role(s) of ApoD in the pathogenesis of AD is still not understood. Here, we demonstrated the role of *Glial Lazarillo* (*GLaz*), a gene for a *Drosophila* mammalian *ApoD* homolog, in the AD-like phenotypes of Aβ 42-expressing flies. *GLaz* transcript level was increased by human Aβ42 expression, as in AD patients. Also, *GLaz* overexpression mitigated the Aβ42-induced phenotypes such as rough eyes, locomotive defect, reduced survivability and neuronal cell death. In addition, increased ROS level and sensitivity to oxidative stress in the AD model flies were significantly reduced by pan-neuronally overexpressed *GLaz*. Among the five different glial-subtypes, only subperineurial and cortex glial-specific *GLaz* knockdown increased cell death in the larval brain, like *GLaz* mutant fly. Taken together, our results suggest that *ApoD* is expressed in specific glial cells and plays a protective role against the AD-like phenotypes of AD model flies and that *ApoD* can be a potential genetic marker and therapeutic target of AD.

P114

Structure and mechanism study of 3-chymotrypsin-like protease of severe acute respiratory syndrome coronavirus 2

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The COVID-19, caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), is threatening global health. Because of its high infectiousness and significant mortality, COVID-19 requires rapid development of specific therapeutics and vaccines. The 3-chymotrypsin-like protease ($3CL^{pro}$) is considered a promising drug target, as it is dissimilar to human proteases and has a specific active site good for developing small molecule drugs. Sequence and structure of the $3CL^{pro}$ are closely related to those from other β-coronaviruses, facilitating drug discovery attempts based on previous lead compounds. $3CL^{pro}$, also named non-structural protein 5 (nsp5), is activated by autoproteolysis and is the main protease responsible for maturing polyprotein by cutting the viral polyprotein into functional units. This study is for investigating sequence-based inhibitors using structural biology. We carried out the cloning, expression, and crystallization of $3CL^{pro}$ and enzyme assay to study the enzyme activity and develop a specific inhibitor.

▶ **Keywords:** 3-chymotrypsin-like protease, COVID-19, Coronavirus SARS-CoV-2, drug design, enzyme kinetics, X-ray crystallography

P115

Expression, crystallization and X-ray crystallographic, HPLC analysis of cystathionine γ-synthase (XometB) from *Xanthomonas oryzae* pv. *oryzae*

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The PLP dependent enzyme has a versatile mechanism and promiscuous character. One of the PLP dependent enzymes, cystathionine γ-synthase (CGS) catalyzes the first step in the trans-sulfuration pathway leading to the formation of cystathionine from O-succinyl homoserine and L-cysteine through a γ-replacement reaction. The *CGS* (*XometB*) gene from *Xanthomonas oryzae* pv. *oryzae* (Xoo) was cloned, and the CGS protein was expressed, purified, and crystallized. The enzyme kinetics study of CGS is in progress via the HPLC assay. *XometB* gene was cloned into the pET15b expression vector containing a 6 x His tag at the upstream of a thrombin cleavage site. The expression vector, yielding the recombinant CGS protein, was transformed into *E. coli* BL21 (DE3). After series of purification steps using nickel affinity chromatography and anion exchange chromatography and cleavage of the His tag, the crystallization of CGS is being carried out. The enzyme assay using HPLC is also established.

▶ **Keywords:** Pyridoxal phosphate, transsulfuration pathway, *Xanthomonas oryzae* pv. *oryzae,* pesticide, enzyme mechanism

P116

NORE1A induces a feedback termination of TNF signaling by antagonizing TNFR1 through ITCH-mediated destruction complex

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Background: NORE1A/RASSF5 is a tumor suppressor that is commonly inactivated in a variety of cancers. NORE1A is frequently down-regulated during tumor development and its inactivation often correlates with up-regulation of Ras activity.

Results: Upon exposure to TNF-a, NORE1A is induced by NF-kB signaling at the level of transcription while its activation suppresses TNF activation of NF-kB, indicating that NORE1A functions as a feedback terminator of TNF-NF-kB signaling. As predicted, NORE1A blocks TNF activation of pro-inflammatory gene transcription, epithelial-to-mesenchymal transition (EMT), invasion and migration. Mechanistically, NORE1A binds directly to TNF receptor I (TNFR1) and ubiquitin E3 ligase ITCH to facilitate ITCH-mediated K48-linked ubiquitination of TNFR1 and subsequent lysosomal degradation. This interaction protects BAX from ITCH-mediated ubiquitination and thus activates its apoptotic function. NORE1A interaction with ITCH plays a crucial role for both TNFR1 degradation and BAX stabilization and activation

Conclusions: In this study, we demonstrate that NORE1A is a feedback terminator of TNF-NF-kB signaling, which directly antagonizes TNFR1 by facilitating the ITCH-TNFR1 interaction. Our study also shows that NORE1A binding to ITCH releases ITCH from BAX and activates BAX-mediated apoptosis. These data illuminate the mechanistic consequence of NORE1A inactivation in tumorigenesis.

P117

FOXO1 mediated FAF1 expression is essential for the host to prevent *T. gondii* infection

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Purpose: Recently, it was reported that FAF1 is involved in the regulation of a virus-triggered IFN-β signaling pathway by inhibiting the nuclear import of phosphorylated IRF3 thus preventing the cellular antiviral response. However, the regulation mechanism of FAF1, especially in the immunity system is not fully understood, yet. Therefore, we studied how FAF1 modulates immune response related transcription factor activity upon infectious pathogen.

Materials and Methods: The phosphorylation level of TBK1/IRF3 and the expression level of the target genes ISGs were measured by western blot and PCR, respectively. The nuclear/cytoplasmic translocation of IRF3 was monitored by Western blot analysis and confocal microscopy. FAF1 expression alteration was analyzed using Western blot, RT-PCR and confocal microscopy.

Results: *T. gondii* growth requires host TBK1/IRF3 pathway activation. Inhibition of PI3K/AKT pathway had no effect on IRF3 phosphorylation level but blocked IRF3 nuclear import and ISGs transcription even in the presence of *T. gondii* or *T.gESA*. FAF1 expression level was reduced by *T. gondii* infection and PI3K/AKT inhibitors reversed *T. gondii* induced FAF1 down-regulation. *In silico* analysis for the FAF1 promoter sequence showed that the presence of FRE which is a conserved binding site of FOXO1 transcription factor, and indeed, FOXO1 overexpression enhanced intracellular FAF1 level meanwhile FOXO1 gene silencing reduced it. We also found that *T. gondii*-induced FAF1 down-regulation is correlated with enhanced transcriptional activity of IRF3.

Conclusion: These results suggest that *T. gondii* infection-driven PI3K/AKT/FOXO1 dependent FAF1 down-regulation is essential for IRF3 nuclear translocation to activate the transcription of ISGs and thereby *T. gondii* proliferation.

P118

A comprehensive analysis of gorilla-specific full-length LINE-1 retrotransposons

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Long interspersed element-1 (LINE-1 or L1) is the most abundant retrotransposons in the primate genome. They have approximately 520,000 copies and make up ~17% of the primate genome. Full-length L1s can mobilize to a new genomic location using their enzymatic machinery. Thus, L1s have contributed to genome diversity and variations during the primate evolution. Gorilla is the second closest species to the human after the chimpanzee, and human-gorilla split time of 7-12 million years ago. The gorilla genome provides an opportunity to explore primate origins and evolution. Here, we aimed to identify gorilla-specific L1s using a more recent version of the gorilla reference genome (Mar. 2016 GSMRT3/gorGor5). We identified 2,002 gorilla-specific L1 candidates through computational analysis. Among them, we manually inspected 694 gorilla-specific full-length L1s, and most of them belong to the L1PA2 subfamily. 12 out of 694 gorilla-specific full-length L1s were structurally intact L1s that could influence genomic variations in the gorilla genome. Interestingly, 12 intact L1s have 18 highly conserved missense mutations, including 7 mutations and 11 mutations in ORF1 and ORF2, respectively.

▶ **Keywords:** Gorilla, Gorilla-specific, LINE-1, Transposable elements, Primate Evolution

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P119

Development of an effective quantification method for human fecal microbe by comparing NGS-based metagenome profiling data

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Metagenome profiling using next-generation sequencing (NGS) is a technique widely used to analyze the diversity and composition of microbes living in the human body, especially in the gastrointestinal tracts. This technique brought remarkable advances in molecular diagnosis on the complex microbial composition associated with various human diseases, but there are problems with a high-cost burden and long analysis period. Among the proven technologies to date, quantitative real-time PCR (qRT-PCR) is most suitable for quantifying and analyzing characteristic microorganisms quickly and efficiently. Many studies have recently been making efforts to develop diagnostic methods with a genus-specific primer that can detect and quantify pathogens presenting in the human mouth, nasal cavity, and pharynx. Therefore, based on NGS metagenome profiling data produced by utilizing 100 GUT samples, we conducted a comparative analysis of quantification accuracy for six bacterial genera (*Akkermansia*, *Bacteroides*, *Bifidobacterium*, *Faecalibacterium*, *Phascolarctobacterium*, and *Roseburia*) through qRT-PCR assay in parallel. Genus-specific primer targeting the particular gene (such as transcription termination/antitermination protein; *NusG*) with one of the genera allows quantification results corresponding with the metagenome profiling data. Our results suggest an efficient quantification method of beneficial or harmful bacteria using qRT-PCR in the microbial diagnosis industry.

▶ **Keywords:** Metagenome profiling, Quantitative real-time PCR (qRT-PCR), Next-generation sequencing (NGS), Genus-specific primers

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P120

Whole-exome sequencing reveals rare genetic variations in Ovarian Granulosa Cell Tumor

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Ovarian Granulosa cell tumor (OGCT) is a rare type of ovarian cancer that accounts for about 5% of all ovarian tumors. Despite the low grade of ovarian cancer, high and late recurrences are common in OGCT patients. In the case of recurrence, the prognosis is poor and conventional chemotherapy is ineffective. This tumor usually occurs in adult women with high estrogen levels, but the cause of OGCT is still unknown. To screen genetic variants associated with OGCT, we collected tumors and matched normal tissues from eleven OGCT patients and carried out whole-exome sequencing (WES) using illumina Hi-Seq 4000 platform. A total of 28,843 single nucleotide polymorphisms (SNPs) and 3,583 insertions/deletions (InDels) were identified in eleven OGCT patients. Among them, 187 SNPs and 19 Indels had a minor allele frequency (MAF) lower than 0.05, 151 SNPs and 14 InDels were common variants, and 36 SNPs and 5 InDels were tumor-specific variants. Furthermore, we used four databases (COSMIC, DisGeNET, OMIM, and TCGA) to investigate whether the candidate genes significantly impacted ovarian cancer. As a result, we found *MUC16,* known to be associated with ovarian cancer in all four databases, which is the most widely used biomarker for recurrent ovarian cancer.

