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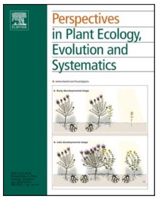

Rare plants sustain communities of visitors with similar diversity but different composition across populations of different size

Héctor Miranda-Cebrián [a,*], Joan Cáliz [b], Jens M. Olesen [c], Adela González Megías [d], Sergio Albacete [e], Francisco Martín [f], Lidia del Arco [g], María Jarne [a,h], Emilio Ortega Casamayor [b], Miguel Verdú [i], María Begoña García [a]

[a] Pyrenean Institute of Ecology (CSIC), Avda Montañana 10005, Zaragoza 50059, Spain
[b] Integrative Freshwater Ecology Group, Centre of Advanced Studies of Blanes-Spanish Council for Research CEAB-CSIC, Blanes E-17300, Spain
[c] Department of Biology, Aarhus University, Ny Munkegade 116, Aarhus C DK–8000, Denmark
[d] Departamento de Zoología, Universidad de Granada, Granada 18071, Spain
[e] Dipartimento di Scienze e Tecnologie Agro-Alimentari, Alma Mater Studiorum Università di Bologna, Bologna 40127, Italy
[f] EarthPulse, St Joan de La Salle, 42, Barcelona 08022, Spain
[g] Centre for Ecological Research and Forestry Applications (CREAF), Bellaterra 08193, Spain
[h] Sociedad Aragonesa de Gestión Agroambiental (SARGA), Spain
[i] Centro de Investigaciones Sobre Desertificación (CIDE, CSIC-UV-GV), Moncada, Spain

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ABSTRACT

Interactions are fundamental pillars of ecosystem functions, and plants often host a multitude of organisms both above- and belowground. However, plant populations of the same species may be visited by different communities depending on their size or local environment. Here we thoroughly surveyed the aboveground arthropod and belowground bacteria communities interacting with six Pyrenean rare plant species. We compared the patterns of alpha and beta diversity between patches of similar size located in small and large plant populations, and explored the relationship between aboveground arthropod and belowground bacterial diversities. Alpha diversity of arthropod visitors did not differ between plant patches, but belowground bacterial diversity was higher in small populations. In addition, significant differences were observed in the composition of arthropod communities, with patches in small populations having communities that differed from those in large populations. Finally, above- and belowground patterns of beta, but not alpha diversity were positively correlated. Our results suggest that isolated small plant populations may sustain communities of similar diversity as similar sized patches located within large populations, although with different taxonomic composition. This highlights the importance of small plant populations, often regarded as having lower ecological value, as hosts to a wide range of species both above- and belowground.

1. Introduction

Biotic interactions play a fundamental role in ecosystems. They are an important part of many mechanisms underlying ecosystem functioning such as energy and nutrient flows due to predation, carnivory or herbivory; as well as influencing species abundances and distribution via pollination, seed dispersal and facilitation (Hooper et al., 2005, Traill et al., 2010). Consequently, interactions are an important part of the dynamics and long-term stability of populations, communities and ecosystems (Valiente-Banuet et al., 2015).

In this context, plants offer a large variety of resources like food and shelter to many species (Borges and Brown, 2001). The diversity and strength of plant-animal interactions are determined by the resources made available by the plants, as well as the local diversity and abundance of the species that may interact with them (Bascompte and Jordano, 2007). More diverse networks of interactions are more robust to disturbances such as the extinction of their constituents, leading to increased ecosystem stability by ensuring the persistence of ecosystem functions through time (Ollerton, 2017). For example, a higher diversity of pollinators or seed dispersers has positive impacts on the reproductive

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* Corresponding author.
E-mail address: hectorm94@gmail.com (H. Miranda-Cebrián).

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success, diversity and productivity of plant communities, which ensures their long-term persistence, and increases the resource availability for all the organisms in the ecosystem (Hale et al., 2020). Even interactions that are seemingly negative for plants, like herbivory, can contribute to maintaining plant diversity by limiting competition between plant species and promoting coexistence under certain conditions (Borer et al., 2014).

The interactions between plants and belowground communities of organisms also play an important role in plant performance (Berendsen et al., 2012). Microbial communities in the soil or rhizosphere are involved in many mutually beneficial interactions with their host plants. For instance, plants offer suitable microhabitats for bacteria and fungi, in addition to a supply of organic carbon in the form of root exudates (Bais et al., 2006). In turn, the activity of microbes may contribute to plant growth by different mechanisms like increasing availability of soil nutrients through organic matter degradation, nitrogen fixation, improving the uptake of soil nutrients through mycorrhizae or preventing the proliferation of root pathogens (Trivedi et al., 2020, Vandenkoornhuyse et al., 2015). Given that plants and the organisms they interact with constitute complex systems comprising many interconnected parts they should be considered in an integrative way (Tylianakis et al., 2010). However, most studies on plant-animal interactions focus on either trophic or mutualistic interactions (García-Callejas et al., 2021), whereas our understanding of how often plants interact with other organisms that approach them to rest, reproduce or forage, remains limited.

