Quantitative field surveys for the selection of biological control agents for *Genista monspessulana,* based on host range and efficacy assessment

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Summary

Surveys for potential biological control agents of weeds provide opportunities to collect detailed quantitative data on the community structure of phytophagous species associated with particular plant species and their close relatives. Such studies are still few and far between, but offer increased understanding of assemblage rules of species with different degrees of host-plant specialization and the numbers and abundances of species in different feeding guilds. Including a range of closely related host plants also allows comparison of natural enemy community structure across similar host-plant species with different local abundances and regional distributions. When such surveys also measure agent impact, they allow agent selection to be based on efficacy as well as specificity. The preliminary results of quantitative surveys of natural enemy communities on species in the tribe Genisteae, particularly *Genista monspessulana* (French, Montpellier or Cape broom), around the Mediterranean, are presented. Sampling consisted of fixed beating-tray samples on up to ten individual flowering plants per site. Seed pods were also collected from the plants when they matured, and then dissected to quantify attack and abundance of seed feeders. Insects collected were sorted to species, and counted and analyzed for species diversity by site and region. Sample sites were selected based on the co-occurrence of two to several host-plant species to allow comparison of host use and abundance. Analysis of the preliminary results is discussed together with the value of quantitative field surveys in biological weed control.

Keywords: agent selection, insect–plant interactions, natural enemy communities, seed predation, species abundance.

Introduction

Surveys of potential biological control agents for weeds are most frequently made by qualitatively listing the natural enemy species found on the target, and perhaps co-occurring species in the same genus, during trips throughout its native range, together with simple descriptions of known feeding habits, likely specificity from literature records and geographical distributions (e.g. Zwölfer 1963), or by listing sites where each insect was sampled (O'Donnell 1986). Syrett & Emberson (1997) extended this approach to quantita-

tive sampling of insects on plants in full flower on all co-occurring species in the same tribe as the target, and analyzing these data to look at likely specificity of the main insects found. For more precision, sampling can then be focused on one or a few sites where agent damage (Hosking 1995) and abundance (Mazay 1993) can be measured more precisely. These approaches allow information on the abundances, specificity and damage levels of the different natural enemies in the community to be relatively quickly obtained without investing years on the detailed ecology of the system (e.g. Waloff 1968).

Quantitative sampling of the invertebrate communities on several closely related hosts also provides explanations of the effects of host-plant phylogeny, architecture, spatial pattern and abundance on natural

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enemy species richness (Lewinsohn 1991, Lawton *et al*. 1993), species packing (Zwölfer 1987, Lawton 1990), guild structure and levels of specificity (Frenzel & Brandl 1998, Prado *et al*. 2002). Such data sets can also be used to explore community assemblage rules (Gaston & Lawton 1990, Hanski & Gyllenberg 1993) and to compare the structure of native communities with those newly developed in the exotic range (Lawton 1982, Moran & Southwood 1982, Memmott *et al*. 2000). Despite this, very few quantitative data sets exist of natural enemy communities across a group of closely related hosts with associated records of abundance, guild structure and specificity that can help understand whether these communities evolved through sequential adaptation or competition (Frenzel & Brandl 1998). Biological-control surveys provide a great opportunity to collect such data to help explain how and why natural enemy communities differ between closely related host plants (Zwölfer 1987)

In this paper, we present the preliminary results of a quantitative survey approach adopted for natural enemies on plants in the tribe Genisteae in the Mediterranean region focused around the target *Genista monspessulana* (L.) L.A. Johnson. This approach goes one step further in complexity than previous studies (e.g. Syrett & Emberson 1997), by attempting to combine field assessment of host range, abundance and damage across the whole native range of the target, thereby incorporating host range and efficacy as equally important in the agent selection process (McFadyen 2003, Sheppard 2003). At each site, quantitative data were separately collected per plant of the natural enemy community present from all plant species in the tribe during peak flowering and within mature seed pods. The specific aim was to develop a prioritized list of potential biological control agents for use against *G. monspessulana* and other widespread Mediterranean weeds in the Genisteae. This approach also provides an opportunity to explain how the phytophagous community attacking species in the Genisteae is organised in relation to local differences in host frequency, abundance and geographical distribution.

Materials and methods

Literature search

To complement the published species lists from previous biological control survey trips against target weeds in the Genisteae (e.g. Zwölfer 1963, O'Donnell 1986, Syrett & Emberson 1997, Syrett *et al*. 1999), a standard online literature search was made of CABI Abstracts and Zoological Record for all references containing the key words either *Genista, Cytisus* or *Ulex*, as well as searching the standard taxonomic reference books on the phytophagous arthropods and plant pathogens of Europe. The results of the literature search was used, in combination with the comparative quantitative survey data, to generate a list of stenophagous to monospecific arthropods found on *G. monspessulana* during field surveys. It was also used to list those genera where separate species are known to occur on *G. monspessulana*, *Cytisus scoparius* (L.) Link and *Ulex europaeus* L.

