

# ECOFLOR 2026: Book of Abstracts



February 6, 2026

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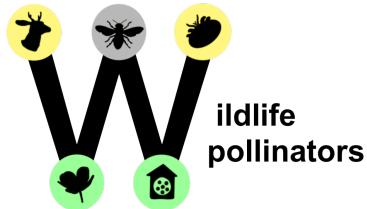
The ECOFLOR 2026 Book of Abstracts. The book may be downloaded as a PDF file from the [ECOFLOR 2026 website](#).

## Scientific Committee

The 23rd edition of EcoFlor meeting was organised by **the Wildlife Pollinators Group**, a research group of the **Wildlife Ecology and Health Lab**, based in the **Veterinary Faculty of the Autonomous University of Barcelona (UAB)**. Additional researchers from different institutions (IRTA, CTFC, IVIA, CREAF) are actively involved in the organisation.

In the Wildlife Pollinators Group we study the relationship between large herbivores (domestic and wild) and plant-pollinator communities and interactions, as well as in pollination function. We are also interested in understanding how other processes operating at large scales (such as wildfires) influence the assemblage of these communities. On the opposite (microscopic scale) side, we are interested in disentangling the mysteries behind solitary bee health. We conduct basic faunistic studies as well as research on bee diversity patterns in multiple types of habitats (including urban ecosystems, riparian ecosystems, and grasslands).

**Organisation committee:** Carlos Hernández-Castellano, Néstor Pérez-Méndez, Jordi Margalef-Marrassé, Alice Casiraghi, Jakub Štenc, Júlia Batlle-Benaiges, Júlia Coromina, Nil Guerrero, Marina Aguilar Grau,





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Jakub Štenc



Júlia Batlle-Benaiges





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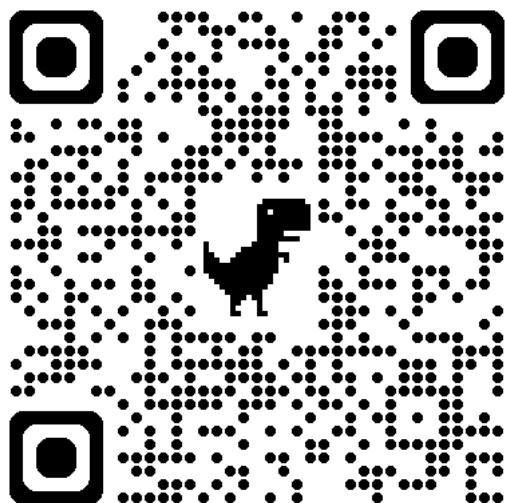


**Ajuntament de Tortosa**



## **Vote for the Best Presentation**

Please vote for the best student oral and poster presentation!



## Oral presentations

### Floral Evolution, Breeding Systems & Reproductive Success

#### Pollinator-mediated floral evolution in the pollination-generalised plant *Viscaria vulgaris*

**Presenting:** Aarushi Susheel

**Authors:** Aarushi Susheel; Felipe Torres-Vanegas; Ciara Dwyer; Yedra Garcia; Sophie Hecht; Magne Friberg; Øystein H. Opedal

**Affiliation:** Department of Biology, Lund University, Sweden.

Pollinator-mediated selection can lead to large variation in floral traits. This has been well researched in specialist systems, where one pollinator species interacts with a flowering species. In generalist systems, where one flowering plant interacts with several pollinator species, changes in the size and composition of the pollinator community can alter the patterns of selection acting on the plant. Through my PhD, I will study how a pollination-generalised flowering plant, *Viscaria vulgaris*, adapts to a functionally diverse pollinator community that varies both spatially and temporally. The study involves measurement of plant and pollinator phenotypes, pollinator visitation, pollinator effectiveness, and plant fitness. Combining these data with selection studies across multiple years in multiple populations, I aim to quantify the importance of functionally distinct pollinators in pollination and floral divergence. Initial data analysis has revealed functionally diverse pollinator assemblages within each plant population, along with evidence for phenotypic selection on floral traits. I plan to link these patterns by presenting findings from single-visit efficiency experiments and pollinator visitation rates to quantify the ‘importance’ of each pollinator in the local pollinator community of various populations. This would pave the way for constructing models that will assess the impact of functionally diverse pollinator assemblages on floral evolution.