We explore the diversity of arthropod communities found aboveground and that of bacterial communities found belowground associated with six rare plant species of conservation interest. First, we describe the community of visitors found in two populations of each plant species that differ in size but close enough to share similar environmental characteristics. In contrast to most studies involving plant interactions, we did not focus on any particular visitor functional group (*i.e.,* pollinators or herbivores) and took a more inclusive approach to better characterize the interactions potentially experienced by the focal plant. To allow direct comparison between populations, we delimited one patch covering most of the small population and three patches spread over the large population with a similar size as the first patch, and then compared the diversity and composition of visitors between patches of each plant species. We expect patches located in smaller populations to offer less resources and thus be less attractive to potential visitors, particularly the more specialized ones, reducing the diversity of their communities of aboveground visitors (Brosi, 2016, Waser et al., 1996). On the other hand, we expect root bacterial communities to have similar diversity and composition between patches of the same plant species due to host specificity regardless of the population they are located in (Berendsen et al., 2012, Eck et al., 2019). Finally, we tested the correlation between above- and belowground diversity metrics to assess if both visitor communities respond in a similar way to plant population size (Trivedi et al., 2020, Wardle et al., 2004).

2. Methods

2.1. Study area and plant species

Our study was carried out in the Spanish side of the Pyrenean range (Fig. 1). We chose six plant species of conservation interest in the region and involved in a wide variety of interactions, such as pollination, seed dispersal, predation, carnivory or parasitism (Table S1): *Borderea pyrenaica* (Dioscoreaceae), *Cypripedium calceolus* (Orchidaceae), *Galanthus nivalis* (Amaryllidaceae), *Gentiana lutea* (Gentianaceae), *Pinguicula longifolia* (Lentibulariaceae), *Ramonda myconi* (Gesneriaceae).

For each plant species, we located one large, continuous population (L) and one small (S) population, separated by 0.7 km - 22 km depending on the species. Populations were chosen after an exhaustive search of the study area according to the records in the Herbarium JACA, one of the largest in Spain (http://www.ipe.csic.es/proyectos-de-investigacion) and specialized in the flora of the region. The two populations of each plant species shared similar climate and soil properties, and before sampling we made sure that there were no other populations of the same species between each pair of focal populations to minimize any mixing between communities of visitors. We defined large an small populations based on an estimate of the number individuals, with large populations having 5–20 times more individuals than small populations (Table S1). In each small population we sampled a square patch of 20–30 m of side length depending on the terrain that covered most of the population area. In the large populations we sampled three patches of similar shape and size as the one sampled in S and separated between 40 and 300 m depending on the population but connected enough to share visitors. In each patch we recorded the density of the focal plant species