Surveys

Conventional survey trips were carried out throughout most of the native distribution of *G. monspessulana* around the Mediterranean, on the north coast from Greece to Portugal, and to Tunisia on the south coast. Areas intensively searched were typical native habitat, i.e. rainfall 600+ mm per annum, less than 1000 m altitude on acid soils that support oak or pine-overtopped maqui vegetation. A separate trip was made to Tenerife and Gomera in the Canary Islands, because, while *G. monpessulana* does not occur there, these islands are a centre for diversification of very closely related *Genista* spp. (= *Teline*), including the exotic weed *Genista stenopetala* Webb & Berth (Percy 2003), and the only native range of *Chamaecytisus proliferus* (L.f.) Link (tagasaste), a key test plant for Australia where it is also grown as a forage species for livestock. The surveyed areas support many co-occurring species in the Genisteae, so sites were selected to include several species in the tribe where possible, and where not, samples were taken in large monospecific stands of the common species present. Particular effort was made to find sites where *G. monspessulana* co-occurred with *C. scoparius* or *U. europaeus* for comparison, as focused survey trips have been made for these species in the past and the natural enemy community found on them is relatively well understood (Zwölfer 1963, Syrett *et al*. 1999).

Quantitative sampling

Two trips were made to each site. On the first "mid-flowering" visit (between March and May) sampling consisted of three sharp taps (with a shortened broom handle) to 10 plants per Genisteae species per site (where possible) with a 1.5 m × 1.5 m beating sheet held under each plant. All arthropods were collected with an aspirator except for very numerous species where a subsample was collected from a random section of the beating sheet and the numbers of individuals calibrated up for the whole sheet. Immature stages of herbivorous species where adults clearly were not present (e.g. Lepidoptera larvae) were placed in separate rearing boxes with the food plant. Attempts were made to rear out adults for identification. Plants were also searched visually to collect any obvious endophagous species not sampled by beating, including leaf miners, gall formers, stem and root borers and obviously pathogenic fungi. Such species were recorded as present or absent. Samples from individual plants by host species by site were kept separately. Herbarium samples were taken to confirm plant identifications.

All arthropods were sorted, counted and identified as far as possible (to family or genus) in the laboratory in Montpellier on return, and voucher specimens were sent for identification from all species clearly on *G. monspessulana* alone and all species in the following orders/families: Lepidoptera, Diptera, Curculionidae, Apionidae, Chrysomelidae, Cerambycidae, Bruchidae, Buprestidae, Aphididae, Cicadellidae, Psyllidae and Miridae.

Another visit was made to each site (except sites in Greece) just before seed-pod maturation (in June to July) in the previous, same or subsequent year and all the pods from 10 randomly selected plants per species were collected and dry-stored separately per plant in ventilated plastic boxes. If arthropod species exited the green pods as larvae to pupate in the soil prior to collection then they were noticed from their emergence holes in the pods. Those larvae that did emerge from the pods soon after collection were placed in rearing dishes of moist vermiculite until adult emergence. After a minimum of three-months storage, the samples were sorted for emerged adult phytophagous arthropod species from the whole sample and then 30 pods per plant were dissected to quantitatively assess the attack rate and impact of the different arthropod species on total plant seed production, by relating damage characteristics to phytophagous species.

Analysis

The quantitative natural enemy species data from the beating trays were combined for each site sampled and the number of each species found per plant that were a) specific to the *G. monspessulana*, b) specific to the tribe Genisteae, c) specific to the family Fabaceae and d) other generalist species (including flower visitors) was calculated for each site and region. These data were then used to calculate Shannon diversity indices, *H*, per plant for each site and region. The pod dissection data were used to calculate the percentage seed loss per plant for each pre-dispersal insect seed predator identified a) for the seven most common Genisteae species sampled across all sites and b) between regions where *G. monspessulana* was sampled.

The data from the first site sampled with high abundance of *G. monspessulana* and several other Genisteae, Romanya de la Selva in north-eastern Spain, were used to assess the efficiency of the sampling regime at locating the total number of species present at a site. This site was also selected because the number of natural enemy species was relatively high (>25) compared with other sites sampled during the early surveys. At this site, two extra beat samples were taken, providing a total of 12 samples. The average number of species sampled from 1 through to 12 samples was calculated for all combinations of sample order. By plotting this against the number of samples, a rarefaction curve was generated, the asymptote of which estimates the number of samples necessary to have captured all the species present at the site (Müller-Schärer *et al*. 1995).

Results

Literature search

The literature search generated a list of 183 insects recorded from hosts in the genus *Genista*, of which 28 had already been recorded from *G. monspessulana*, and 134 insects recorded from hosts in the genus *Ulex,* of which 87 had already been recorded from *U. europaeus*. The literature search found no significant additions to the known list of 243 insect species recorded from *C. scoparius* (Syrett *et al*. 1999). This search supported the argument that historical sampling effort on *U. europaeus* and *C. scoparius* had led to much higher known natural enemy communities on these weeds, but that a similar sampling effort on *G. monspessulana* and other species in the Genisteae would improve understanding of the natural enemy community within the tribe.

Sites and sampling

The coastal surveys have so far included 10 sites in Spain (in the north-east and south-west), four sites in Portugal, four sites in coastal France, 10 sites in Corsica, three sites in Sardinia, five sites in western Italy and Sicily and four sites in Greece. The density of sampling reflected the frequency and abundance of *G. monspessulana.* Sampling was also carried out at 16 sites in the Canaries and six sites in Tunisia on other species in the Genisteae. Species in the Genisteae sampled throughout these surveys are included in Table 1. Sites surveyed and analysed in this paper are given in Figure 1. Beat samples were taken at 30 sites containing *G. monspessulana* and pod samples were taken at 25 of these sites. The remaining unsurveyed regions within the native range of *G. monspessulana* include the eastern coast of Italy and the Balkan coast, Turkey and Morocco.