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P121

Establishment of BiTE antibody platform and functional study of CD3ε / CD19 Bispecific BiTE antibody secreted from *Pichia pastoris*

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Blinatumomab (BLINCYTO) is an anti-cancer BiTE (Bispecific T cell Engager) antibody drug approved by the FDA for targeting Acute Lymphoblastic Leukemia (ALL). Blinatumomab targets CD3ε, which is expressed on normal T cells and at the same time targets CD19, which is specifically expressed in B cell leukemia. T cells bound by Blinatumomab are activated to secrete perforin and granzyme, which induces apoptosis of B cell leukemia. Blinatumomab is produced in the Chinese hamster ovary (CHO) Cell expression system in consideration of post translational modification (PTM) and immunogenicity. Although the PTM of CHO cells is similar to that of mammalian cells, it has disadvantages of low yield and high production cost. In this study, a BiTE antibody targeting CD3ε / CD19 was produced from the yeast species *Pichia Pastoris* at a yield of about 1 mg/L using a pHIL-S1 plasmid vector encoding a sequence of Blinatumomab, and the production yield was about 444 times higher than that produced in CHO cell expression system. Purified protein was confirmed to have almost the same level of antigen-binding affinity as BLINCYTO produced in CHO cells through ELISA and flow cytometry analysis. As a result, we suggest that the *Pichia pastoris* is a useful expression system that can express and produce BiTE antibody platform for therapeutic drugs in biotechnology.

▶ **Keywords:** Blinatumomab, Bi-specific T cell Engager (BiTE), *Pichia Pastoris*, Acute Lymphoblastic Leukemia (ALL), Chinese hamster ovary (CHO)

P122

Anticancer peptide with anti-microbial effect against multidrug-resistant bacteria

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Multidrug-resistant bacteria, which are resistant to a variety of antibiotics, are now a threat to human health around the world. Since conventional antibiotics have several limited antibiotic mechanisms, the development of antibiotics with similar mechanisms cannot be a fundamental solution to multidrug-resistant bacteria. We have previously reported on Anti-cancer peptides that exhibit cancer specific anticancer effects. This Anti-cancer peptide is composed of a peptide that exhibits anticancer effect by binding to the transcription factor CP2c and a cell penetrating peptide. Considering that various antimicrobial peptides have anti-cancer effects, it was evaluated whether anti-cancer peptides have anti-microbial effects. As a result, anti-microbial effects were shown in Gram-positive and Gram-negative bacteria. In particular, significant Minimum inhibitory concentration (MIC, 3.125~6.25uM) was shown in multidrug-resistant bacteria including MRSA, MDRPA, VREF. It was also confirmed through cytoplasmic membrane depolarization that it did not destroy the outer membrane of bacteria, unlike the mechanisms of conventional antibiotics. Additionally, the results showed that anticancer peptides were not toxic to normal cells and yeast, and did not show hemolytic effect on human red blood cells. This has the potential as a new Antimicrobial peptide to overcome multidrug-resistant bacteria and can be suggested as an effective antibiotic against various types of bacteria.

▶ **Keywords:** Antimicrobial peptide, Multidrug-resistant bacteria, MRSA, MDRPA, VREF, cytoplasmic membrane depolarization

P123

XAF1 directly antagonizes ERa through the assembly of a BRCA1-mediated destruction complex to direct apoptotic switch of estrogen function

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Purpose: To explore XAF1's candidacy for a suppressor in breast tumorigenesis, we investigated its expression status in tumor cell lines and tissues, effect on ERα regulation of cell growth, and the molecular basis for its function.

Results: XAF1 expression shows an inverse correlation with ERα expression. In ERα-expressing cells, restoration of XAF1 expression increased cellular sensitivity to estrogen-induced, ERα -mediated apoptosis. Likewise, in ERα-non expressing cells, restoration of ERα led to the recovery of apoptotic response to estrogen in XAF1-dependent fashion. XAF1 was found to directly bind to and destabilizes ERα and this interaction is crucial for its apoptosis-promoting activity. XAF1 interacts with BRCA1 and subsequently stimulates BRCA1 binding to ERα and BRCA1-mediated K48 polyubiquitination of ERα. Using a series of deletion mutants, we determined the domains of XAF1, ERα and BRCA1 that are required for the assembly formation. Additionally, XAF1 was identified to be upregulated by estrogen at the transcription level through the p38, JNK and NF-kB signaling pathway.

Conclusion: XAF1 is induced by estrogen and its activation directs the apoptotic switch of estrogen function through the assembly of BRCA1-mediated ERα destruction complex. Our study illuminates the mechanistic consequence of epigenetic inactivation of XAF1 in human breast tumorigenesis.

P124

VitaminD antagonize *Toxoplasma gondii* growth by reducing host Programmed cell death protein 5 (PDCD5) in ARPE-19 cells

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Introduction: Vitamin D is a fat-soluble steroid synthesized from a cholesterol precursor (7-dehydrocholesterol), which has a chemical secosteroid structure. Vitamin D (VitD) has been known as a key regulator of host defense against infections by activating genes and pathways that enhance innate and adaptive immunity. PDCD5 (programmed cell death 5), was first identified as an apoptosis-promoting protein, displays multiple biological activities. However, the biological effect of vitamin D and PDCD5 on parasite infection is not entirely elucidated. Therefore, we examined the effect of interaction between vitamin D and PDCD5 on *T. gondii* infection and proliferation in ARPE-19 cell, a model for ocular toxoplasmosis.

Material and Method: The alteration of TBK1/IRF3 activity and the PDCD5 level in host cell by *T. gondii* infection or by Vitamin D were monitored by Western blot and RT-PCR. The effect of vitamin D on T. gondii infection and growth was measured by Confocal Microscopy.

Result: We found that T. gondii infection increase host PDCD5 expression in a moi dependent manner. In addition, we found that *T. gondii* can induce TBK1/IRF3 signaling pathway in similar context with nucleotide antigens, such as, cyclic di-AMP (c-di-AMP) or Poly(dA:dT) in ARPE-19. We also found that vitamin D3 is an effective agent for suppressing T. gondii replication in ARPE-19. The anti-parasitic mechanism of vitamin D included the inhibition of TBK1/IRF3 activation, followed by lowering of host PDCD5 level.

Conclusions: Our data exhibited that the *T. gondii* can induce host PDCD5 expression which is under control of TBK1/IRF3 signaling pathway. Vitamin D was proven to have a capability of reversing the TBK1/IRF3 stimulating effect of *T. gondii* infection or nucleotide antigens. By suppressing the TBK1/IRF3 activity and PDCD5 expression, vitamin D restricted *T. gondii* from invasion and proliferation in ARPE-19 cells. Therefore, our findings indicate that the TBK1/IRF3 signaling pathway or PDCD5 might has a pharmaceutical potential as a target in developing anti-parasite drug.

P125

Anti-parasite effect of 4-Hydroxyacetophenoneis mediated by regulation of HIF-1α and Akt

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Introduction: Many medicinal plants or their active compounds have been evaluated *in vitro* and *in vivo* for their ability as novel drugs candidate in the parasite control. Previous investigations indicate that 4-Hydroxyacetophenone (well-known as piceol), a key compound in *Cynanchi atrati Radix* (*C. atrati*), has an anti-virus function and some anti-inflammatory effects. Nevertheless, the bioactivity of 4'HAP remains to be identified in parasites prevention. This research aims to find out its pharmacological effect on the growth of *T. gondii* in ARPE-19 cell.

Material and Method: The effect of 4'HAP on *T. gondii* infection and growth was analyzed using fluorometric determination, microscopy and FACS. The activity of GSK3β/ HIF1α and Akt/ FoxO1/ NOX4 pathway was detected by Western blot and RT-PCR. ROS-induction by 4'HAP was measured by fluorescent microscopy with DHE and DCFDA.

Results: 4'HAP, revealed similar effect with *C. atrati* to suppresses *T. gondii* (an obligate intracellular protozoan pathogen) proliferation without side effect to host. In the activity of anti-inflammatory signaling pathway analysis, 4'HAP significantly inhibited HIF-1α pathway, and loss of HIF-1α stability was responsible for the effect since protease inhibitor MG-132 reversed the inhibiting effect of 4'HAP on *T. gondii* proliferation. Gene silencing of HIF-1α restrained the growth of *T. gondii* and inhibition of GSK3β, which is known to directly mediates HIF-1α degradation improved *T. gondii* proliferation. The cytokines IL-1β, IL-6 and TNF-α levels were significantly inhibited in the pre-treatment with 4'HAP, while, IL-10 level was dramatically increased. In addition, it is found that 4'HAP elevated intracellular ROS level by inhibiting Akt activity, followed by the NOX4 expression level increase.

Conclusions: The results suggest that GSK3β/HIF-1α & PI3K/Akt are indispensable for *T. gondii* growth and survival. 4-HAP is capable of suppressing *T. gondii* growth by inactivating HIF-1α or induce ROS generation. Our results indicate the pharmaceutical potential of 4'HAP as a candidate for anti-parasite drug for *Toxoplasma gondii*.

P126

Depolymerization of filamentous actin by LRRK2 negatively regulates actin dynamics of microglia

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Actin dynamics is the key feature of active migrating cells such as microglia of brain. Here, we report LRRK2, the major familial Parkinson's disease-associated gene, negatively regulates actin dynamics in microglia. By in vitro biochemical approaches, we showed the depolymerization activity of filamentous actin (F-actin) of LRRK2/Lrrk2 in either direct binding to the F-actin or an indirect pathway by inhibiting Rac-PAK signaling of microglia. Knockdown of Lrrk2 resulted in the reduced ruffle and enhanced lamellipodia formation of ADP-activated microglia, leading to the strong migration activity of microglia toward damaged cells. These results collectively suggest that the negative regulation of actin dynamics through LRRK2 is essential in inhibiting the large process elongation of stimulated microglia, moderating the response of micro-damaged site of the brain by microglia.