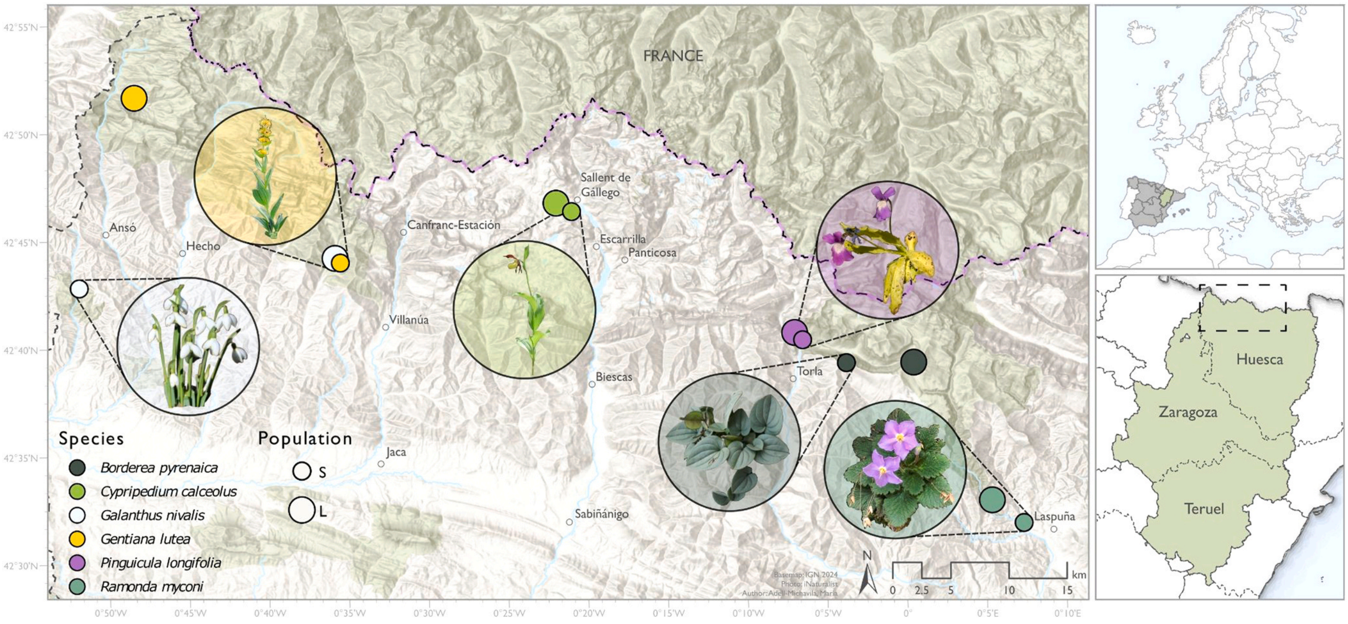

Fig. 1. Study area and location of populations S and L of each plant species.

as well as the diversity and composition of accompanying plant species to test for any possible effects on visitor diversity, as higher density plant density is associated with increased availability of resources for visitors and thus higher diversity (Mustajärvi et al., 2001). We assessed the diversity of accompanying plants by recording the cover of all plant species found in an area of 5 by 5 m at the center of each patch using the Braun-Blanquet scale. Focal plant density was similar across patches of each plant species and did not show a relation with visitor diversity (Table S2, Supplementary Material B), thus, we focused on differences between small and large host plant populations.

2.2. *Aboveground interactions survey*

The aboveground arthropod community was surveyed in 2016, 2017, and 2018 during the flowering season of the host plants. Sampling area and length of surveys varied among plant species, depending on size of plants and frequency of interactions, but at least 20 surveys of 15 min were performed at each site, resulting in more than 9000 minutes and 638 surveys overall (Table S1). Sampling effort varied among plant species because they differed in the abundance or detectability of interactions (*e.g., G. nivalis* was sampled for a shorter period because it has very few visitors; flowering occurs at the end of winter, when temperatures keep visitor activity low). However, sampling effort was always kept similar among patches of the same plant species. All arthropods visiting any part of flowering and non-flowering plants over an area covered visually by the observer were visually identified or sampled to confirm identification later on. These included, among others, individuals nesting on the plant, eating or sucking on plant tissue, pollinating or predators waiting for prey. In addition, specific methods were used to unveil interactions that are not easily visible, like those by very small or hidden organisms (Table S2). For example, acari sheltered under leaves of *R. myconi* were sampled by Berlese funnel traps. Cafeteria experiments were used for *B. pyrenaica* and *G. nivalis*, given that their seeds have an elaiosome attractive to ants. Fruits of *G. lutea* were also wrapped in mesh fabric to capture arthropods emerging from eggs laid inside the fruit (Table S2). In the particular case of the carnivorous *P. longifolia*, arthropods trapped by three sticky leaves of 15 plant individuals in each patch were also identified (sampled three times during the summer of 2018). Individuals not identified *in situ* were collected and sent to expert taxonomists to be identified. When identification at species level was not possible, morphospecies were used (*e.g.,* diptera_1, diptera_2). The abundance of each visitor was measured as the number of times it was observed interacting with plants of the focal species.

2.3. *Belowground interactions survey*

Belowground prokaryotic communities were characterized for each plant population from samples of root material from several individuals within each patch, collected during the aboveground surveys (10–20 samples, depending on plant species but taking the same amount in patches of each species). Roots were shaken vigorously, and their growing tips were cut and frozen until analysis. Root material of each patch was mixed, and DNA extraction was carried out from three samples with 0.05–0.1 g of root material using a Mobio PowerSoil DNA Isolation Kit (Mobio Laboratories). PCR and sequencing of the 16 rRNA gene was done with Illumina MiSeq (NGS) following the methods from the central genomic services of RTSF-MSU (Michigan State University, USA) (https://rtsf.natsci.msu.edu/). We analyzed the V4 variable region of the 16S rRNA gene (250 nucleotides) using primers F515 (5′-GTGCCAGCMGCCGCGGTAA-3′) and R806 (5′-GGACTACHVGGGTWTCTAAT-3′) (Caporaso et al., 2011). Raw rRNA gene sequences were processed using the UPARSE pipeline (Edgar, 2013) to identify zOTUS (zero-radius operational taxonomic units). Taxonomic assignment used the naive Bayes scikit-learn classifier implemented in QIIME2 (Caporaso et al., 2010) and the SILVA 132 database (Quast et al., 2012). Chloroplast, mitochondrial, and unclassified sequences were excluded from further analyses. The original zOTU table was normalized by rarefying the sequences of all samples to a minimum threshold of 14,000 sequences/sample. The abundance of each zOTU was measured as the mean number of sequences detected across samples in each plant population after rarefaction.