The assessment of the efficacy of the beating tray sampling is presented in Figure 2 from the site in north-eastern Spain. According to this relationship, the sample size of 10 plants per site used throughout the surveys would be expected to find 93% of the total number of species estimated to be present at that site. It appears that the sample size chosen was sufficient to collect the vast majority of species during this survey at the time of sampling.

Natural enemies of *G. monspessulana*

The quantitative beating-tray and pod-sample surveys in the northern Mediterranean region have so far found 85 species of phytophagous arthropod on *G. monspessulana*. Of these, 26 are considered to be specific to the level of the tribe Genisteae and 8 are specific to the genus *Genista* (Table 2). The rust *Uromyces genistae* Fuckel was also observed attacking old leaves in late spring and summer (Guynot & Massenot 1958).

Table 1. Species of Genisteae sampled since January 1999 and whether or not arthropods were found. Surveys included Greece, France, Italy, Spain Portugal and Tunisia. Nomenclature follows <http://www.ildis.org/LegumeWeb/>.

Species	Number of sites sampled alone	Number of sites sampled together with other Genisteae	Total number of sites sampled	Number of sites where arthropods were found on the plant
Genista monspessulana [a]	9	34	43	42
Genista stenopetala [b]	0	3	3	2
Genista canariensis [b]	0	1	1	1
Genista corsica	0	2	2	1
Genista ferox	2	0	2	2
Genista linifolia [a]	0	1	1	0
Genista microcephala	3	0	3	3
Genista tricuspidate	2	0	2	2
Cytisus villosus	5	16	21	21
Cytisus scoparius [a, b]	1	8	9	7
Cytisus arboreus	0	7	7	7
Chamaecytisus proliferus [a]	4	7	11	10
Spartium junceum [a, b]	2	6	8	6
Calicotome spinosa [a]	0	3	3	3
Calicotome villosa	4	10	14	14
Adenocarpus foliolosus [b]	0	4	4	2
Adenocarpus telonensis	0	4	4	4
Spartocytisus filipes [b]	0	1	1	1
Stauracanthus boivinii	0	1	1	1
Retama raetam [a, b]	1	1	2	0
Ulex europaeus [a, b]	1	7	8	8

[a] Species that are also exotics.
[b] Species only (or also) sampled in the Canary Islands.

Figure 1. Map of the sample sites (O) of agent prospecting surveys for the biological control of *Genista monspessulana* around the Mediterranean. Quantitatively sampled sites are shaded.

Most foliar damage observed was caused by the psyllid *Arytinnis hakani* (Loginova). The psilid fly *Chyliza (Chyliza) leptogaster* (Panzer) and the buprestid *Agrilus antiquus* Mulsat et Rey (Schaefer 1949) were the only species observed killing mature plants, although only in a restricted part of the native range in south-eastern France. Amongst the seed feeders, the bruchid beetle, *Bruchidius lividimanus* (Gyllenhal) was the commonest species, followed by the apionid *Lepidapion (Lepidapion) argentatum*

(Gerstäcker) and weevil *Pachytychius sparsutus* (Olivier). A population of *Bruchidius villosus* (F.) in north-eastern Spain was found restricted to *G. monspessulana* despite the presence of *Cytisus villosus* Pourret. *Cytisus scoparius* is the commonest host of this species in northern Europe (Haines *et al*. 2004), but our surveys also found a second population restricted to *Spartium junceum* despite the presence of *G. monspessulana* in southern France. This suggests *B. villosus* may also attack these other species in the Genisteae in

Australia, New Zealand and North America, where it has been introduced as a biological control agent for *C. scoparius*.

A comparison of Table 2 with a similar list for *C. scoparius* (Syrett *et al*. 1999), suggests it contains very few species in all orders except the Coleoptera and that there remain many species not yet detected in our surveys from *G. monspessulana*. Several species were also found during the literature search (e.g. Emmet & Heath 1992), which have not yet been seen

Table 2. The abundance and frequency of the 32 phytophagous arthropod species that the literature suggests are at least specific to the tribe Genisteae, and that were sampled during the beating-tray survey of 30 *Genista monspessulana* sites in Greece, Italy, France, Spain and Portugal. Information includes their likely specificity, their phytophagous feeding guild and other genera of the Genisteae from which these species were also collected during these surveys.