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#### Beyond Seed Set: What Shapes Seed Quantity and Viability in Wild Plant Assemblages?

**Presenting:** Estefanía Tobajas

**Authors:** Estefanía Tobajas<sup>1</sup>; Luis J Chueca<sup>1</sup>; Christian Gostout<sup>1</sup>; Brais Hermosilla<sup>1</sup>; Jennifer Rose<sup>1</sup>; Xabier Salgado-Irazabal<sup>1</sup>; Celia Baigorri<sup>1</sup>; Montserrat Muriana<sup>1</sup>; Jon Poza<sup>1</sup>; Ainhoa Magrach<sup>1,2</sup>

**Affiliation:** <sup>1</sup> BC3 - Basque Centre for Climate Change - Klima Aldaketa Ikergai. Sede Building 1, 1st floor | Scientific Campus of the University of the Basque Country 48940 Leioa (Spain). <sup>2</sup> Ikerbasque, Basque Foundation for Science, Bilbao (Spain).

Understanding the drivers of plant reproductive success is crucial for predicting population dynamics and ecosystem functioning. Reproductive success depends not only on the number of fruits and seeds produced, but also on the viability of these seeds, an aspect that is seldom considered in pollination studies. In this study, we investigated the factors influencing both seed production and seed viability within a diverse plant community. During 2024, we marked and collected fruits from multiple plant species across 16 sites in Gorbea Natural Park (N Spain), quantified their seed production, and assessed seed viability using tetrazolium staining. Preliminary results show that plant species richness has a positive effect on seed set, although the magnitude of this effect varies among species. We also find evidence of a trade-off between seed quantity and seed quality: fruits with more seeds tend to produce a lower proportion of viable seeds. Next steps will incorporate additional mechanisms, including temporal and resource use overlap among plant species, functional diversity, and pollinator community structure, to better understand the pathways shaping reproductive outcomes. Overall, this study highlights the value of integrating seed production and viability to understand plant reproductive success, and underscores the influence of community composition and biotic interactions on reproductive performance in natural plant communities.

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### Integrated fitness pathways expose concealed habitat-loss impacts in sexually deceptive orchid

**Presenting:** Joshua Borràs

**Authors:** Joshua Borràs<sup>1</sup>; Miquel Capó<sup>1,2</sup>; Yedra García<sup>3</sup>; Øystein H. Opedal<sup>3</sup>; Amparo Lázaro<sup>4</sup>; Joana Cursach<sup>1</sup>

**Affiliation:** <sup>1</sup> Botany on Mediterranean Islands Research Group, Department of Biology, Universitat de les Illes Balears, Palma, Spain. <sup>2</sup> Plant & Animal Ecology Lab. Centro para la Conservación de la Biodiversidad y el Desarrollo Sostenible, Departamento de Sistemas y Recursos Naturales, Universidad Politécnica de Madrid, Madrid, Madrid, Spain. <sup>3</sup> Department of Biology, Division of Biodiversity and Evolution, Lund University, Lund, Sweden. <sup>4</sup> Global Change Research Group, Mediterranean Institute for Advanced Studies (IMEDEA; UIB-CSIC), Esporles, Balearic Islands, Spain.