2.4. *Taxonomic diversity assessment*

Alpha diversity of the communities in each patch was estimated using Hill numbers (Hill, 1973), a measure of diversity that varies based on the weight given to the relative abundance of taxa by changing the parameter q. If $q = 0$, no weight is given to species abundance and as q increases, more weight is given to abundance and thus rare species have less importance in the community. Here, we calculated alpha diversity (${}^{q}D$) for each patch separately and each population as a whole using q values of 0, 1 and 2, which are equivalent to classic diversity indices like species richness ($q = 0$), the inverse Simpson diversity index ($q = 1$) and the exponential of Shannon entropy ($q = 2$).

2.5. *Change in community composition*

We assessed the changes in community composition of visitors above- and belowground among plant species and patches with the Bray-Curtis dissimilarity and then calculated the degree of turnover and nestedness between patches and populations using the *betapart* package (Baselga and Orme, 2012).

2.6. *Relationship between aboveground and belowground diversity*

We used Pearson's correlation coefficient to assess the relationship between each aboveground alpha diversity metric (${}^{0}D$, ${}^{1}D$, ${}^{2}D$) and its belowground counterparts across species. The relationship between aboveground and belowground beta diversity was tested using the Mantel test on the community dissimilarity matrices.

2.7. *Analysis of differences between plant patches*

First, we assessed sampling completeness using the *iNEXT* package (Hsieh et al., 2025). Then, we checked for any possible confounding effects on the diversity and composition of interacting species caused by differences in altitude, host plant density, co-occurring plant diversity and soil conditions (pH, granulometry and carbon, nitrogen, phosphorus and organic matter content) between host plant populations (Supplementary Material B). Since we did not find any statistically significant effect of these confounding factors, we excluded host plant density, co-occurring plant diversity and soil conditions from downstream analyses. Then, we tested the differences in alpha diversity of above- and belowground interacting species between patches using two methods. First, we calculated rarefaction curves for each patch as well as the aggregated L patches of each host using the *iNEXT* package. Then, we assessed the overlap of the 95% confidence intervals of each plant species curve for S against the whole L populations and S against L1, L2 and L3. Second, we tested the differences in diversity between S and L patches using Gaussian generalized mixed-effects models (GLMM) for ${}^{1}D$ and ${}^{2}D$, and Poisson GLMMs with a log link function for ${}^{0}D$ with R package *lme4* (Bates et al., 2015). We included host plant species as a random variable to account for any differences in diversity between plant species caused by factors external to population size as well as any pseudoreplication or differences in sampling effort between plant species. Before proceeding any further, we tested for the spatial autocorrelation of each model's residuals (Supplementary Material B). Since we did not find any significant autocorrelation, we deemed it unnecessary to account for it in our models. To further test the robustness of our results against the small sample size of S patches we validated the results from the GLMMs by testing if the difference in mean diversity between L and S patches differed from 0 using bootstrapping stratified by host plant (Supplementary Material E).

Multivariate analysis of variance (PERMANOVA) on the dissimilarity matrices was used to test the differences in community composition between plant patches. We used the *adonis2* function in the *vegan* package (Oksanen et al., 2026) with permutations stratified by plant species to control for differences in visitor community composition between host plant species.

Although our sampling approach is more inclusive in terms of visitor diversity than traditional studies of plant interactions, this might mask diversity patterns in more narrowly defined functional groups of visitors. Thus, to test if our results were consistent across different types of aboveground interactions, we repeated all our analysis but only considering pollinators (Supplementary Material F).

3. Results

For the 6 plant species and 24 patches sampled, a total of 5876 interactions between arthropods and the focal plant in each patch were observed aboveground, which involved 636 arthropod morphospecies. The average sampling completeness per population was 87.3% (SD = 5). Most visitors were identified to species (36.5%) or genus level (18.1%), while 28.5% were identified to family level and 16.4% to order level. The remaining taxa were identified to the class level. The most abundant orders were Diptera (27.3% of interactions), Hymenoptera (16.9%), and Hemiptera (13.8%) (Table S7). The belowground bacterial diversity consisted of a total of 3691,306 DNA sequences in roots, corresponding to 35,283 zOTUs. Average sampling completeness per population was 96.7% (SD = 1.7). Alphaproteobacteria were the most abundant bacterial group (21.3% of interactions), followed by Gammaproteobacteria (16.2%) and Bacteroidia (9.8%) (Table S8). Given that diversity patterns between the whole dataset, and the subsets of only pollinators were similar (Supplementary Material F), here we only present results concerning the full community of visitors found at each patch.