Species	Specificity[a]	Guild[b]	Insects plant^{-1}	Frequency (%)[c]	Other Genisteae genera
Hemiptera					
Arytaina genistae (Latreille)	2	1	4.00	3	*Cytisus*
Arytinnis hakani (Loginova)	1	1	11.98	70	*Cytisus, Calicotome*
Acyrthospihon pisum ssp. *spartii* (Koch)	2	1	0.15	7	*Genisteae*
Gargaria genistae (F.)	1	1	0.43	37	*Cytisus, Spartium*
Heterocordylus ? leptocerus (Kb)	2	1	8.05	7	*Cytisus*
Orthotylus ? adenocarpi (Perris)	2	1	11.82	40	*Cytisus*
Diptera					
Chyliza leptogaster (Panzer)	1?	7	1.5	16	
Asphondylia sp. (galls)[d]	2	3	0.22	53	
Lepidoptera					
Agonopterix nervosa (Haworth)	2	2	0.71	17	*Calicotome*
Agonopterix scopariella (Heinemann)	1	2	0.09	25	*Cytisus*
Callophrys rubi (L.)	2	2	0.04	3	
Pseudoterpna pruinata (Hufnagel)	2	2	0.10	3	*Cytisus, Calicotome*
Oecophoridae sp.[d]	2	2	0.08	13	
Pyralidae sp.[d]	2	2	0.12	13	*Cytisus*
Tortricidae sp.[d]	2	2	0.19	13	*Genista, Cytisus, Calicotome*
Coleoptera					
Chrysomelidae					
Gonioctena (*Spartoxena*) sp.[d]	2	2	0.20	7	
Bruchidae					
Bruchidius villosus (F)	2	5	0.67	33	*Cytisus, Calicotome, Spartium*
Bruchidius lividimanus (Gyll.)	2	5	3.61	57	*Genista, Cytisus, Calicotome*
Buprestidae					
Anthaxia sp., *Agrilus antiquus* & *Agrilus cinctus*	2	7	0.09	7	
Apionidae					
Exapion fuscirostre (F)	1	5	0.20	3	*Cytisus, Calicotome*
Exapion nr. *putoni* (Ch. Brisout)	1	5	0.60	7	*Genista, Calicotome*
Lepiapion argentatum (Gerstäcker)	1	5	1.39	37	
Oryxolaemus ? scabiosus (Weise)	1	3	0.20	3	*Cytisus, Calicotome*
Pirapion ? immune Kirby	2	3	0.13	3	*Cytisus*
Protopirapion attratulum (Gemar)	2	4	0.08	7	
Curculionidae					
Pachytychius sparsutus (Ol)	2	5	0.38	7	*Cytisus, Calicotome*
Peritelus senex (Boheman)	2	6	0.93	3	
Pleurodrusus carinula (Olivier)	2	6	0.09	7	*Cytisus, Spartium*
Sitona gressorius (F.)	2	6	1.00	3	
Sitona regensteinensis (Herbst)	2	6	0.84	20	*Cytisus, Calicotome, Spartium*

[a] Specificity: 1 = specific to genus, 2 = specific to tribe.
[b] Guild: 1 = sap sucker, 2 = defoliator, 3 = leaf miner/galler, 4 = flower feeder, 5 = seed feeder, 6 = root feeder, 7 = stem feeder.
[c] Percentage of *G. monspessulana* sites where species sampled.
[d] Detailed rearing and identification required.

in the field. Table 3 summarises the currently known specialist arthropod community on *G. monspessulana, C. scoparius* and *U. europaeus* developed from both the literature search and field collections from *G. monspessulana.* This table focuses on arthropod genera where the literature suggests there are different species using these three closely related hosts.

Table 3. A comparison of the specialist arthropod community on *Genista monspessulana,* and the previously documented community on *Cytisus scoparius* (Syrett *et al.* 1999) and *Ulex europaeus* (Zwölfer 1963) generated from the literature search and field collections. Species in bold type are the extreme specialists that appear to be restricted to one host or the other.

Family	Genus	Species on *G. monspessulana*	Species on *C. scoparius*	Species on *U. europaeus*
Eriophyidae	***Aceria***		**genistae**[a]	**genistae**
	Tetranychus			**lintearius**[a]
Psyllidae	***Arytaina***		**genistae**	
	Arytinnis/Arytainilla	**Arytinnis hakani**[a]	**Arytainilla spartiophila**[a]	
Aphididae	*Acyrthosiphon*	*?spartii*	*spartii*	
	Aphis	**genistae**	**sarothamni**	**ulicis**
Membracidae	*Gargaria*	*genistae*	*genistae*	*genistae*
Pentatomidae	*Piezodorus*	*lituratus*	*lituratus*	*lituratus*
Miridae	***Heterocordylis***	**genistae,** *leptocerus*	**tibialis,** *leptocerus*	*parvulus*
	Globiceps	*fulvicollis,* **genistae**	*fulvicollis*	
	Orthotylus	*adenocarpi, beieri, virescens*	*adenocarpi, beieri, virescens,* **concolor**	
	Platycranis	**boreae**	*bicolor*	*bicolor*
Geometridae	***Chesias***		**legatella**	
	Isturgia		**limbaria**	
	Pseudoterpna		*pruinata*	*pruinata*
Oecophoridae	***Agonopteryx***	*scopariella, nervosa*	**assimilella,** *scopariella, nervosa*	**ulicetella,** *nervosa*
Lyonetiidae	***Leucoptera***	**laburnella**	**spartifoliella**[a]	
Nepticuliidae	***Trifurcula***	**serotinella**	**immundella**	
Gelechiidae	***Mirificarma***	**cytisella**	**mulinella**	**ulicinella**
Gracillariidae	***Phyllonorycter***	**stainoniella**	**scopariella**	**uilicicolella**
Tortricidae	***Cydia***	*succedana*	*succedana,* **scopariana**	*succedana*[a], **ulicetana, internana**
Psilidae	***Chyliza***	**leptogaster**		
Cecidomyiidae	***Asphondylia***		**sarothamni, pilosa**	**ulicis**
Tenthredinidae	*Rhogogaster*		*genistae*	
Cerambycidae	*Deilus*	*fugax*	*fugax*	*fugax*
Buprestidae	*Agrilus*	*antiquus, cinctus*	*antiquus, cinctus*	
	Anthaxia	*funerula*	*funerula*	*funerula*
Bruchidae	*Bruchidius*	*lividimanus, villosus*	*lividimanus, villosus*[a]	*lividimanus*
Chrysomelidae	*Gonioctena*	**sexnolatus, gobanzi,** *variabilis*	**olivacea,** *variabilis*	
Apionidae	***Lepidapion***	**argentatum,**[a] *squamigerum*	*squamigerum*	**pseudogallaecianum,** *squamigerum*
	Exapion	*?plutoni*	**fuscirostre,**[a] *plutoni*	**ulicis**[a]
	Pirapion	*immune*	*immune*	*immune*
	Protopirapion	*attratulum*	*attratulum*	*attratulum*
Curculionidae (roots)	***Sitona***	*regensteinensis,* **gressorius**	*regensteinensis,* **puberulus**	*regensteinensis,* **striatellus**
	Polydrusus	***?cervinus,** prasinus*	**confluens,** *prasinus*	
	Peritelus	*senex*	*?*	*?*
Curculionidae (seeds)	***Tychius***		**parallellus**	
	Pachytychius	*sparsutus*[a]	*sparsutus*	*sparsutus*