Natural habitat loss is one of the main threats to biodiversity. Understanding how landscape degradation affects reproductive success is essential for plant conservation, especially for species involved in specialized pollination systems. We evaluated how habitat loss influences reproductive fitness in the sexually deceptive *Ophrys balearica* using two years of data from six populations, three in conserved and three in disturbed landscapes. We quantified herbivory

affecting flowers and inflorescences, pollinaria removal and deposition, fruit production, plant traits, and the composition of co-flowering species. A path-analytical modelling framework tracked each reproductive stage to assess how habitat loss, herbivory and pollination shape reproductive output. Herbivory was the strongest constraint on reproductive fitness. Both herbivory and pollinator visitation were higher in disturbed landscapes, with visitation varying across sites and years with no differences in observed fitness. Floral display increased visitation and improved both male and female fitness components, although morphological traits explained little fitness variation once herbivory and visitation were accounted for. Overall, orchid populations in disturbed landscapes showed cumulative reductions in relative fitness when all reproductive stages were integrated. This study shows that habitat loss alters herbivore pressure and pollinator visitation, leading to reduced reproductive success in this sexually deceptive orchid.

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### **Phylogeography of an invasion to track rapid floral evolution**

**Presenting:** Maria Clara Castellanos

**Authors:** Romero-Bravo, A., J. O'Flaherty, J. Green, L. Unwin & M.C. Castellanos

**Affiliation:** Department of Ecology & Evolution, University of Sussex, UK.

Recent plant range expansions where pollinators change provide a unique opportunity to study the potential and speed of floral adaptive change. We have been studying the common foxglove, *Digitalis purpurea*, to investigate convergent floral changes after the addition of hummingbirds as pollinators when naturalised in tropical mountains. In addition to our previous reports of morphological changes, we now have new evidence of changes in nectar traits consistent with bird pollination. To confirm the convergent nature of these changes, here we use a phylogeographic approach to reconstruct the invasion of focal Colombian and Costa Rican populations from the native European range. We used genotyping-by-sequencing on individuals from eleven native populations in Europe and three populations in the introduced range. Our phylogeographic reconstruction points at Central Europe as the source of two recent and independent introduction events to South and Central America. Within the native range, population structure is consistent with a historic northward expansion from southern European populations and the colonisation of Norway from Britain across the North Sea. Our phylogeographic analysis provides the most comprehensive insight onto the colonisation history and the genetic relationships across populations of *Digitalis purpurea*, an emerging model species to study adaptive changes in novel pollinator environments.

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## **Gene expression plasticity across regulatory pathways for flowering time in *Arabidopsis thaliana***

**Presenting:** Patricia Roca Villanueva

**Authors:** Patricia Roca-Villanueva<sup>1</sup>; Ana García Muñoz<sup>1</sup>; A.Jesús Muñoz-Pajares; Mohamed Abdelaziz; Xavier Picó<sup>2</sup>

**Affiliation:** <sup>1</sup> Departamento de Genética, Universidad de Granada, Granada. <sup>2</sup> Departamento de Ecología y Evolución, Estación Biológica de Doñana (EBD-CSIC), Sevilla.

Gene expression plasticity can be defined as the ability of a single gene to adjust its expression in response to changes in the environment. Understanding how environmental cues affect gene expression plasticity in field conditions is a major challenge, which may help grasp the complexity of genotype-phenotype relationships. Nevertheless, gene expression plasticity in natural conditions has barely received attention due to the logistical complexity to estimate gene expression outdoors. In this study, we investigated how environmental conditions modulate the expression of flowering-related genes from all known regulatory pathways in natural accessions of *Arabidopsis thaliana* across multiple timescales relevant for gene expression. Using generalized linear mixed models (GLMMs) on a previous whole-genome gene expression dataset obtained from locally-adapted accessions in natural conditions, we evaluated gene expression plasticity across diurnal (morning vs. afternoon), seasonal (across developmental stages: vegetative, inductive, and reproductive), and annual timescales (over two different years). Our analysis focused on a set of 306 known genes in *A. thaliana* related to flowering time to estimate their expression plasticity and to quantify the differences across accessions and various regulatory pathways. Overall, our work provides valuable insights to understand how genes and regulatory pathways for flowering respond to natural environmental variation to complete the vegetative-to- reproductive transition in plants, which is a major trait under strong selection in annuals and short-lived perennials.