3.1. Alpha diversity

The average aboveground arthropod richness (^{0}D) was 50.5 (SE = 7.67), and was highest for *G. lutea* (mean = 118; SE = 4.73) and lowest for *G. nivalis* (mean = 8.5; SE = 1.94) (Fig. 2A). The average zOTU

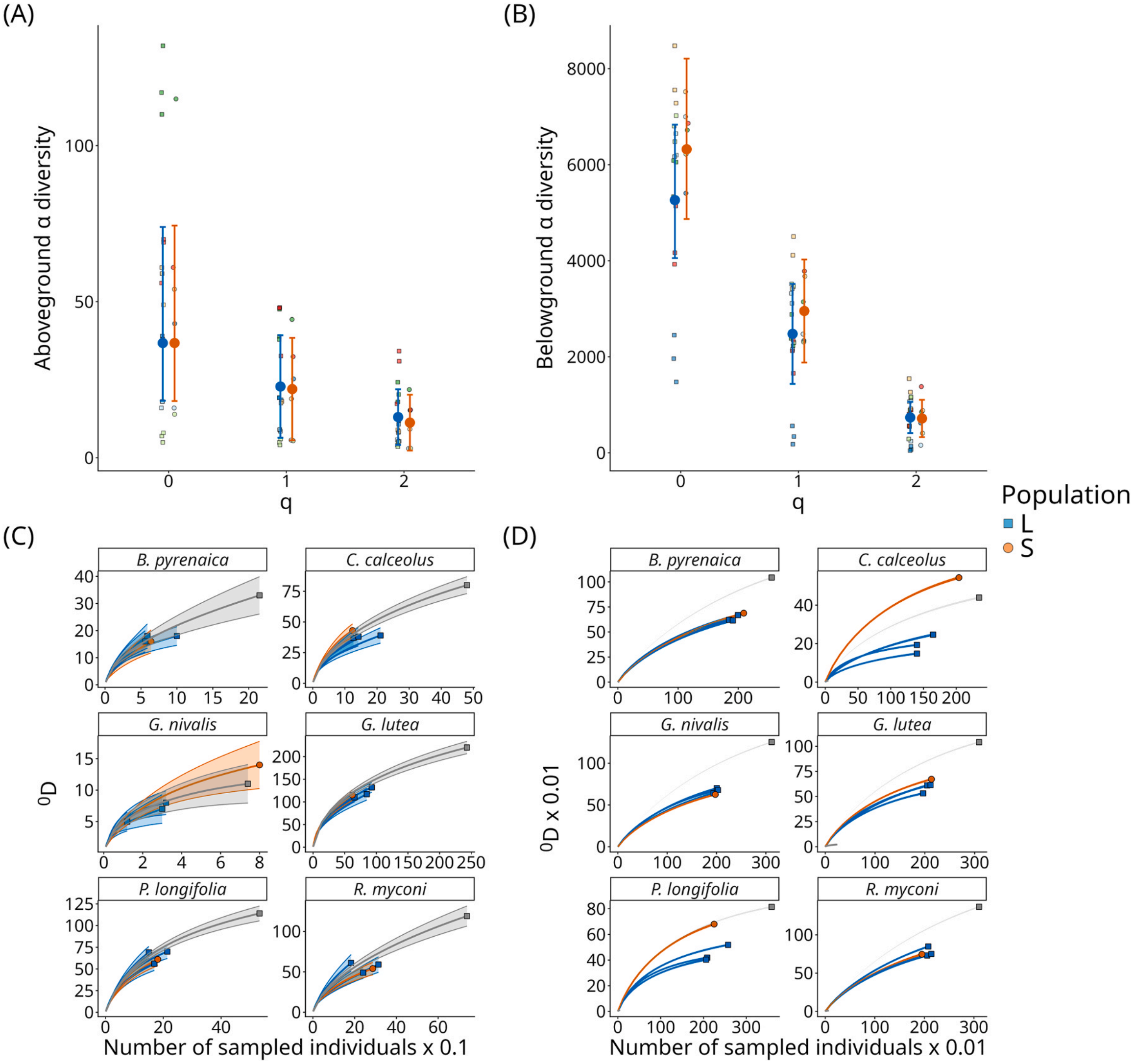

Fig. 2. Alpha diversity of arthropods (A) and zOTUs (B) for Hill numbers of $q = 0$, 1 and 2, and host plant patch size (S and L). Species richness rarefaction curves according to the number of individuals sampled in each community with their 95% CI for aboveground arthropod (C) species and belowground zOTU (D) richness (^{0}D) in the S (orange) and L (blue for each patch and grey for the combination of them) populations of each plant species. In panels (A) and (B), orange and blue dots indicate the mean value and its 95% confidence interval from the GLMM for S and L plant populations, respectively. Smaller symbols indicate the diversity values for each population and species. X and Y-axes in panel (D) are multiplied by 0.01 for easier visualization. X-axis in panel (C) is multiplied by 0.1.

richness was 5780.7 (SE = 368.01) and the highest values per species were found in *R. myconi* (7701.6; SE = 263) while the lowest were observed in *C. calceolus* (2822; SE = 883). The average ^{1}D, which considers the abundance of zOTUs and is better suited for comparisons between microbial communities, was 2596.5 (SE = 228.65); with the highest values found in *R. myconi* (3898.1; SE = 240) and the lowest in *C. calceolus* (850.4; SE = 500).

We found no statistically significant differences in aboveground species richness when comparing the rarefaction curves for S *vs* L nor S *vs* L1, L2 and L3 in most plant species, with the exception of *R. myconi* where the combination of the L patches was richer (Fig. 2C). The comparison of zOTU rarefaction curves indicated that all patches differed in richness regardless of plant species (Fig. 2D). These results were confirmed by the mixed-effect ANOVA, which showed no statistically significant differences between patches in any of the alpha diversity metrics for q values 0, 1, and 2, except for zOTU richness (^{0}D), in which small populations were richer (Fig. 2B, Table S9). Bootstrap analysis of the differences in diversity between L and S further supported this conclusion (Supplementary Material E).

3.2. Composition of visitor communities