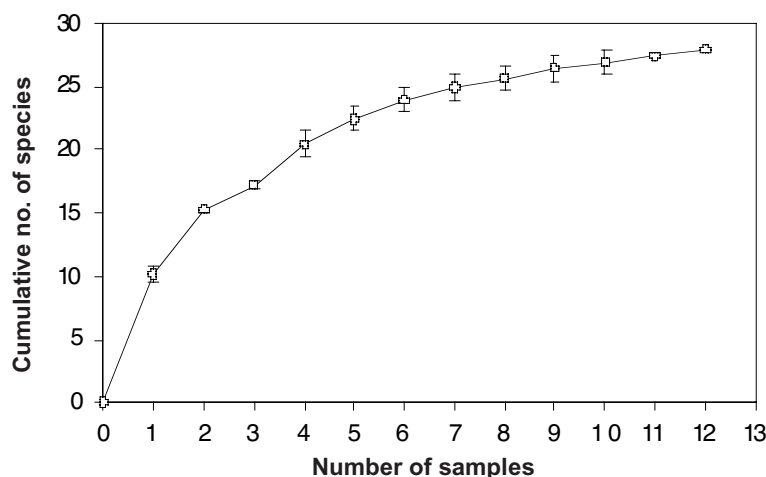[a] Released or studied as a biocontrol agent.

Figure 2. The rarefaction curve for the number of herbivorous arthropod species detected on *Genista monspessulana* against the number of plants sampled using the described beating method at Romanya de la Selva, Sierra de Gavarres, south-eastern Girona, south-western Spain. This analysis includes all arthropod species collected; both specialists and generalists.

Quantitative analysis

The percentage of beat samples from *G. monspessulana* that included each natural enemy specific at least to the tribe Genisteae and the number of individuals of that species per sampled plant are given in Table 2. The average number of species found per site in each region and the total number of species sampled per region are presented in Figure 3 for species sampled that were a) specific to the *Genista monspessulana*, b) specific to the tribe Genisteae, c) specific to the family Fabaceae and d) all other insects found including generalist flower visitors. Shannon diversity index *H* mean values calculated for each region surveyed are presented in Figure 4 for a) species found at least specific to tribe Genisteae, b) species found at least specific to the family Fabaceae and c) all insects found including generalist flower visitors. The diversity of the largely specialist insect species collected suggests that the centre of origin of *G. monspessulana* is in the western Mediterranean.

Data from the pod dissections from each of the 25 *G. monspessulana* sites were used to estimate predispersal seed losses to insects for the different Genisteae species sampled across sites (Table 4) and variation in seed loss per site to the different pod feeding insects between regions (Figure 5). The overall average seed predation level in the pods of *G. monspessulana* was 22%. This was higher than for any other co-occurring species in the Genisteae except *Calicotome spinosa* (L.) Link, although only two populations of this were sampled. *Lepidapion argentatum* damage was the highest, but bruchids also caused comparable losses (Table 4). There was large variation is seed losses to the different seed predators across plants and sites and in overall seed losses per seed predator species between

native range region where *G. monspessulana* occurs (Figure 5), ranging from 6 to 39% across regions and 1 to 63% across sites.

Discussion

Quantifying the natural enemy community

A comparative approach is starting to show how communities of natural enemies differ between closely related host plants (e.g. Table 3). We have also started to turn a qualitative picture of the natural enemy community into a quantitative description of the patterns of abundance and diversity of all species in this community in relation to their specificity and host use. With such a description, community assemblage rules can be explored that may explain what determines the abundance and number of highly specific and damaging species using individual hosts (Gaston & Lawton 1990, Hanski & Gyllenberg 1993). Understanding community assemblage rules would also assist biological control in its attempts to create stable natural enemy communities on weeds in their exotic range that have the capacity to suppress host populations.