P127

Structural insights into CYP107G1 from Rapamycin-Producing *Streptomyces rapamycinicus*

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Rapamycin is a clinically important macrolide agent with immunosuppressant and anti-proliferative properties, produced by the actinobacterium, *Streptomyces rapamycinicus*. Two cytochrome P450 enzymes are involved in the biosynthesis of rapamycin. CYP107G1 and CYP122A2 catalyze the oxidation reactions of C27 and C9 of pre-rapamycin, respectively. To understand the structural and biochemical features of P450 enzymes in rapamycin biosynthesis, the *CYP107G1* and *CYP122A2* genes were cloned, their recombinant proteins were expressed in *Escherichia coli*, and the purified enzymes were characterized. Both enzymes displayed low spin states in the absolute spectra of ferric forms, and the titrations with rapamycin induced type I spectral changes with K_d values of 4.4 ± 0.4 and 3.0 ± 0.3 μM for CYP107G1 and CYP122A2, respectively. The X-ray crystal structures of CYP107G1 and its co-crystal complex with everolimus, a clinical rapamycin derivative, were determined at resolutions of 2.9 and 3.0 Å, respectively. The overall structure of CYP107G1 adopts the canonical scaffold of cytochrome P450 and possesses large substrate pocket. The distal face of the heme group is exposed to solvents to accommodate macrolide access. When the structure of the everolimus-bound CYP107G1 complex (CYP107G1-Eve) was compared to that of the ligand-free CYP107G1 form, no significant conformational change was observed. Hence, CYP107G1 has a relatively rigid structure with versatile loops to accommodate a bulky substrate. The everolimus molecule is bound to the substrate-binding pocket in the shape of a squeezed donut, and its elongated structure is bound perpendicular to a planar heme plane and I-helix.

▶ **Keywords:** P450, CYP, CYP107G1; *Streptomyces rapamycinicus*, rapamycin, everolimus, macrolide, X-ray crystal structure

P128

MicroRNA 34a-AXL axis regulates vasculogenic mimicry formation in breast cancer cells

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Targeting the tumor vasculature is an attractive strategy for cancer treatment. However, the tumor vasculature is heterogeneous, and the mechanisms involved in the neovascularization of tumors are highly complex. Vasculogenic mimicry (VM) refers to the formation of vessel-like structures by tumor cells, that can contribute to tumor neovascularization, and is closely related to metastasis and a poor prognosis. Here, we report a novel function of AXL receptor tyrosine kinase (AXL) in the regulation of VM formation in breast cancer cells. MDA-MB-231 cells exhibited VM formation on Matrigel cultures, whereas MCF-7 cells did not. Moreover, AXL expression was positively correlated with VM formation. Pharmacological inhibition or AXL knockdown strongly suppressed VM formation in MDA-MB-231 cells, whereas the overexpression of AXL in MCF-7 cells promoted VM formation. In addition, AXL knockdown regulated epithelial-mesenchymal transition (EMT) features, increasing cell invasion and migration in MDA-MB-231 cells. Finally, the overexpression of microRNA-34a (miR-34a), which is a well-described EMT-inhibiting miRNA and targets AXL, inhibited VM formation, migration, and invasion in MDA-MB 231 cells. These results identify a miR-34a-AXL axis that is critical for the regulation of VM formation and may serve as a therapeutic target to inhibit tumor neovascularization.

▶ **Keywords:** Breast cancer, Vasculogenic mimicry, Epithelial-mesenchymal transition, AXL, miR-34a

P129

Hypoxia-inducible factor 2α is a novel inhibitor of chondrocyte maturation

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Hypoxic environment is essential for chondrocyte maturation and longitudinal bone growth. Although hypoxia-inducible factor 1 alpha (Hif-1α) has been known as a key player for chondrocyte survival and function, the function of Hif-2α in cartilage is mechanistically and clinically relevant but remains unknown. Here we demonstrated that Hif-2α was a novel inhibitor of chondrocyte maturation through downregulation of Runx2 stability. Mechanistically, Hif-2α binding to Runx2 inhibited chondrocyte maturation by Runx2 degradation through disrupting Runx2/Cbfβ complex formation. The Hif-2α-mediated-Runx2 degradation could be rescued by Cbfβ transfection due to the increase of Runx2/Cbfβ complex formation. Consistently, mesenchymal cells derived from Hif-2α heterozygous mice were more rapidly differentiated into hypertrophic chondrocyte than those of wild type mice in a micro-mass culture system. Collectively, these findings demonstrate that Hif-2α is a novel inhibitor for chondrocyte maturation by disrupting Runx2/Cbfβ complex formation and consequential regulatory activity.

▶ **Keywords:** Hif-2α, Runx2, Cbfβ, Proteosomal degradation, chondrocyte maturation

P130

Cbfβ is an anabolic regulator for blocking osteoarthritis progression during aging

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Objective: Transcription and translation are frequently dysregulated in osteoarthritis. Core binding factor β (Cbfβ), a partner protein of the Runx family transcription factor, encodes Runx transcription activity to control endochondral ossification and bone formation. However, the role of Cbf β during osteoarthritis progression and the mechanism of Cbfβ action has not been well elucidated.

Methods: To explore the *in vivo* function of Cbfβ in articular cartilage, we generated articular cartilage-specific Cbfβ-deleted mice (*Cbfβ*$^{\triangle ac/\triangle ac}$) by crossing Gdf5 promoter-driven Cre mice with Cbfβ floxed mice. Surgical destabilization of the medial meniscus (DMM) was performed on both knees of 12-week-old male mice and severity of OA was determined by histological analysis according to the Osteoarthritis Research Society International (OARSI) guidelines. Spontaneous OA progression were performed in the *Cbfβ*$^{\triangle ac/\triangle ac}$ at the 12 months. To assess the role of Cbfβ in osteoarthritis progression, we conducted Type II collagen Mmp13 expression using Real time PCR, Immunohistochemistry and western blotting. Primary articular chondrocytes from the *Cbfβ*$^{\triangle ac/\triangle ac}$ mice hind limb joint at day 5-6 were used for mechanism identification.

Results: Expression of Cbfβ was decreased in the mouse OA or human OA compared to normal joints. Specific deletion of Cbfβ in articular cartilage resulted in down-regulation of Runx1, type II collagen and up-regulation of Mmp13 expression in articular cartilage tissues and progressive OA development in *Cbfβ*$^{\triangle ac/\triangle ac}$ mice at surgical induced OA or aging process OA. Mechanistically, Cbf β deletion inhibited Tgfβ transduced type II collagen expression through inducing Runx1 proteosomal degradation in articular chondrocytes *in vitro*. Rescue of Cbfβ stabilized Runx1 expression, therefore, increased Type II collagen expression and decreased MMP13 expression in Cbfβ -deficient articular chondrocytes.

Conclusion: These results indicate that Cbfβ acts as an anabolic regulator for maintaining articular cartilage integrity to protect from osteoarthritic cartilage destruction via stabilizing of Runx1 expression.

▶ **Keywords:** Osteoarthritis, Dysregulation, Core binding factor β, Runx1, proteosomal degradation

P131

TDAG51 is a negative regulator of PPARg-mediated adipocyte differentiation

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Adipogenesis is mainly induced by the coordinated interplay among transcriptional factors, such as CCAAT/enhancer binding proteins and peroxisome proliferator-activated receptor g (PPARg). PPARg, a member of the nuclear receptor gene family, acts as the master transcriptional regulator in adipogenesis. PPARɣ forms a heterodimer with retinoid X receptor (RXR), to form an active transcriptional complex. In this study, we identified T-cell death-associated gene 51 (TDAG51) as a novel negative regulator of PPARg-mediated adipocyte differentiation. Forced expression of TDAG51 inhibited adipocyte differentiation in 3T3-L1 cells. We identified that TDAG51 physically interacts with PPARg. In deletion mutant analyses, the region between residues 1 and 201 of the TDAG51 ia involved in the interaction with the region between residues 140 and 506 of the PPARg. The heterodimer formation of PPARg-RXRa was competitively inhibited in a ligand-independent manner by TDAG51 binding to PPARg. Thus, these results indicate that TDAG51, which could determine adipogenic cell fate, is a ligand-independent competitive inhibitor of PPARg in adipogenesis, expanding the importance of TDAG51 in the regulation in metabolic diseases, including obesity and diabetes.

P132

GJA1 depletion causes ciliary defects and abnormal laterality

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Cilia is essential for the embryonic development and physiological maintenance of the human body. Disruption of cilia formation or function caused syndromic disorder, ciliopathy, in humans. Gap junction alpha 1 (GJA1), also known as connexin 43, is a major subunit of gap junction, among connexin family. But mechanism and role of GJA1 in the formation and function of cilia is yet to be determined. In this study, we examined functions of GJA1 during ciliogenesis in RPE1 cells and *Xenopus laevis*. GJA1 is localized at the pericentriolar materials around primary cilium of RPE1 cells and the multi-cilia in *Xenopus* epithelial tissues. Knockdown of GJA1 showed decreased primary cilia formation frequency in RPE1 cells and caused severe malformation of motile cilia elongation and assembly in *Xenopus*. Moreover, knockdown of GJA1 in the gastrocoel roof plate (GRP) showed shorten GRP cilium length, which caused disrupted left-right asymmetry. Additionally, through IP-MS, we found putative GJA1 binding partners, which were previously reported to be critical for ciliogenesis. These findings suggest that GJA1 is necessary for proper ciliogenesis and axis specification during embryonic development.

P133

Study on the functions of ERAD pathway in cartilage formation

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Endoplasmic reticulum-associated degradation (ERAD) complex functions at the endoplasmic reticulum and removes misfolded and unfolded proteins using proteasome-mediated degradation. ERAD complex is composed of Sel1L, HRD1, EDEM1, and Derlin-1/2. ERAD pathway is critical to eliminate misfolded or unfolded protein to maintain ER homeostasis. Previously, we have shown that the central domain of Sel1L, which composed of 5 to 9 SLR motif, mediates oligomerization of Sel1L and oligomerization of Sel1L is necessary for the ERAD pathway. Also, Sel1L C-terminus, which composed of 10 to 11 SLR motif, is an HRD1 binding domain. In this study, we discovered that malfunction of ERAD pathway elevates ER stress and disrupts craniofacial cartilage development in a vertebrate. Furthermore, we show that ERAD genes are significantly downregulated in human OA patients. Also, the depletion of SEL1L in mouse articular tissues caused OA-like joint destruction. These data suggest that ERAD pathway is a critical disease factor for OA development.

▶ **Keywords:** ERAD, Cartilage, ER stress, Xenopus

P134

Developmental and molecular studies of the arms formation in *Octopus minor*

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Cephalopods (e.g. cuttlefish, nautilus, octopus, squid) belong to a class of the phylum Mollusca. In general, cephalopods as advanced invertebrates have interesting biological characteristics such as extraordinary rapid growth, short lifespan, large brain, and sophisticated sense organs with complex nervous system. *Octopus minor*, commonly called long arm octopus has eight arms, each of which also carry out common function and its own role. In this study, we performed the transcriptome analysis on the embryo of the *Octopus minor* in the development stage. We selected genes with very high expression level in each arm of the analysis. Based on gene data, we conducted molecular biological experiments such as *in situ* Hybridization, Immunohistochemistry and Histological analysis. These results are the first step to understanding the complex functions of the *Octopus minor*'s arms and will valuable resource for analyzing the functions of gene repertoires in various developmental phases.