Patches of each plant species appeared clustered in the NMDS based on the Bray-Curtis dissimilarities of aboveground arthropod visitors, suggesting that the composition of these communities differs between plant species (Fig. 3). This clustered pattern was weaker but also present in belowground bacteria communities. Based on visual inspection of the NMDS, the composition of visitors in S patches differed from those in L patches except for *G. lutea* in aboveground communities and *R. myconi* in both communities (Fig. 3). PERMANOVA tests confirmed statistically significant differences between population types in the composition of aboveground but not belowground communities (Table S10). When we differentiated between the turnover and nestedness components of community composition between plant populations, we found that the species turnover accounted for the majority of the differences between S and L as a whole, with an average of 97.1% (nestedness = 2.9) for aboveground visitors and 93.1% (nestedness = 6.9) belowground. In addition, species turnover represented an average of 97.6% (nestedness = 2.4) of the dissimilarity between patches S, L1, L2 and L3 aboveground and 94.8% (nestedness = 5.2) belowground. The composition of visitor communities differed not only at the species level but also at higher taxonomic levels. For example, in the S populations of *B. pyrenaica* and *G. nivalis* the vast majority of the interactions corresponded to Hymenoptera and Diptera respectively (Fig. S3), whereas the L populations tended to be more varied in composition. In contrast, the S populations of other plant species like *P. longifolia* had a more even community of visitors in terms of the abundance of taxa they interacted with, at least at the order level. Regarding the root communities, some groups of bacteria, like Betaproteobacteriales, Sphingomonadales and Rhizobiales, were common to all plant species, although the relative proportion of each bacterial group changed between hosts, with *C. calceolus* interacting with more diverse groups of bacteria (Fig. S3). However, the relative abundance of major bacterial groups was similar between patches of each plant species.

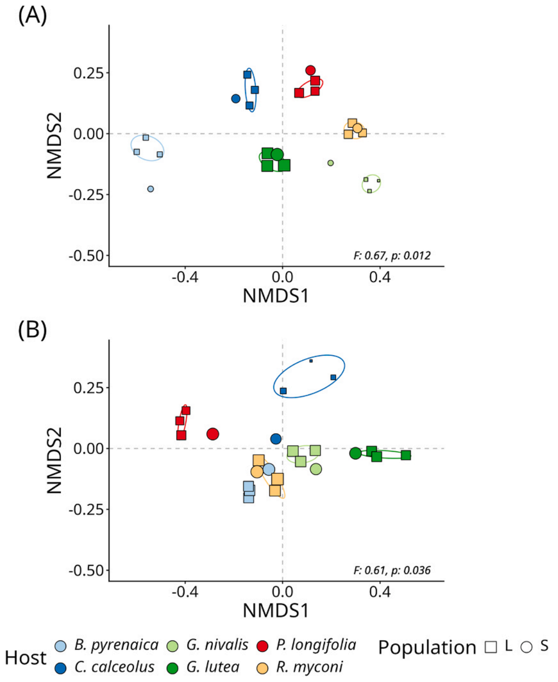

Fig. 3. Nonmetric multidimensional scaling based on the taxonomic composition dissimilarities between each plant species' community of visitors above- (A) and belowground (B). Symbol size indicates taxa richness. The *F-statistic* and *p*-value of the PERMANOVA analysis between plant patches are shown in the lower right corner of each plot.