Quantitative biological control surveys also provide valuable information on the potential damage species may inflict on their hosts if released. Here we have started to show the variation in damage levels observed for seed feeders as well as the mean. Natural enemies that show wide variation in the damage they inflict across many sites are more likely to be suppressed by extrinsic bottom up (plant density) or top down (predation) ecological processes, which they might escape from following release. This assists agent efficacy evaluation prior to release (Sheppard 2003).

Table 4. Percentage seed loss per plant overall and for the five seed predators across 7 species of Genisteae at 25 sites containing natural populations of *Genista monspessulana* in the native range in Spain, France and Italy.

Genisteae	n	Mean total % seed loss per plant	*Bruchidius lividimanus*	*Bruchidius villosus*	Apionid spp.[a]	*Pachytychius sparsutus*	Lepidoptera
Genista monspessulana	25	22.03 ± 3.40	5.33 ± 1.18	2.92 ± 1.12	8.38 ± 3.49	2.00 ± 0.55	3.40 ± 0.96
Cytisus villosus	8	9.73 ± 4.54	4.76 ± 1.24	0.06 ± 0.05	4.74 ± 4.49	0.02 ± 0.02	0.15 ± 0.12
Cytisus scoparius[b]	2	1.19 ± 0.26	1.01 ± 0.43	0.00	0.00	0.00	0.17 ± 0.17
Cytisus arboreus	2	12.78 ± 4.56	8.60 ± 1.90	0.00	2.05 ± 1.81	0.88 ± 0.77	1.25 ± 0.08
Calicotome villosa	6	16.35 ± 5.14	10.94 ± 5.65	0.00	4.78 ± 3.58	0.36 ± 0.40	0.03 ± 0.03
Calicotome spinosa	2	34.27 ± 2.02	2.94 ± 1.87	0.00	0.00	31.02 ± 0.16	0.31 ± 0.31
Adenocarpus telonensis	2	4.36 ± 3.52	0.00	0.00	0.00	0.00	4.36 ± 3.52

[a] *Lepidapion argentatum* on *G. monspessulana*, *Exapion ? subparallelum* (Dbr.) on *C. villosa*, *Exapion ? fuscirostre* on *C. villosus* and *C. arboreus*.
[b] Data only for sites where *C. scoparius* co-occurs with *G. monspessulana* (Corsica); other studies in the native range have estimated seed loss of *C. scoparius* to be 15−23% (Hosking 1995), 0.4−24% (Mazay 1993), 26% (Hinz 1992).

Selecting effective agents also requires clear understanding of the population dynamics of the target weed in the exotic environment. There is good understanding of the population dynamics and ecology of *G. monspessulana* (Pareja 1999, Lloyd 2000), *C. scoparius* (Rees & Paynter 1997, Sheppard *et al.* 2002) and *U. europaeus* (Rees & Hill 2001). All these studies suggest that the best agent for these woody weeds with seed-based reproduction is an agent that can reduce lifetime seed production. A stem or root borer that prematurely kills adults would therefore receive a high priority, but these studies also show that agents that directly reduce seed production can also be very useful, particularly in habitats of low fertility or where seedling mortality is naturally high (Sheppard *et al.* 2002). They would also be useful for weeds that are still spreading significantly, by both reducing rate of population spread and reducing the control efforts required for other management strategies.

Selecting agents for *G. monspessulana*

The preliminary results of these surveys suggest that the most damaging agents are the psyllid *A. hakani* attacking the foliage, the fly *C. leptogaster* and buprestid *A. antiquus* attacking the stems and roots, and the beetles *B. lividimanus*, *L. argentatum*, *B. villosus* and *P. sparsutus* attacking the seeds. The only pathogen found so far was only present in significant amounts on old leaves.