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## **Kinship, cross pollination and self-incompatibility: exploring the fitness costs of genetic viscosity.**

**Presenting:** Camilo Ferrón

**Authors:** Camilo Ferrón<sup>1,2</sup>; Ana García-Muñoz<sup>1,2</sup>

**Affiliation:** <sup>1</sup> Departamento de Biología y Geología, Física y Química Inorgánica, Universidad Rey Juan Carlos (URJC), Móstoles, 28933, Spain. <sup>2</sup> Instituto de Investigación en Cambio Global (IICG-URJC), Universidad Rey Juan Carlos, Móstoles, 28933, Spain.

In cross-pollinated systems lacking seed-dispersal mechanisms, pollinator activity strongly determines the spatial arrangement of individuals within a population. Consequently, neighbouring plants often exhibit greater genetic similarity than expected by chance, increasing the likelihood of mating among relatives. Such inbreeding can reduce fitness due to the expression of recessive deleterious alleles associated with higher genetic homogeneity between pollen donor and receptor. We used *Moricandia moricandoides*, an allogamous, hermaphroditic and self-incompatible species, to (i) characterize the degree of self-incompatibility, (ii) evaluate the costs of reproduction between related individuals, and (iii) assess how the parental neighbourhood influences offspring performance. We worked with a parental generation with known spatial genetic structure and a second generation of 320 individuals with known relatedness. A total of 820 directed controlled crosses were performed, varying the genetic distance between donors and receptors and accounting for parental neighbourhood. We assessed the success of forced self-pollination and cross treatments by measuring fruit set, seed number and seed set. Our results show that forced self-pollination succeeded more often than expected for a self-incompatible system, and that cross success increased with genetic distance between parents. These patterns suggest a partially relaxed self-incompatibility system that may promote reproduction within familial patches, while favouring genetically more distant crosses.

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## Traits, Plasticity & Signals

### Flower economic spectrum: A key to understanding the floral diversity of alpine plants

**Presenting:** Lucie Holzbachová

**Authors:** Lucie Holzbachová<sup>1</sup>; Petr Sklenář<sup>1</sup>; Jakub Štenc<sup>1,2</sup>

**Affiliation:** <sup>1</sup> Faculty of Science, Charles University, Prague. <sup>2</sup> CREAf, Spain.

Flowers of zoogamous plant species are subject to combined selection pressures from abiotic and biotic factors, yet their impact on floral diversity has mostly been studied separately. The concept of the Flower Economic Spectrum (FES) has been recently proposed to understand the evolutionary phenotypic variation and diversity of functional traits in flowers that evolved under multiple selection factors. The world's mountainous regions are home to a large part of global biodiversity and mountain environments impose strong pressures on flowering, such as extreme climatic conditions and low abundance and diversity of pollinators. However, not all alpine regions share the same conditions. Tropical and temperate mountains differ in many important ecological factors that strongly influence generative plant reproduction. We studied more than 50 herbaceous and woody species from two mountain regions (Ecuador and the USA). The study examines the phenotypic variability of alpine flowers through the lens of the FES, i.e. relationship between flower longevity and investment into flower biomass (cost of

flower production). Our preliminary results show a positive association between flower biomass investment and flower longevity, with differences in longevity patterns between the two alpine regions. Together, these findings provide empirical support for the proposed Flower Economic Spectrum.

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### **Flower orientation influences wild pollinator behaviour: a field study on natural and artificial flowers**

**Presenting:** Chiara Buonanno

**Authors:** Chiara Buonanno<sup>1</sup>; Giannetti Daniele<sup>1</sup>; Marta Barberis<sup>2</sup>; Marta Galloni<sup>2</sup>; Donato A. Grasso<sup>1</sup>

**Affiliation:** <sup>1</sup> Department of Chemistry, Life Sciences and Environmental Sustainability, University of Parma, Italy. <sup>2</sup> Department of Biological, Geological and Environmental Science, University of Bologna, Italy.