▶ **Keywords:** *Octopus minor*, arms, arm formation, Transcriptome analysis, *in situ Hybridization*

P135

Developmental studies and head regeneration of *Perionyx excavatus*

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Regeneration is a biological process restoring lost or amputated body parts. The capability of regeneration varies among organisms, and the regeneration of the central nervous system (CNS) is limited to specific animals, including the earthworm, *Perionyx excavatus*. Thus, it is crucial to establish *P. excavatus* as a model system to investigate mechanisms of the CNS regeneration. Here, we set up the culture system to sustain the life cycle of *P. excavatus*, and characterize the development of *P. excavatus*, from embryo to juvenile, based on its morphology, myogenesis, and neurogenesis. During development, embryos have EdU-positive proliferating cells throughout the whole body, whereas juveniles maintain proliferating cells exclusively in the head and tail regions, not in the trunk region. Interestingly, juveniles amputated at the trunk, which lacks proliferating cells, are able to regenerate the entire head. In this process, a group of cells, which are fully differentiated, reactivates cell proliferation. Our data suggest that *P. excavatus* is a model system to study CNS regeneration, which is dependent on dedifferentiation of cells.

▶ **Keywords:** *Perionyx excavatus*, earthworm, embryonic development, head regeneration, juvenile

P136

Accumulation of mitochondrial *RPPH1* RNA is associated with cellular senescence

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Post-transcriptional gene regulation is an important step in the regulation of eukaryotic gene expression. Subcellular compartmentalization of RNA species plays a crucial role in the control of mRNA turnover, spatial restriction of protein synthesis, and the formation of macromolecular complexes. Although long noncoding RNAs (lncRNAs) are one of the key regulators of post-transcriptional gene expression, it is not heavily studied whether localization of lncRNAs in subcellular organelles has functional consequences. Here we report on mitochondrial lncRNAs whose expression fluctuates in the process of cellular senescence. One of the mitochondrial lncRNAs, *RPPH1* RNA, is overexpressed and accumulates in mitochondria of senescent fibroblasts, possibly modulated by the RNA binding protein AUF1. In addition, *RPPH1* RNA overexpression promotes spontaneous replicative cellular senescence in proliferating fibroblasts. Using MS2 aptamer-based RNA affinity purification strategy, we identified putative target mRNAs of *RPPH1* RNA and revealed that partial complementarity of *RPPH1* RNA to its target mRNAs prevents those mRNAs decay in proliferating fibroblasts. Altogether, our results demonstrate the role of mitochondrial noncoding RNA in the regulation of mRNA stability and cellular senescence.

P137

Structure and mechanism study of Npu intein for protein splicing

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Protein splicing has interesting merits to stabilize proteins and advantages on industrial application for many therapeutics and biocatalysts. Inteins from Nostoc punctiforme (Npu) DnaE has been widely used for the protein splicing due to the high activity. We study the structure and function relationship of inteins to increase the protein splicing activity. All inteins share common structural features such as a horseshoe-like pseudo two-fold symmetric fold, several canonical sequence motifs, and similar splicing mechanisms. The splicing efficiencies and substrate specificity of different inteins vary considerably, reflecting subtle changes in the chemical mechanism of splicing, linked to their local structure and dynamics. The understanding of structural and dynamical aspects of inteins is crucial for intein engineering and the improvement of intein-based technologies.

▶ **Keywords:** Npu inteins, protein splicing, protein stability, structure and mechanism

P138

In vivo evaluation of scaffolds compatible for colonoid engraftments onto injured mouse colon epithelium

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Colonoids are known to be similar to colon tissue in structure and function, which makes them useful in the treatment of intestinal de-epithelialized disease. Matrigel, which is used as a transplantation scaffold for colonoids, cannot be used clinical applications due to its undefined composition and tumorigenicity. This study identifies clinically available scaffolds that are effective for colonoid transplantation in damaged intestinal mucosa. The colon crypt was isolated and cultured from CAG-EGFP mice into EGFP+ colonoids and subsequently transplanted into the EDTA colitis mouse model using gelatin, collagen, or fibrin glue scaffolds. To identify scaffolds suitable for colonoid engraftment in injured colon mucosa, the success rates of transplantation and secondary EGFP colonoid formation were measured, and the scaffolds' mediated toxicity *in vitro* and *in vivo* were observed in recipient mice. When colonoids were transplanted with gelatin, collagen, and fibrin glue into the EDTA colitis mouse model, all groups were found to be successfully engrafted. Especially, Fibrin glue showed significant increase in engrafted area compared to Matrigel after 4weeks. The scaffolds used in the study did not induce colonic toxicity after transplantation into the recipients' colon and were thus deemed safe when locally administrated. This study suggests new methods for and provides evidence of the safety and utility of the clinical application of colonoid-based therapeutics. Furthermore, the methods introduced in this study will be helpful in developing cell treatment using the esophagus or a stomach organoid for various digestive-system diseases.

▶ **Keywords:** Colonoid, Fibrin glue, Collagen, Gelatin, Organoid transplantation

P139

Deficiency of early growth response-1 (EGR1) cause irregular decidual reaction during implantation

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A receptive environment of uterine endometrium suitable for embryo implantation is accomplished by the physiological-specific steroid hormonal balance and their receptors on endometrium. In mice, decidual reaction can induced after 4 day of pregnancy when embryos adhere to the uterine luminal epithelium. It include the change of shape from a fibroblast-like cell to an epithelioid-like cell, and accumulation of lipid and glycogen. In addition, a diploidy cell undergoes an endoreduplication cycle to become polyploidy. Previously, we showed the spatio-temporal expression of early growth response-1 (EGR-1) during pregnancy. EGR-1 is a zinc finger transcription factor belonging to the *Egr* family.. It well evaluated that the Egr1 is involved in cell proliferation and differentiation. Few groups showed the expression regulation by estrogen during decidualization but still is not fully evaluated its function during pregnancy. In this study, using the in vitro decidualization model, the role of *Egr1* in decidualization was studied. The molecular decidual markers *Dtprp*, and alkaline phosphatase activity were low in Eg1 null uterine stromal cells. The cytoplasmic accumulation levels of lipid and glycogen were also low compared with the wild type stromal cells. The cell shape index(CSI) was not different between null stromal cells and wild-type stromal cells. Interestingly, the Annexin V-PI positive cells were increased significantly in *Egr-1* nulled stromal cells. Even though, needed more study for the reason of decreased decidual response in *Egr-1* null stromal cells, those results suggest that *Egr-1* has a role in regulation of the decidual cell reaction.

P140

Reproductive characteristics of a new animal model for study of prion protein: Establishment of replaced bank vole Prnp knock-in ($Prnp^{hr(bvprnp\text{-}I109)cdpr2}$) mice

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Prions are infectious proteins that cause destructive neurodegenerative. It is composed of PrP^{SC}, a misfolded form of cellular prion protein (PrP^{C}). The PrP^{C} Inhere,thephysiologicalphenotype,expressionofprionproteingene(Prnp)invariousorgans,andreis a normal protein located on the exterior cell surface and is attached to the plasma membrane via a glycosylphosphatidylinositol (GPI) anchor. Prion transmission between species is limited by species barrier. To create a model with a low barrier between species, we generate knock-in mouse model which replaced with bank vole PrP^{C}(I109) included GPI anchor region ($Prnp^{hr(bvprnp\text{-}I109)cdpr2}$). In here, the physiological phenotype, expression of prion protein gene (Prnp) in various organs, and reproductive characters were evaluated on new model. Compared with wild type (WT), body weight was reduced on knock-in (KI) mice at 5 week. Whereas, the female KI mice was increase at 20 week. The expression levels of mouse and bank vole prion protein gene (PRNP) transcripts were screened with qRT-PCR in brain, heart, lung, liver, kidney, spleen, thymus, muscle, and reproductive tissue such as ovary and testis. There was no significant difference in the reproductive characteristics such as vaginal opening time after birth and cyclicity and period of estrus cycle between WT and KI. Average litter size of F1 generation was 5.65 and the sex ratio of pups was 1.101 : 1.00 (male : female) and followed Mendelian inheritance law. In summary, while the new model showed some physical differences, the others are not affected. Based on the results, it is expected that this new mouse model may contribute to the prion disease therapeutic agent discovery and the studying of the developmental role of PRNP.

▶ **Keywords:** Prion protein, Bank vole, Reproduction, Estrous cycle, Mendelian inheritance law

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Characteristics of replaced bank vole Prnp knock-in mouse in embryo development and fertility

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It is known that cellular prion protein can be cause of neural diseases and involved in embryogenesis. Cellular isoform, which is non-infectious PrP^{c} undergoes conversion to infectious PrP^{Sc} in neuronal cells and may modify the cellular signaling. Replacing KI is a useful model to evaluate the replaced gene. We generate knock-in animal model replaced the PrP^{c} mRNA coding with the bank vole PrP^{c} mRNA coding. There are a few isotype of cellular prion protein. In this study, the bank vole prion protein with 109 methionine was examined. We identified various reproductive character such as, estrous cycle, pregnant rate, the sex ratio and litter size of the pups. To evaluate the effect of PrPc on the developmental competence of the fertilized ooytes, in vitro cultrue were performed in the standard culture condition with agonist or antagonist. f knock-in mouse embryo, and analyzed the expression of some marker genes. The shorten diestruous stage was a character of KI mice. The average litter size was 6.31 and the sex ratio of pups wss 1.12 : 1.00 (male : female). Recombinant $bvPrP^{C}$ inhibit the development to the blastocyst. Amyloid inhibited the blastocyst development more severely than that of KI. Based on these results, it is suggested that prion protein may have the role for early stage embryo development with compensation factors.

▶ **Keywords:** Prion protein, early stage embryo, development, reproduction

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A study on the cryopreservation method and container development for stability of primary cells

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As various studies on primary cultured cells have progressed, techniques for isolation and culturing cells from tissues have also been developed remarkably. However, research on cell storage methods such as cryopreservation agents has been slowly developed compared to other parts. Recently, as the field of therapeutic drug development gets attention, devices for cryopreservation such as controlled rate freezer(CRF) or vapor-phase LN2 tank have been developed to maintain cell viability and prevent contamination. We observed temperature change inside and outside the cell storage container when the therapeutic products were moved to the vapor-phase liquid nitrogen tank after cooling down to - 80℃ ~ -90℃ using CRF. As a result, the difference in temperature decrease rate between the bottom side and the inlet side of the vapor-phase LN2 tank was large and also the cell storage container which interferes with the circulation of the vaporized nitrogen was a factor which hinders the stability of the cells. Therefore, suitable storage container and cryopreservation method for cell stability are needed in vapor-phase LN2 tank because it is an important reason for deciding the activity and efficacy of advanced bio-therapeutics products.