That a psyllid appears on this list is highly desirable from a specificity perspective. The genera *Lupinus* and *Ulex* in the Genisteae have no recorded psyllid species and the four genera of arytainine psyllids known to feed
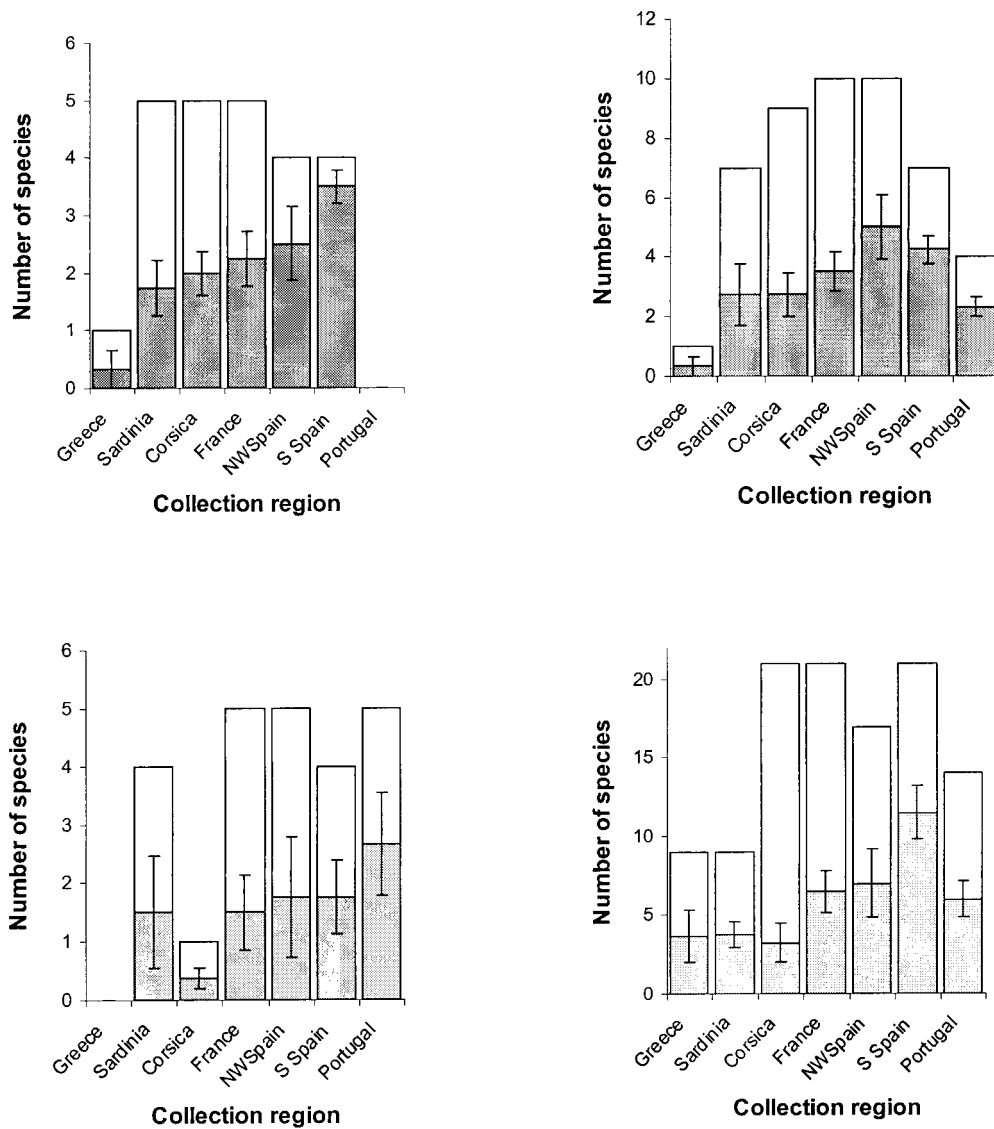

Figure 3. Mean number of species sampled on *Genista monspessulana* per site (filled section ±SE) and total number (bar height) for each region sampled for species a) specific to *Genista*, b) specific to the Genisteae, c) species specific to the Fabaceae and d) generalist flower visitors etc.

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on host plants in the Genisteae are restricted within the tribe (Hodkinson & Hollis 1987, Burckhardt 1989) with a high percentage of monospecific species (Percy 2003). Only one species in the genus *Arytinnis*, *Arytinnis modica* (Loginova) comb. n., has hosts in two genera (*G. stenopetala* and *C. proliferus*) and an analysis using the molecular phylogeny of arytainine psyllids to date the separation of these two host races suggests divergence occurred 70,000–121,000 years ago (D. Percy unpublished data). *Arytinnis hakani* has only ever been recorded from *G. monspessulana* and has a relatively wide geographical distribution (northern and southern coasts of the western Mediterranean from Portugal to Italy and Morocco to Algeria). As molecular and morphological evidence suggests the genus *Arytinnis* probably originates from the Canaries (Percy 2001), where *G. monspessulana* does not occur, the association between this psyllid and *G. monspessulana* may be recent. We found *A. hakani* only on *G. monspessulana* and only in the western Mediterranean. We found no evidence of other species of psyllids using *G. monspessulana* as a host. *Arytaina genistae* (Latreille) was found on *C. scoparius* at sites where this co-occurred with *G. monspessulana*, but *A. genistae* was clearly not using *G. monspessulana* (though this species will develop on *C. proliferus*; S. Fowler, pers. comm.). Evidence from California, where *A. genistae* has been accidentally introduced, but is only found on *C. scoparius* and not *G. monspessulana*, supports this.

Of the stem borers, the psilid fly *C. leptogaster* was only observed through the Massif des Maures in France, but appears to be a significant cause of early plant population decline at this sample site. The larvae tunnel under the bark, either ring-barking whole branches or causing widespread necrosis of cambium tissue. This genus of 57 species worldwide (Iwasa 1989) from a small family are considered to be bulb and stem miners,

however, very few of these have known host plants. *Chyliza leptogaster* has been recorded from nut-like wood galls on *Physocarpus* and *Spiraea* sp. (Rosaceae) in northern Europe, however Collin (1944) talks about slight morphological differences between his *C. leptogaster* and a "southern form" described by Rondani in Italy in 1876 which the latter called *Chyliza premixta* Rondani. Rondani records no host plant for his species. Chandler (1975) comments that this genus had fairly "chaotic taxonomy". However, a slight concern is the tendency of some species in the genus to appear to only oviposit into existing wounds (e.g. *Chyliza annulipes* Macquart on *Pinus*, Lyneborg 1987).

The buprestid *A. antiquus*, found in the same region as *C. leptogaster*, was also observed to be associated with plants that had died prematurely in low density populations of *G. monspessulana*. Like *C. leptogaster*, it was not found in nearby *C. villosus* and *Calicotome villosa* (Poiret) Link stands, although the literature suggests it will attack many species in the Genisteae.