The foraging activity of bees is a complex behaviour that depends, among other factors, on some physical features of flowers. Of particular importance are accessibility of floral rewards, floral proportions, symmetry and orientation. Several studies have investigated the effects of flower orientation using colonies of bees under experimental controlled condition. In the present study we performed field experiments employing both artificial and natural flowers (different species of the genus *Salvia*) characterized by zygomorphic symmetry. By altering the orientation of flowers, we analysed how different species of wild bees approached and interacted with them. The results showed that pollinators visiting artificial flowers, especially of family Halictidae, preferred those with a horizontal landing surface. Concerning real flowers, several species of Apidae visited significantly more flowers with natural orientation or those turned of 90°. Our results, including observations on insect approach and visiting methods, showed that even minor alterations in flower orientation can markedly affect pollinator behaviour, providing new perspectives into the ecological and evolutionary mechanisms shaping plant-pollinator interactions.

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### **Floral Trait Thermal Plasticity in a Common Crop**

**Presenting:** Lucy Unwin

**Authors:** Unwin, L. A., Millerchip, E. K., Dadswell, C., Castellanos, M. C

**Affiliation:** University of Sussex, United Kingdom.

Plasticity in floral traits, particularly those related to pollinator reward and attraction, can influence both the types of pollinators that visit a flower and the nature of those interactions. As flowers commonly exhibit suites of traits that align with pollinator preferences, environmentally driven (=plastic) changes in floral traits can alter plant-pollinator interactions in both crop and wild plants. Whilst floral nectar traits have frequently been cited as ‘highly plastic’, many studies do not measure true plasticity - that is, variation in trait expression across environments within the same genotype. Consequently, the true extent of plasticity in floral nectar traits remains poorly understood. Understanding this is central to predicting the resilience of plant–pollinator interactions in the face of environmental change. We used an experimental setup to measure plasticity in response to temperature in floral nectar volume, flower size, and nectar sugar characteristics in the common bean *Phaseolus vulgaris* L., a globally important crop in the Fabaceae family. *P. vulgaris* individuals were grown in controlled greenhouse conditions, then allowed to flower at temperatures of 16, 23, and 30°C for 3-day periods. Individual plants experienced multiple temperature treatments to assess plasticity in floral traits. Both nectar volume and flower size show significant plasticity in response to temperature. For both traits, the response to temperature was quadratic, consistent with the presence of a thermal optimum. Interestingly, plants varied in their baseline nectar production, but the shape of the plastic response was highly consistent across plants, suggesting plant-level physiological control of this trait. For flower size, plastic responses were less consistent and there was variation across flowers within plants. Understanding the plasticity of floral traits in crop species provides key information on the potential to breed cultivars with stable reward production that can benefit both yields and pollinators.

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## Community Ecology, Networks & Niche Partitioning

### How is the buzz-pollination niche partitioned among co-flowering plants?

**Presenting:** Agnes Dellinger

**Authors:** Benjamin Lazarus; Agnes S. Dellinger

Co-flowering plants may overlap or diverge in pollination niche, with traits related to pollinator attraction (e.g., color, scent) and fit (e.g., herkogamy) regarded as particularly important in mediating pollination niche position. Buzz-pollinated flowers are particularly interesting in this context since they have a third, invisible and understudied trait component determining niche position: their vibrational properties. Buzz-pollination is a functionally highly specialized pollination mechanism where large quantities of pollen can only be dislodged when bees apply vibrations in the range of 100-400 Hz to the flowers. Whether co-flowering, buzz-pollinated

species are “tuned” to different bees, or rely on common strategies of niche partitioning such as differential attraction and fit, remains unclear. In my talk, I will explore these questions using community-level plant-pollinator interaction studies of the plant family Melastomataceae as a model. Melastomataceae are among the largest plant families worldwide (close to 6000 species), almost exclusively buzz-pollinated (96% of species, adaptive plateau) and multiple species are commonly co-flowering in diverse tropical habitats. Using comparative assessments of plant-pollinator interactions, single visit experiments and artificial vibration experiments (mimicking bees), we find that co-flowering Melastomataceae often overlap in their bee visitor assemblages, but that size-matching with bees (herkogamy) plays a critical role in niche differentiation. Our artificial vibration experiments further indicate that different species have different vibration optima, and that differential “tuning” may indeed be an important mechanism of pollination niche differentiation.