3.3. Correlation between aboveground and belowground diversity patterns

All the correlation coefficients between aboveground alpha diversity metrics and their belowground counterparts were close to zero, with 95% confidence intervals overlapping zero (^{0}D: r = -0.03 CI$_{95}$[-0.43, 0.37]; ^{1}D: r = -013 CI$_{95}$[-05, 0.29]; ^{2}D: r = -0.03 CI$_{95}$[-0.43, 0.38]). On the other hand, the Mantel test comparing Bray-Curtis dissimilarities of above– and belowground community composition between patches showed a positive and statistically significant correlation (Mantel's: r = 0.6, CI$_{95}$[0.56, 0.66]).

4. Discussion

Here, we studied in-depth the aboveground arthropod and belowground bacteria communities interacting with six plant species of conservation interest, and explored the differences in alpha and beta diversity of these communities between patches in plant populations of different sizes. Host plants had a wide community of visitors, but we found no major differences in alpha diversity between plant patches after controlling for possible confounding factors. However, we did find differences in the composition of arthropod communities in most plant species, with patches in small populations being visited by communities distinct from those in larger populations of the same plant species. We found extremely weak correlations between the alpha diversity above- and belowground, but we observed that community dissimilarity was positively correlated between both, with patches that resembled more one another in their aboveground visitor community also being more similar in their belowground composition.

4.1. Rare species as hubs for biodiversity

Rather than discriminating towards any specific group of organisms such as pollinators or herbivores, in this study we tried to characterize as much of the universe of interactions of each plant as possible. In doing so, we observed that rare plants do not only interact with many species that visit the plant seeking a direct benefit, like herbivores and pollinators, but also with plenty of species displaying more subtle interactions such as using the plant as shelter, to hunt or lay eggs. Although these interactions might not directly benefit the host plant, they support other species not seeking specialized resources (Valiente-Banuet et al., 2015). Thus, the loss of rare plant species may negatively affect organisms that are usually overlooked in classical plant-animal interactions studies because they are not easily observed interacting with their host plants (Terry and Lewis, 2020). This highlights the importance of rare plant species as maintainers of biodiversity and interactions that might be relevant to ecosystem functioning, which has potential consequences for conservation biology (Bracken and Low, 2012, Mouillot et al., 2013). Given that rare species and small populations have a higher risk of extinction (Davies et al., 2004, Matthies et al., 2004), their visitors are more susceptible to losing important resources than others. The precise extent of that impact, however, depends on the degree of specialization of the visitors towards the host (Valiente-Banuet et al., 2015).

4.2. *Aboveground patterns of arthropod diversity*

We did not find any significant differences between the richness and abundance of aboveground arthropod communities visiting patches in small host plant populations and those visiting larger plant populations. This challenges our initial hypothesis that the visitors of patches located within smaller populations would be less diverse than those in larger plant populations because those patches offer less resources, especially to visitors specialized on a particular plant (Waser et al., 1996). This lack of difference may be explained by the fact that the plant species in our study are neither highly specialized nor restricted in their interactions with particular organisms. As a result, small plant populations are able to attract generalist visitors despite offering less resources (*e.g.* pollen) than larger populations, or compensate for their lower appeal by sharing visitors with other, more attractive plant species in the vicinity (Brosi, 2016).

Even though the richness and abundance of visitor species was similar between patches in different sized populations, the composition of aboveground arthropod visitors differed. More precisely, the patches in large populations were visited by communities that resembled one another more than they did the patch in the small population, following the idea that neighboring plant patches tend to interact with similar sets of species (Trøjelsgaard et al., 2015). Species turnover was the main driver of changes in visitor composition between plant patches, a pattern observed in other plant-pollinator interaction networks and habitats (Souza et al., 2021, Trøjelsgaard et al., 2015). This suggests that plant species in our study were visited by distinct assemblages of arthropod species en each patch rather than by subsets of a common pool of visitors.