▶ **Keywords:** Primary Cells, Cryopreservation, Stability, vapor phase, liquid nitrogen tank, Storage container

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P143

RBM47-regulated alternative splicing of TJP1 promotes cell migration during epithelial-to-mesenchymal transition

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Epithelial-mesenchymal transition (EMT) is an important process in embryonic development, cancer metastasis, and organ fibrosis. Morphological and functional changes during the EMT process have been demonstrated to be regulated by alternative splicing. However, splicing factors involved in EMT and their regulatory mechanisms are largely unknown. Here, we showed that an isoform of tight junction protein 1 (TJP1), which is lacking exon 20, is predominantly expressed in cancer tissues, and that TGF-b induced EMT in A549 cells. In addition, the expression level of RNA binding motif protein 47 (RBM47) was downregulated by TGF-b treatment. We found that alternative splicing of exon 20 of TJP1 was regulated by RBM47. Biochemical studies revealed that RBM47 promoted the inclusion of exon 20 via its direct binding to (U)GCAUG sequence in the downstream intronic region of exon 20. We confirmed that RBM47 competes with Rbfox2 for the (U)GCAUG sequence, which has been demonstrated to be a binding motif for the Rbfox family proteins, even though Rbfox2 has been shown to be irrelevant in the regulation of TJP1 splicing. Furthermore, we examined several genes that contain the (U)GCAUG sequence in a downstream intronic region of an alternative exon. The inclusion of these alternative exons were increased due to the overexpression of RBM47. Finally, we found that phenylalanine residues (amino acid 115 in RBM47) within the first RRM domain among three RRM domains were critical for its binding to the pre-mRNA of TJP1. Taken together, we demonstrated the regulatory mechanism for the alternative splicing of TJP1 pre-mRNA by RBM47 during EMT, thus providing a basis for studies related to EMT modulations in diseases involving cancer metastasis and fibrosis.

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Dual-mode detection of miRNA based on graphene oxide

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Graphene oxide (GO), one of the most widely used 2-dimensional materials, is an oxidized version of graphene and is laced with oxygen-containing groups. It has been utilized in numerous fluorescence biosensors of nucleic acids because of its strong affinity for single-stranded nucleic acids and efficient fluorescence quenching capability. In this study, we established an advanced GO-based fluorescence/colorimetric dual sensing platform for miRNA by employing a newly designed probe in an existing fluorescence platform. The probe was designed to form a hairpin-like configuration with a fluorescent dye-labeled long tail, possessing a G-rich DNAzyme domain in loop region and target binding domain over the stem region and tail. This platform enables sensitive fluorescent miRNA detection even below the nanomolar levels as well as visual detection by direct observation in a single solution without an additional separation step.

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Development of zebrafish lexA-inducible Ab-SPOP system

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The targeted protein degradation system 'Ab-SPOP' has been recently developed in our lab to regulate gene expression at the protein level. Ab-SPOP is comprised of nanobody and SPOP that is the adapter protein of the curling-ring E3 ubiquitin ligase complex, and was shown to have the rapid ubiquitination and degradation effects of target nuclear proteins in zebrafish embryos and animal cells. Zebrafish is an ideal animal model to study early development and organogenesis through imaging with its rapid development and transparency during embryogenesis. In this study, we generated the inducible transgenic zebrafish of which gene expression is controlled using the SPOP synthetic ligase to efficiently degrades a target protein using its nanobody in vivo. We added a LexA system under the cmlc2 promoter to induce Ab-SPOP expression in the heart during a desired time. Our results show the sustainable maintenance of target expression through generations using the inducible transgenic lines.

P146

I-pesticide causes microcephaly in zebrafish development

Giyoung Lee[p,1], Anamika Wardatul Jannat[2], and Yun Kee[c,1,3]

[1]Division of Biomedical Convergence, College of Biomedical Science, Kangwon National University, Chuncheon 24341, Korea
[2]Department of Molecular Bioscience, College of Biomedical Science, Kangwon National University, Chuncheon 24341, Korea
[3]Interdisciplinary Graduate Program in Environmental and Biomedical Convergence, Kangwon National University, Chuncheon 24341, Korea

Understanding the basis of neurological disorders related to prenatal exposure to harmful environmental chemicals requires the precision analysis to reveal the unseen neurobehavioral toxicity at the organism level. Zebrafish larvae is small and transparent allowing the high-throughput larval behavior analysis and the live imaging of anatomical malformations in organ development during early development. Here we investigated the neurodevelopmental toxicity of I-pesticide, which is widely used in agriculture worldwide, using zebrafish as animal model. The behavioral monitoring revealed the abnormal larval behavior in a concentration-dependent manner. To identify the basis of the neurobehavioral toxicity of the substance, we combined the traditional teratogenicity testing with advanced imaging technology including the light-sheet microscopy and revealed the I pesticide-specific neurodevelopmental defects including microcephaly, implicating the risk associated with prenatal exposure to the environmental substance in humans and wildlife animals.

P147

Assessment of the neurodevelopmental toxicity of D synthetic compound using zebrafish

Amit Banik[p,1] and Yun Kee[c,1,2]

[1]Interdisciplinary Graduate Program in Environmental and Biomedical Convergence, College of Biomedical Science, Kangwon National University, Chuncheon 24341, Korea
[2]Division of Biomedical Convergence, College of Biomedical Science, Kangwon National University, Chuncheon 24341, Korea

D synthetic compound is a fungicide that is widely used in the agriculture field. It has been shown that the necrotic cell death occurs in Saccharomyces cerevisiae treated with D synthetic compound. Zebrafish larvae are small and transparent allowing high-throughput behavior analysis and live imaging of organ development. The goal of the present study is to investigate the neurotoxic effect of D synthetic compound to human and wildlife, and morphological and neurobehavioral changes were monitored in the developing zebrafish embryos treated with D synthetic compound. The results showed D synthetic compound caused the early developmental defects including the short body length, small eye and otic structure, reduction in muscle mass and altered locomotor activity in the zebrafish larval development. Interestingly, exposure to D synthetic compound dramatically reduced the hindbrain interneuron in the larval brain while the early neurogenesis was intact, implicating that this chemical may alter the neuronal differentiation of the specific cell type, causing the possible neurological disorder.

후원업체 광고

thermoscientific

써모피셔사이언티픽

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FAQ

Q1. 새로운 실험실을 개관하고 싶은데 관련 지식이 없어 막막합니다.

써모피셔 사이언티픽에서는 바이오 벤처 기업의 인재 육성을 위해 관련 교육을 제공하고 있습니다. 언제든지 문의 주시면 스타트업, 연구 분야와 관련된 교육을 제공해드리겠습니다.

Q2. 비용절감 효과는 어떤가요?

신규 연구에 있어 비용절감은 무엇보다 중요합니다. 절대적인 구매비용은 물론 각 단계별로 최적의 조건, 상품을 찾는 탐색비용이 줄여드립니다. 이는 상담과정에서 직접 확인해 보실 수있습니다. 이러한 절감효과가 중첩되어 고객의 순이익을 증대시켜드릴 것입니다.

Q3. 한꺼번에 많은 과정을 처리하려면 계약과정이 복잡하지 않은가요?

고객의 연구목적에 맞는 이상적인 실험실 구축을 위해서는 많은 단계들이 필수적으로 소요됩니다. 뉴랩스타트업 팀이 까다롭지만 반드시 짚고 넘어가야 하는 조항들을 더욱 꼼꼼하게 챙겨드리겠습니다.

표준 계약서를 기반으로 변경이 필요한 조항을 고객 상황에 맞추어 수정할 수 있습니다. 이는 각 단계 별로 여러 업체와 다수의 계약을 진행하는 것에 비해 더욱 효율적입니다.

홈페이지에서 자세한 정보를 확인하실 수있습니다

nlsu@thermofisher.com
더 많은 정보가 궁금하시다면 써모피셔사이언티픽 뉴랩스타트업 팀에 문의하세요.

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- 기존 실험실을 이전하거나 혹은 확장을 원하시는 분
- 바이오텍, 제약 및 학교 실험실 등에서 위와 같은 일들을 하고자 하시는 분들

이제 경쟁 우위의 솔루션을 직접 만나보세요.

Youtube 영상으로 더욱 쉽게 확인해 보세요.
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01 Minimum Vibration

무진동 환경을 제공함으로서 세포성장의 최적환경 제공

02 Infrared CO_2 sensor

습도에 영향을 받지 않는 IR sensor를 통한 보다 정확한 CO2 농도 측정, 고온 멸균 프로세스시 센서 제거 불필요 (AutoZero 기능)

03 Advanced Direct Heat system

4 개의 독립 히팅 컨트롤러,
-> 최고의 정확성
6개 표면 모두 부착된 73미터의 열선 -> 최고의 균일성

04 Fully removale shelving system

완전히 제거 가능한 shelving system을 통해 확실한 멸균작업을 진행가능

05 Fanless construction

열대류를 이용한 부드러운 공기 순환을 통한 시료증발 및 스트레스 최소화

06 Seamless Chamber with rounded angles

라운드 코너의 하나의 챔버는 청소의 편리성, 강한 부식의 저항성, 최대의 오염방지효과 제공

07 High Temp Decontamination Cycle

고온 (125 ℃) 멸균싸이클을 통한 완전한 멸균

강산과학 충청남도 천안시 동남구 해솔2길 17
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Homepage. Kangsansci.com E.mail. Kangsanbio@naver.com

Kangsan Science

생물발광 단백질 센서를 이용한 광역학 치료 연구

한양대학교 생명과학과 김영필 교수
(Tel: 02-2220-2560, E-mail: ypilkim@hanyang.ac.kr)

개요

1. 한양대 나노바이오 연구실 소개

Aptamer-Based Sensors/Regulators

- **GNP-SELEX**
  : Hormones (endocrine, growth, and disruptors)
- **Cell-SELEX** (with FACS/MACS)
  : Dendritic cells (CD11c+/–)
  : Astrocyte (for direct conversion to Neuron)

Cancer-Targeted Therapy

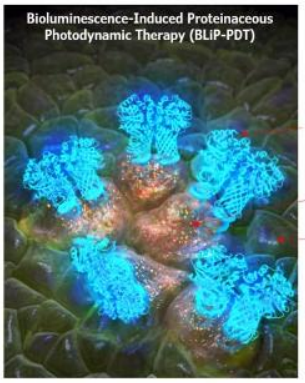
- **Light-Activated Photodynamic Therapy**
  : Bioluminescence or UCNP-driven cancer therapy
- **Protein Delivery**
  : Cyclized proteins, Mt/ER-target, and nanomaterials