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### **Plant–pollinator networks in a riparian and an adjacent terrestrial ecosystem: rivers as biodiversity hotspots and refuges**

**Presenting:** Nil Guerrero Kersten

**Authors:** Nil Guerrero<sup>1</sup>; Jordi Margalef-Marrasé<sup>2,3</sup>; Mariona Cuesta<sup>1</sup>; Jorge López<sup>1</sup>; Joan Pérez<sup>1</sup>; Carlos Hernández-Castellano<sup>4</sup>

**Affiliation:** <sup>1</sup> Wildlife Ecology & Health (WE&H), Servei d’Ecopatologia de Fauna Salvatge (SEFaS), Universitat Autònoma de Barcelona, Cerdanyola del Vallès, Spain. <sup>2</sup> Centro de Investigaciones Sobre Desertificación (CSIC-UV-GV), Moncada, València E46113, Spain. <sup>3</sup> Centre de Ciència i Tecnologia Forestal de Catalunya (CTFC), Solsona, Catalunya E25280, Spain. <sup>4</sup> Department of Ecology, Faculty of Environmental Sciences, Czech University of Life Sciences Prague, Kamýcká 129, Praha – Suchdol, 165 00, Czech Republic.

Riparian ecosystems may function as key biodiversity refuges for pollinators, especially in the Mediterranean, where droughts are recurrent. However, research on plant-pollinator systems in riparian ecosystems is extremely rare. This study aimed to (1) characterize the plant-pollinator network of a riparian ecosystem, and (2) compare it with those of an adjacent terrestrial ecosystem.

We conducted plant-pollinator surveys along a 500 m stretch of the Algars River (NE Spain) in August, during the flowering peak. We calculated several metrics of community and network complexity, and compared them with those from an adjacent terrestrial ecosystem monitored monthly from March to October.

In August, all community and network variables in the riparian ecosystem were higher than in the terrestrial ecosystem. Moreover, community and network complexity of the riparian

ecosystem was similar or even exceeded that observed in the flowering peak (May) of the terrestrial ecosystem.

Our study demonstrates that riparian ecosystems may act as biodiversity hotspots and biodiversity refuges for pollinators.

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### **Pasture size and grazing intensity shape bee diversity patterns in a Mediterranean ecosystem**

**Presenting:** Júlia Batlle-Benaiges

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In human-dominated Mediterranean ecosystems, open habitats result from anthropogenic activities such as livestock grazing. Because bees rely on open habitats, understanding how bee diversity responds to pasture features is important for their conservation. We evaluated how bee richness relates to flower richness, pasture size, and grazing intensity. We conducted flower-bee censuses during the flowering peak in seven pastures of varying size (0.1-1 ha) and intensity (extensive vs. intensive). We calculated  $\alpha$ ,  $\beta$ , and  $\gamma$ -diversity of bees and built linear models to link bee and flower richness and evaluate species-area relationships. Bee richness was determined primarily by  $\beta$ -diversity, with each pasture hosting many idiosyncratic species, and increased linearly with flower richness (slope ~1). Bee richness showed opposed species-area relationships depending on grazing intensity: negative for extensive pastures, and positive for intensive pastures. As such, there is a threshold at 0.65 ha –below it, conversion from intensive to extensive results in a colonisation credit; above it, in extinction debt. While in small intensive pastures flower shortage may be limiting, in large extensive pastures, flower dominance may result in the simplification of bee communities. Therefore, bee conservation in pastures should establish a network of spatially scattered patches with diverse floral resources.