There are many factors that may affect the diversity and composition of aboveground visitors, like local climate, habitat structure, host plant density or the composition of the surrounding vegetation (Joern and Laws, 2013). Our sampling design and statistical analyses controlled for the first two, and neither the density of host plants nor the diversity of the plants that co-occurred with our focal plants had a significant effect on visitor richness. However, we did find a significant positive correlation between the dissimilarities in the composition of arthropod visitors and the plants accompanying each host plant, suggesting that plant species that co-occur with similar plant communities also tend to be visited by similar sets of arthropods (Bascompte and Jordano, 2007).

4.3. *Belowground diversity patterns*

Following our initial expectations, we did not find any differences in the composition of root bacterial communities between patch types, whereas host plant species was the most important variable to explain community dissimilarity. These results support the idea of host plant specificity in root microbiota, in which plants of the same species tend to share bacterial communities of similar diversity and composition (Goberna and Verdú, 2016). This is further supported by the slightly higher proportion of nestedness that we observed in bacterial communities in comparison to aboveground visitors, which indicates that plants of the same species have a tendency to share subsets of a common bacterial community. We did observe significant differences in alpha diversity of microbial communities between patch types, with those within the small populations having richer communities than L patches. The diversity of these communities depends on several factors than can vary between plant patches like soil properties, the health status of the host plant or within-species specialization (Berendsen et al., 2012, Eck et al., 2019, Sasse et al., 2018). Unmeasured differences in any of these factors between small and large plant populations might favor bacteria with specific traits leading to the small differences in richness that we observed in bacterial communities.

4.4. *Aboveground vs belowground patterns*

The alpha diversity of aboveground arthropods visiting the studied host plants was not correlated with underground bacteria communities. On the other hand, the dissimilarity between aboveground visitors across plant patches showed a positive and statistically significantly correlation with the dissimilarity of belowground bacteria communities. The factors that determine the diversity of organisms visiting plants tend to be different aboveground (local climate and vegetation) and belowground (host plant characteristics and soil properties) (Wardle et al., 2004). However, above- and belowgorund communities are not entirely independent, as changes aboveground may affect the host plant and influence its belowground interactions, and vice versa. For instance, a healthy rhizosphere contributes to the good condition of its host plant, making it more attractive to potential visitors aboveground (Pineda et al., 2010). Furthermore, pathogens or herbivores can trigger defensive mechanisms in the plant that can affect the bacteria living in the roots as well as the visitors above through the release of different chemical compounds (Mithöfer and Boland, 2012, Pineda et al., 2010). Hence, changes in the composition of aboveground arthropods could affect the microbiota in the roots and vice versa, leading to the positive correlation between dissimilarity measures that we observed (Berendsen et al., 2012, Dedeyn and Vanderputten, 2005).

5. Conclusions

In this exhaustive study on the diversity of aboveground arthropod and belowground bacteria visitor communities of six rare plant species we found that local species richness and abundance of visitors did not differ between patches in small or large populations aboveground. However, small populations tended to have more diverse communities of bacteria. The composition of arthropod communities in large plant populations differed from those in small populations, with most of that variation being associated with species turnover. Although these differences were not found in bacteria communities, metrics of above- and belowground visitor community dissimilarity between plant patches were positively correlated, suggesting the existence of some common underlying factors or feedback loops between communities that shape changes in their composition. These results add new evidence and insights on the assembly patterns of arthropod and bacteria communities visiting rare and endangered plant species in populations of different sizes. In the current situation of global change, in which habitats and plant populations are becoming smaller and more fragmented due to human pressures, our results contribute to a better understanding of how a decrease in the size of plant populations could affect the diversity and composition of the communities they interact with. Our results challenge the intuitive idea that small populations should maintain less diverse communities of visitors, emphasizing the role of small plant populations as valuable reservoirs of biological diversity both above- and belowground.

CRediT authorship contribution statement

Adela González Megías: Data curation. **Sergio Albacete:** Data curation. **Joan Cáliz:** Writing – review & editing, Writing – original draft, Formal analysis, Data curation. **Jens M Olesen:** Writing – review & editing, Writing – original draft, Supervision, Methodology, Data curation, Conceptualization. **Francisco Martín:** Data curation. **Lidia del Arco:** Data curation. **María Jarne:** Data curation. **María Begoña García:** Writing – review & editing, Writing – original draft, Supervision, Project administration, Funding acquisition, Data curation, Conceptualization. **Héctor Miranda-Cebrián:** Writing – review & editing, Writing – original draft, Formal analysis. **Emilio Ortega Casamayor:** Writing – review & editing, Writing – original draft, Funding acquisition, Data curation. **Miguel Verdú:** Writing – review & editing, Writing – original draft.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.ppees.2026.125930.

Data availability

Data are available at DIGITAL.CSIC (http://hdl.handle.net/10261/287600).

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