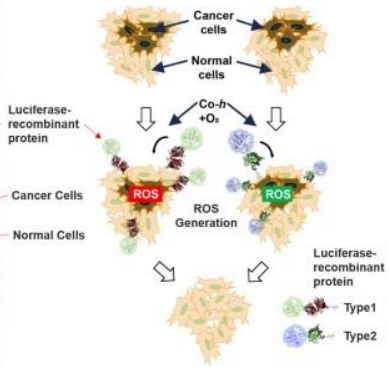
Molecular Imaging/Labeling

- **Targeted Cell Imaging**
  : Dopamine-induced amplification imaging
- **Intracellular/Extracellular Reporters**
  : FRET/BRET reporters
- **ROS-Mediated Protein Proximity Labeling**

2. 생물발광 기반 광역학 치료법 소개

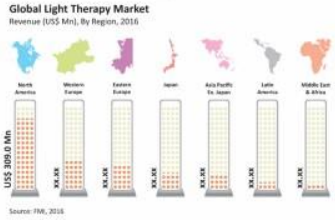
Bioluminescence-Induced Proteinaceous Photodynamic Therapy (BLiP-PDT)

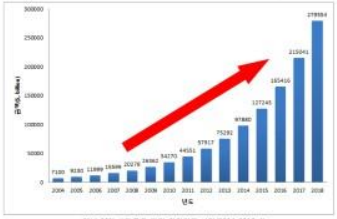




Sci. Adv. **2020**, 6(37); ebaba3009

암 치료를 목표로 하는 광감각제의 시장은 매년 30% 성장률을 보임.
광감각제 암치료 시장은 2004년 $7,100billion으로 2018년 $270,000billion 예상.





주요 연구 내용

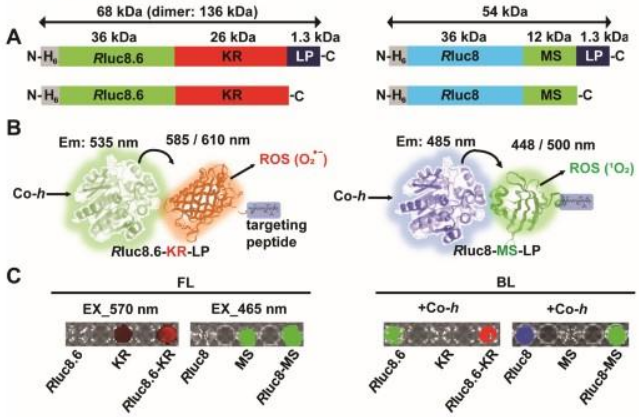
1. 현 광역학 치료법의 문제점

- 화학적 광민감제 (photosensitizer; PS)의 느린 생체 분해 속도 및 체내 축적
- 강한 광조사 (light irradiation) 필요 및 낮은 조직 투과성
- 광민감제의 암조직 주변 passive targeting

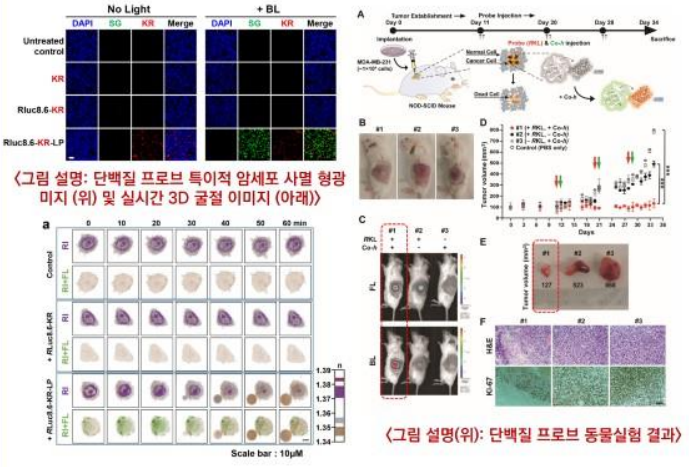
2. 연구 목표

- 빠른 분해와 높은 ROS발생 효율 단백질 광민감제 사용: Protein photosensitizer
- 외부 광조사가 필요 없는 생물발광 원리 적용: Bioluminescence (BL)
- 암세포/조직 특이적 전달체 구성: Cancer cell receptor-targeting ligand

3. 연구 결과



〈그림 설명(위): 단백질 프로브 구성, 발광단백질 + 광수용체 단백질 + 암세포표적 펩타이드〉



〈그림 설명: 단백질 프로브 특이적 암세포 사멸 형광 미지 (위) 및 실시간 3D 굴절 이미지 (아래)〉

〈그림 설명(위): 단백질 프로브 동물실험 결과〉

4. 기대효과 및 활용방안

- 다양한 암종류에 선택적인 치료기술로서 확대
- 병원균 및 감염성 질환 치료에 응용
- 생물발광을 이용한 유전자/약물 전달체로 활용
- 치료이외에 ROS를 이용한 조직재생 및 제어 기술로서 활용

한국연구재단 중견연구자 지원사업 (No. 2019R1A2C2004858)

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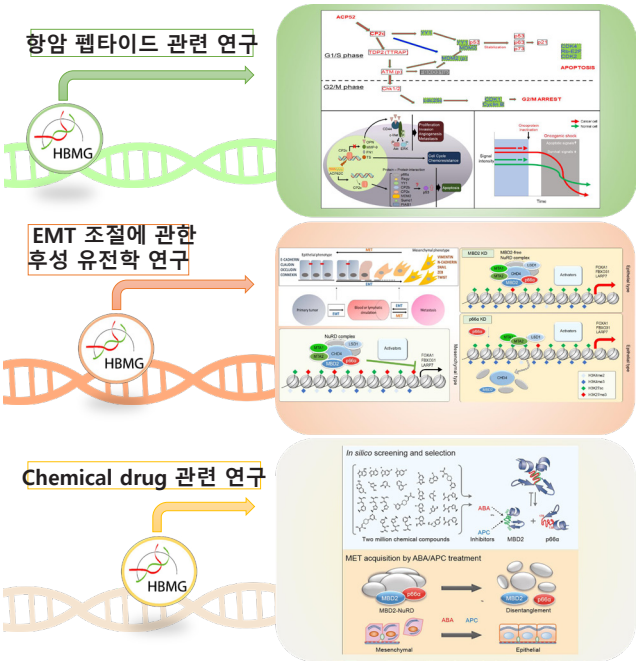
Dept. of Life Science in Hanyang University

크로마틴 리모델러와 암줄기세포의 가소성

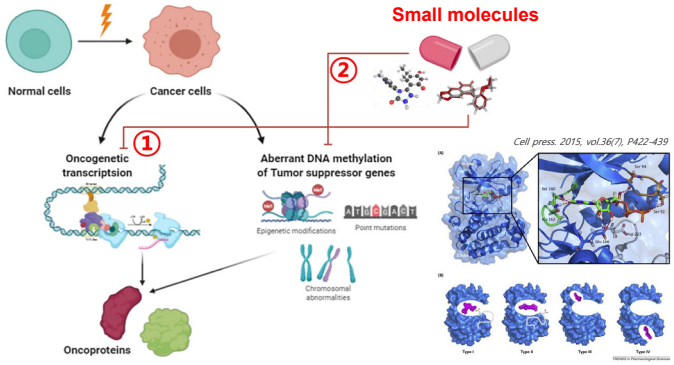
한양대학교 생명과학과 김철근 교수
분자유전학연구실
(Tel: 02-2220-0957, E-mail: cgkim@hanyang.ac.kr)

개요

1. 한양대 분자유전학 연구실 소개



2. 종양 유전자 전사/발현 억제제 개발연구 소개



Small molecules ① Inhibitor of Oncogenic Transcription Factor
② Epigenetic Modulators (Activator/Inhibitor)

- 암의 형성 및 유지에 관여하는 전사조절인자들의 다양한 기능이 보고됨
- 전사조절인자 표적 약물 개발이 다방면으로 진행중
  - Protein-Protein interaction disruption
  - Proteasome mediated degradation modulation
  - Protein-DNA interaction disruption

- 유전자발현조절에 관여하는 후성조절인자의 종류와 기능의 다양성
- 암에서 후성조절인자 (염색체 리모델링 복합체; NuRD 및 BAF complex)의 기능
  - BAF complex: Tumor suppressor & oncogene으로 작용

연구내용

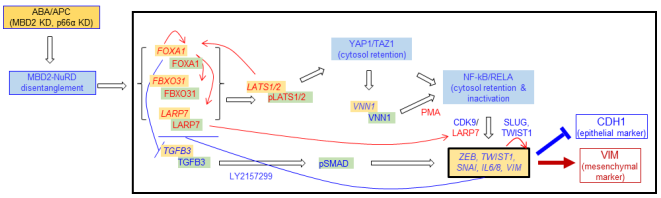
1. 배경

- 암 전이와 암줄기세포: 암줄기세포와 암 전이의 관련성
- 암줄기세포 가소성(EMT/MET)과 후성유전적 조절
- 후성유전적 조절에 관여하는 크로마틴 리모델러

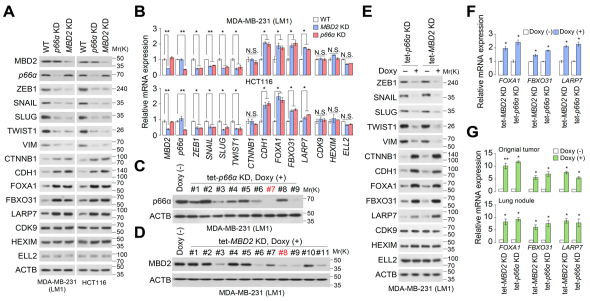
2. 연구 목표

- NuRD 크로마틴 리모델러 경유 CSC 내재성 EMT/MET circuit 확인과 검증
- EMT/MET circuit 에서 BAF 크로마틴 리모델러 및 PRC 복합체의 역할 규명
- EMT/MET circuit 조절 크로마틴 리모델러 인자의 Druggability 분석