Of the seed feeders, *B. lividimanus* appears to have too broad a host range to be useful in countries where native or commercially important species in the Genisteae occur. The seed-feeding apionid *L. argentatum* is also likely to be highly specific to *G. monspessulana*. The genus *Lepidapion* has *ca.* 16 Mediterranean and Canary Island species and two subgenera and shows a high degree of monospecificity. Hosts in the genus include members of *Genista, Ulex, Retama, Spartocytisus* and *Cytisus* (Alonzo-Zarazaga 1985, Ehret 1990). A major revision of the genus is required. Currently, *Genista umbellata* (L'H & eacute; r.) Poiret and *Adenocarpus* sp. have been included in the host range of *L. argentatum*, and *Lepidapion acuminatum* (Schilsky) has also been recorded attacking *G. monspessulana* near Cadiz in southern Spain (Alonzo-Zarazaga 1985), but there is probably only one highly
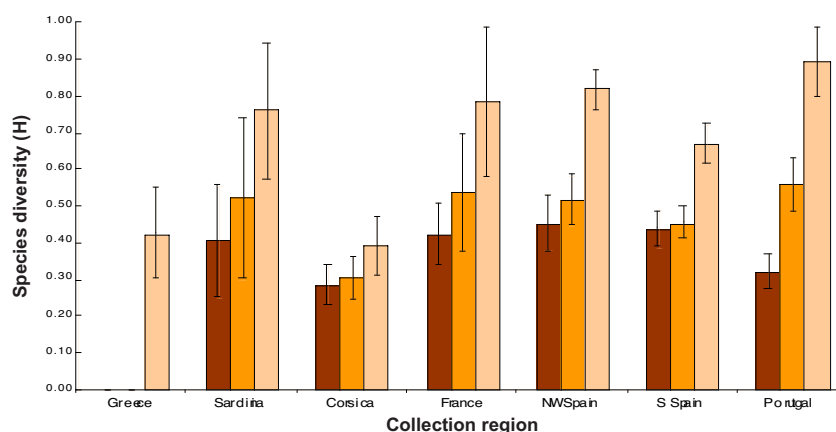

Figure 4 Mean Shannon species diversity indices per *G. monspessulana* plant for each region sampled at flowering for natural enemies a) at least restricted to the tribe Genisteae (dark shading), b) at least restricted to the family Fabaceae (mid-shading) and c) all natural enemies found (light shading) (±SE).
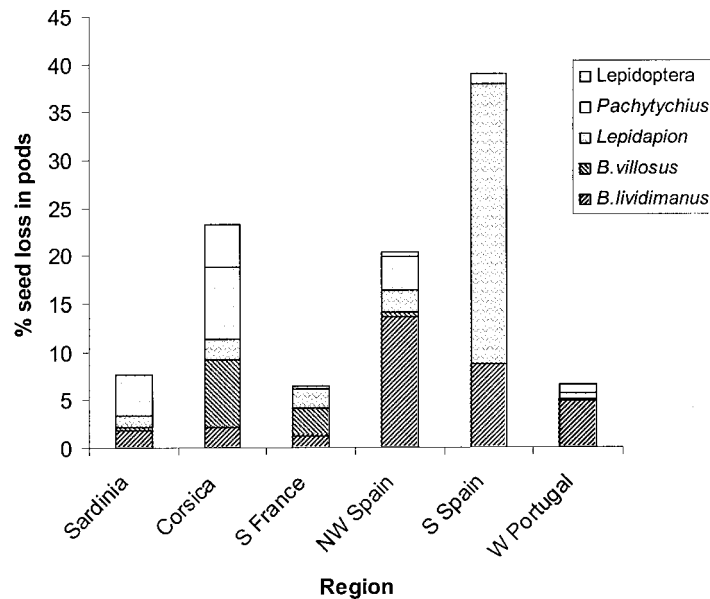
Figure 5. Percentage seed loss per plant in *Genista monspessulana* to pre-dispersal seed predators (Lepidoptera, the weevil, *Pachtychius sparsutus*, the apionid *Lepidapion argentatum* and the two bruchids, *Bruchidius villosus* and *B. lividimanus*) at 25 sites in 6 distinct geographical regions throughout south west Europe.

specific species on *G. monspessulana* and *L. argentatum* may not be its correct name (M. Alonzo-Zarazaga, pers. comm.). Molecular and morphological comparisons will need to be made of *Lepidapion* species on Genisteae throughout the Mediterranean to clearly understand both the taxonomy and host range of species in this genus. *Pachytychius sparsutus* is less specific, but also has potential as a biological control agent. The currently known hosts do not include either *Lupinus* or *Ulex* (Hoffmann 1958, Freude *et al.* 1981), although it would probably feed on *C. proliferus*.

There remain several groups and species, notably the Lepidoptera, that are still too poorly understood, but may have potential for the biological control of *G. monspessulana*.

Conclusion

In this paper, we have tried to emphasize how quantitative agent surveys can be a valuable way of understanding both the host range and damage capacity of natural enemies on target weeds in their native range. This can provide benefits for agent selection, which we are applying in the case of *G. monspessulana*, but we have also outlined the benefits the resulting databases may offer to our general ecological understanding of the structure of natural enemy communities on plants.

Acknowledgements

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