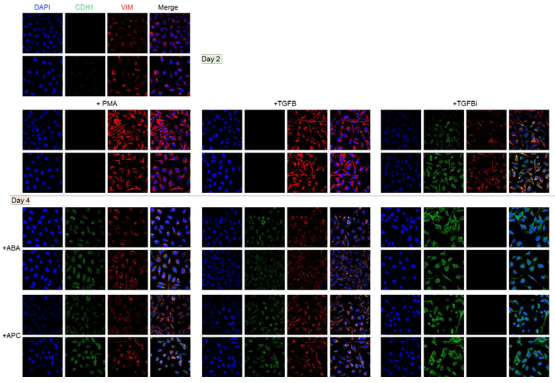
3. 연구 내용 및 결과



< MBD2-NuRD 크로마틴 리모델러 경유 EMT/MET circuit 가설>



< MBD2-NuRD 기능 억제에 따른 EMT/MET circuit 상의 유전자 위상 분석 >



< EMT/MET circuit 상의 signal 조절에 따른 세포의 marker 분석 >

4. 기대효과 및 활용방안

- 암줄기세포에서의 MBD2-NuRD 발현 억제 기반 EMT/MET circuit 검증
- Mi-2/NuRD 와 BAF 및 PRC 복합체의 상호작용 및 역할 분석의 연구적 독창성
- 기존 암치료제와 차별화된 암줄기세포의 가소성을 조절하는 암 전이 억제제 개발

한국연구재단 중견 연구자 지원사업 (No.2020R1A2C2009112)

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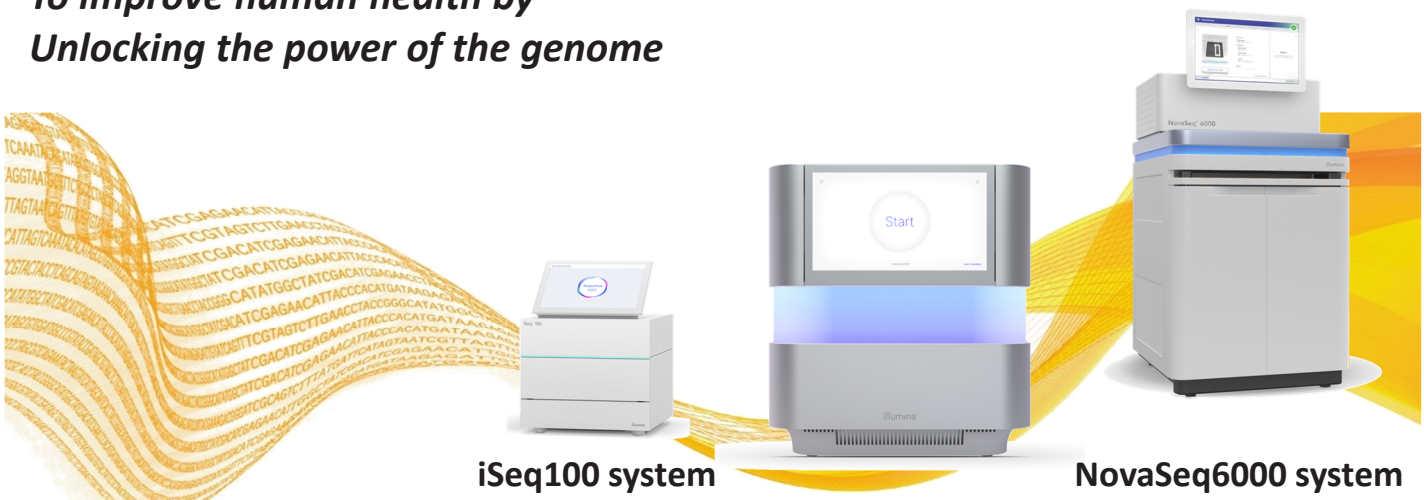

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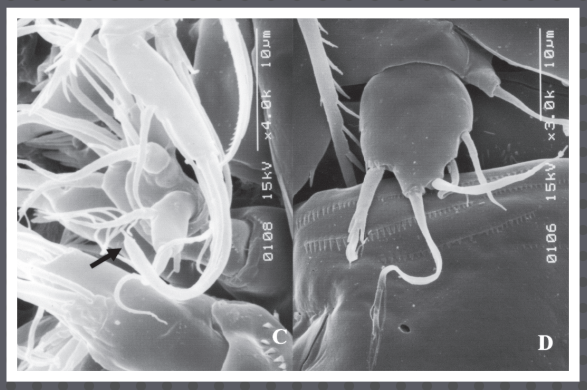
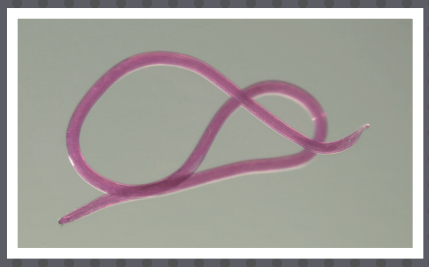
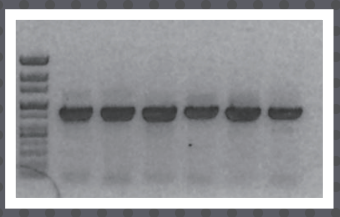
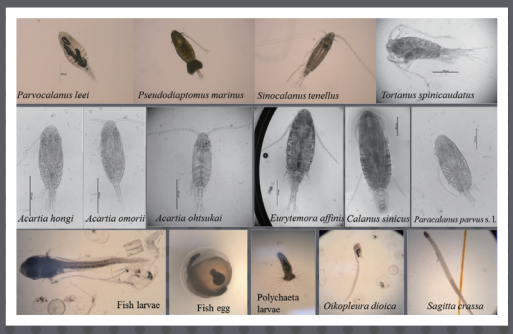
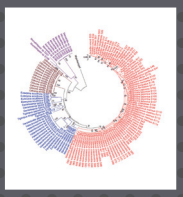
Contact)
E-mail) nextgene@nextgene.co.kr
Tel) 042-823-9353~4 / Fax) 042-823-9351











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RNA Genomics Lab.

한양대학교 생명과학과 최준호 교수

(Tel : 02-2220-0966, E-mail : jcho2711@hanyang.ac.kr)

Lab members

Graduate Student 한승훈

Undergraduate Student 신희식, 송인영

LETTER 2018 nature

mRNA circularization by METTL3–eIF3h enhances translation and promotes oncogenesis

▶Cancer Discovery 지에 소개됨(2018.09)
METTL3 promotes mRNA Translation to Drive Tumorigenesis

2016 Molecular Cell

The m^{6}A Methyltransferase METTL3 Promotes Translation in Human Cancer Cells

Shuibin Lin[1,2,*], Junho Choe[1,2,*], Peng Du[1,2], Robinson Triboulet[1,2], and Richard I. Gregory[1,2,3,4,5]

▶Cancer Discovery 지에 소개됨(2016.05)
The RNA Methlytransferase METTL3 Promotes Oncogen Translation

2020 CellPress REVIEWS

Review

Molecular Mechanisms Driving mRNA Degradation by m^{6}A Modification

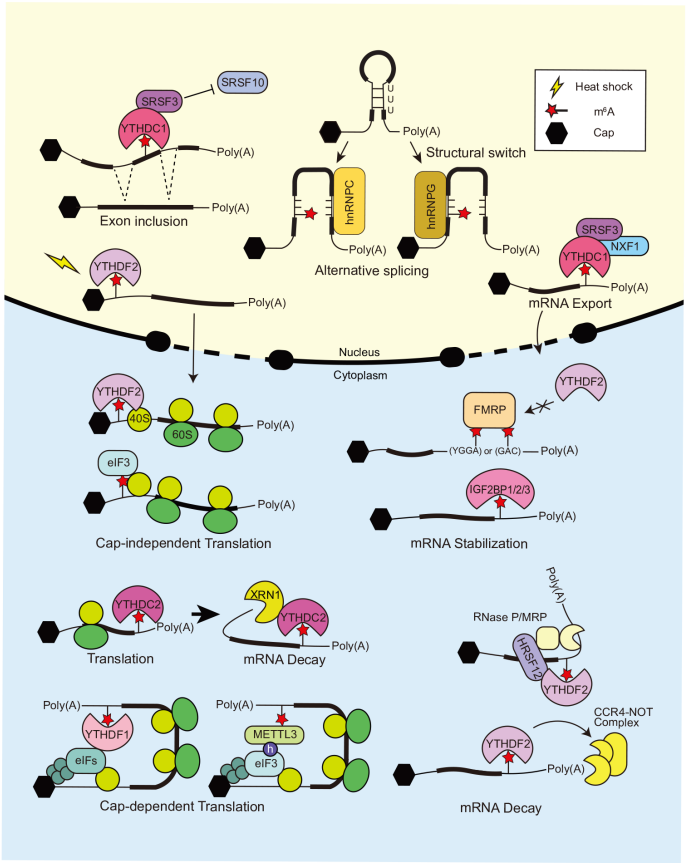
Yujin Lee,[1,2,3] Junho Choe,[3,4,5] Ok Hyun Park,[1,2] and Yoon Ki Kim[1,2,*]

EMM Experimental & Molecular Medicine 2020

REVIEW ARTICLE Open Access

Diverse molecular functions of m^{6}A mRNA modification in cancer

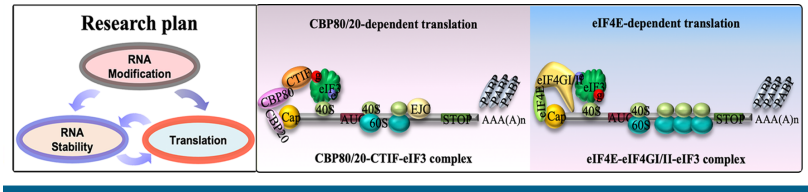
Seung Hun Han[1,2,3] and Junho Choe[2,3]



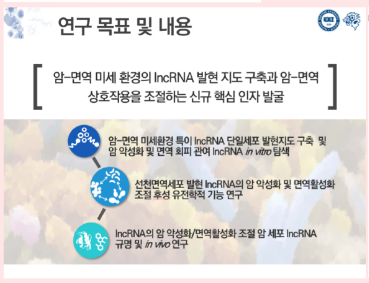
:연구분야 (Research field)

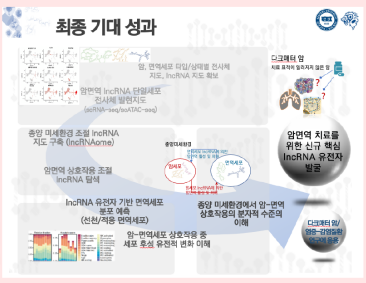
☛ RNA 유전체 연구를 통한 유전자 발현 조절 기전 연구

1. RNA 후성유전체학 (Epitranscriptomics)
2. mRNA 안정성 조절 및 단백질 발현 조절 기전 연구
3. 유전자 발현 조절을 통한 종양형성 (Tumorigenesis) 연구
4. 마우스 배아줄기세포에서의 유전자 발현 조절을 통한 다능성 (pluripotency) 및 분화 (differentiation) 조절 기전 연구



기초연구실 (Basic Research Laboratory)





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(Oxy-hemoglobin Method)

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(Spherical Gold Nanoparticles Method)

피어스 래피드 골드 BCA 정량화
(Pierce Rapid Gold BCA Method)

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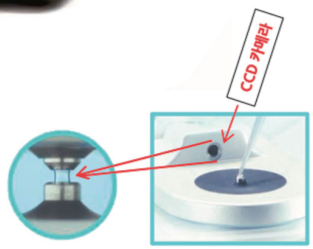
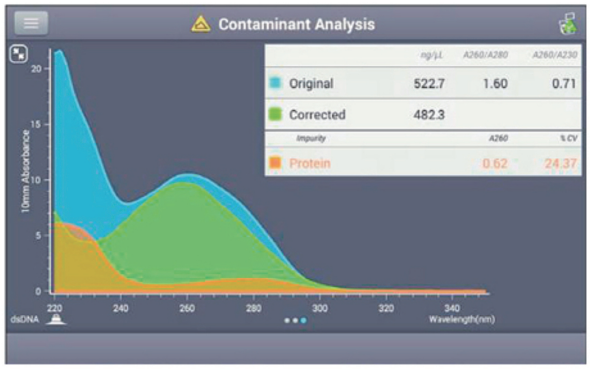
- **Walk-Up Convenience**
  고해상도의 터치스크린과 인터페이스를 독립형 장치에 담아 연구원 여러분들의 소중한 시간과 공간을 절약해드립니다.
- **Minimal Sample Preparation**
  Dynamic range(0.2 – 27,500ng/μL dsDNA)에서의 측정이 가능하기 때문에 샘플 농도에 대한 사전 지식이나 희석이 필요 없습니다.
- **Versatile Data Management**
  Thermal printer 혹은 tag를 이용하여 결과를 인쇄하시거나 USB, Ethernet, 컴퓨터를 통해서 자유로운 데이터 이동이 가능합니다.
- **★Acclaro Sample Intelligence**
  내장된 CCD 카메라로 오염을 감지하고, 샘플 칼럼의 버블 유무를 확인하여 troubleshooting을 위한 sample quality 정보를 feedback해드립니다.



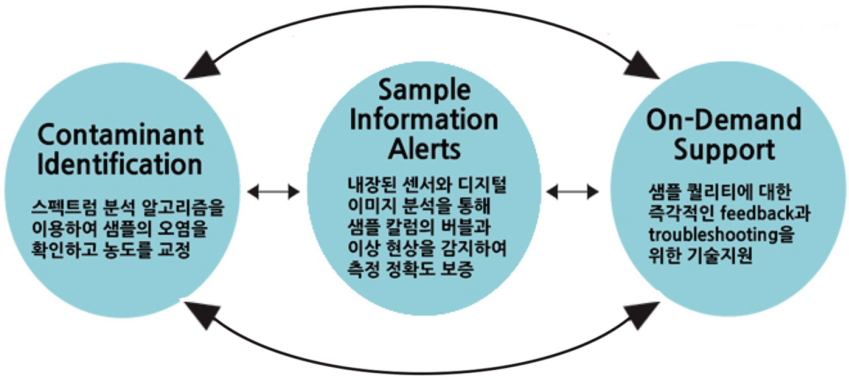
측정 화면에서 여러 개의 샘플을 한 번에 확인할 수 있습니다.
Acclaro가 dsDNA 3번 샘플에서 오염을 감지한 것을 알 수 있습니다.

Acclaro contaminant alert



dsDNA샘플이 protein 오염되어 있을 경우, original result(blue)로부터 protein absorbance 값(orange) 부분이 빠지고 정확한 dsDNA 농도 값(orange)이 얻어집니다.

★Acclaro란??



★ 분광광도 구매시 꼭 체크해야될 사항 ★

1. 샘플에 페놀같은 오염물질이 섞여있는지 확인할 수 있는 장비인지
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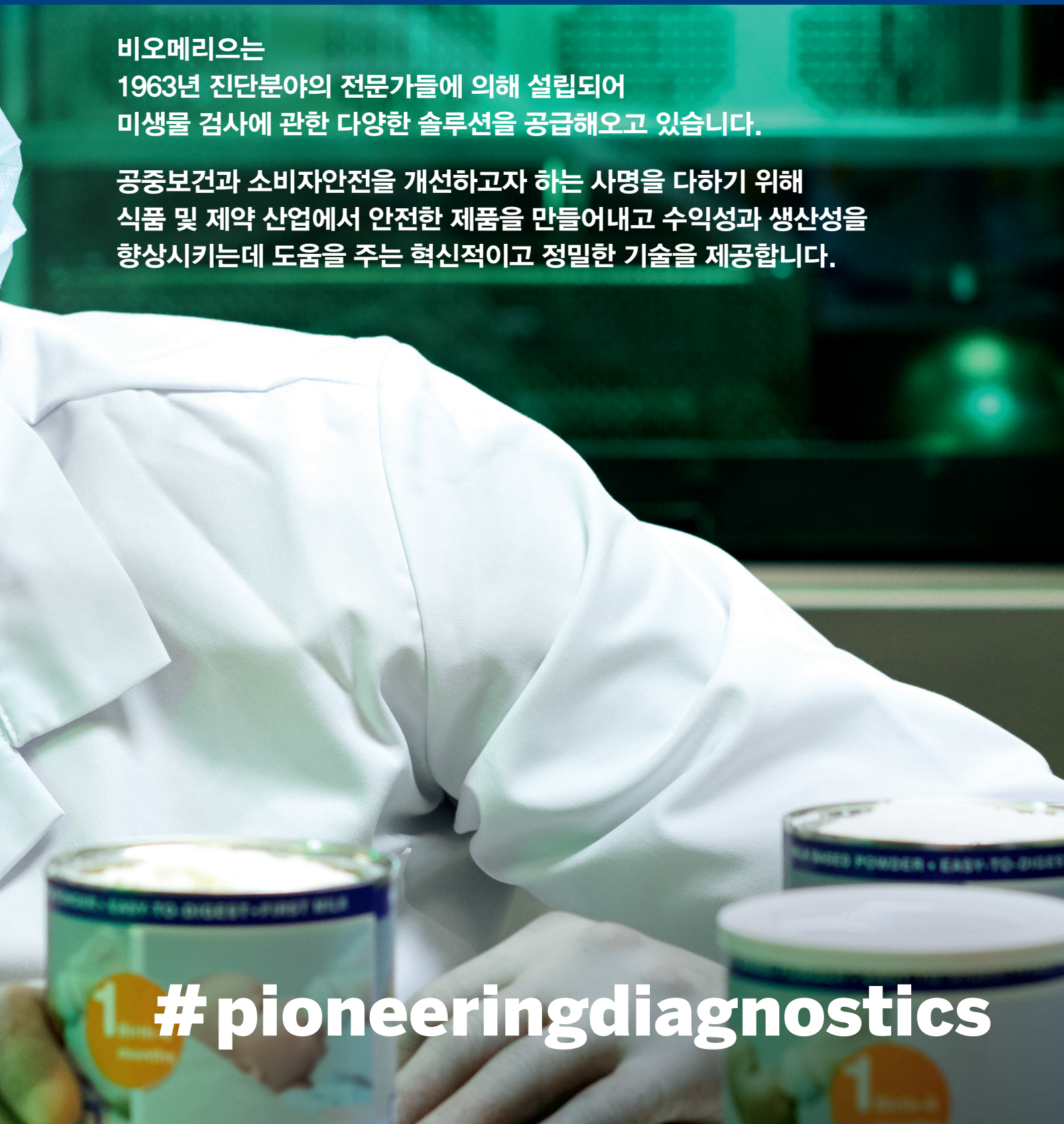

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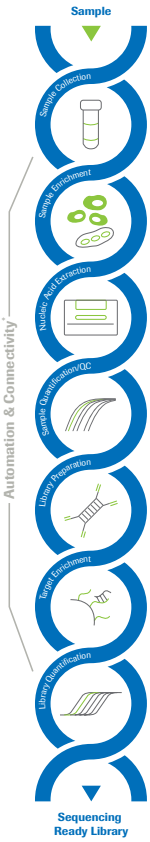
Roche Sample Prep Solutions for RNA-Seq

Sequence what matters



KAPA RNA Hyper/Library Prep

NGS workflow에서 가장 첫번째 단계는 샘플의 잠재력을 풀어내는 열쇠와 같은 단계입니다. 소중한 NGS Sample로부터 더 많은 정보를 얻어내기 위해서, 샘플이 성공적으로 library 제작까지 잘 진행되는 것이 매우 중요합니다. 로슈의 Sample Prep solution은 다양한 샘플 타입과 RNA-Seq application에서 증명되었고, 간단하며 완성형입니다.

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- 적은 input 양과 degraded 된 어려운 샘플에서도 높은 Success rate
- RNA부터 Sequencing 에 바로 사용 가능한 library 제작까지 모든 과정을 아우르는 Service &Support

Cat. No	KAPA Code	Description	Kit Size
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8098123702	KK8581	KAPA mRNA HyperPrep Kit	96rxn
8098140702	KK8561	KAPA RNA HyperPrep Kit with RiboErase (HMR)	96rxn

*Products in development
Data on file. PMR-200714T113719
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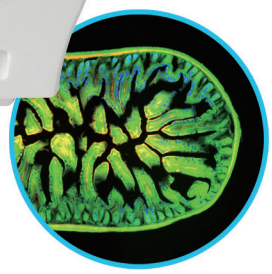
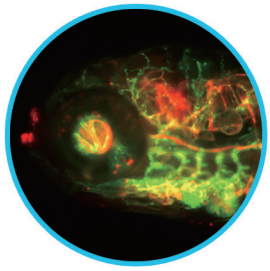
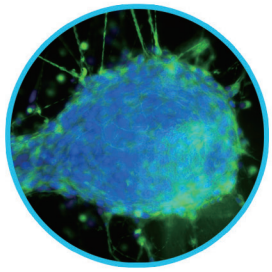
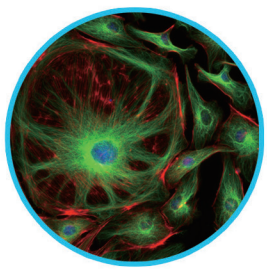
cell imaging multi-mode readers

Seeing is Believing


4x Mouse kidney


4x Zebrafish


20x Neurite 3D image


20x BPAE Cells

BioTek Cytation5는

이미징과 Microplate Reading 기능이
하나로 통합된 시스템으로 **High Contents Screening,**
3D Cell Culture 이미징, Live cell Imaging등
다양한 Application 수행과 전문분석이
가능한 기기입니다.

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