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## **A multidimensional approach reveals pollination niche partitioning among terrestrial orchids**

**Presenting:** Aurélien Caries

**Authors:** Caries Aurélien; Friberg Magne; Opedal Øystein; García García Yedra

**Affiliation:** <sup>1</sup> Department of biology, Lund University, SE-223 62 Lund, Sweden.

Pollinator-mediated reproductive interactions between co-flowering species are increasingly recognized for their role in community structure. Pollination traits, flowering phenology and spatial distribution are key axes of the pollination niche, yet few studies have assessed their combined effects on community assembly. We quantified pairwise overlap in pollination niches among 16 orchids, including rewarding and deceptive species, using floral traits related to pollinator attraction and pollination efficiency measured at two sites on Öland (Sweden). We collected flowering times and spatial co-occurrence data from a citizen-science database. At the local level, we compared the coefficient of variation per trait between pollination strategies (deceptive vs. rewarding) and trait values across sites. Most species pairs overlapped in at least one axis of the pollination niche. Typically, species with high overlap across multiple niche dimensions represented cases where the literature suggests pollinator niche partitioning. Three food-deceptive species overlapped strongly in niche space, despite sharing pollinators. While character displacement for unmeasured traits via competition may occur, we hypothesise that trait divergence may instead promote facilitation by maintaining pollinator deception and increasing visitation. Our findings highlight the complementary role of different niche dimensions in enhancing species coexistence and support emerging evidence that deceptive orchids may facilitate each other.

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## **The impact of *Impatiens glandulifera* (Himalayan Balsam) on the pollination of the native *Stachys sylvatica* (Hedge Woundwort) in the UK**

**Presenting:** Samira Ben-Menni Schuler

**Authors:** Samira Ben-Menni Schuler<sup>1</sup>; Laura Mary White<sup>2</sup>; George Horn<sup>2</sup>; Rocío Pérez-Barrales<sup>1,2</sup>

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Invasive plants can alter pollination dynamics by attracting shared pollinators away from native flora, potentially reducing reproductive success. *Impatiens glandulifera* (Himalayan balsam) is a widespread invader in the UK whose large, nectar-rich flowers attract bumblebees and may disrupt native pollination. We assessed its impact on the pollination of the native

*Stachys sylvatica* through (1) observations in pristine and invaded sites and (2) an experimental introduction of *I. glandulifera* into an uninvaded habitat. Across natural sites, *S. sylvatica* stigmas in invaded areas received ~3.5 times less conspecific pollen than in pristine sites. In the introduction experiment, the arrival of *I. glandulifera* caused a rapid decline in conspecific pollen deposition, decreasing by ~80% within four days, while invasive pollen appeared on up to 70% of stigmas. Combined visitation and pollen data indicate that behavioural diversion of bumblebees better explains the reduction in conspecific pollen than heterospecific pollen deposition. Our results provide experimental evidence that *I. glandulifera* can swiftly disrupt native pollination processes during early invasion stages, highlighting the vulnerability of co-flowering natives and the need for management strategies that limit Himalayan balsam establishment in sensitive riparian habitats. away from native flora, potentially reducing reproductive success. *Impatiens glandulifera* (Himalayan balsam) is a widespread invader in the UK whose large, nectar-rich flowers attract bumblebees and may disrupt native pollination. We assessed its impact on the pollination of the native *Stachys sylvatica* through (1) observations in pristine and invaded sites and (2) an experimental introduction of *I. glandulifera* into an uninvaded habitat. Across natural sites, *S. sylvatica* stigmas in invaded areas received ~3.5 times less conspecific pollen than in pristine sites. In the introduction experiment, the arrival of *I. glandulifera* caused a rapid decline in conspecific pollen deposition, decreasing by ~80% within four days, while invasive pollen appeared on up to 70% of stigmas. Combined visitation and pollen data indicate that behavioural diversion of bumblebees better explains the reduction in conspecific pollen than heterospecific pollen deposition. Our results provide experimental evidence that *I. glandulifera* can swiftly disrupt native pollination processes during early invasion stages, highlighting the vulnerability of co-flowering natives and the need for management strategies that limit Himalayan balsam establishment in sensitive riparian habitats.

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### **Lower Disturbance Correlates with Higher Robustness and Reduced Connectance in Plant–Pollinator Networks in Es Trenc Natural Park (Mallorca)**

**Presenting:** Fortunato Fulvio Bitonto

**Authors:** Bitonto F. F.<sup>1</sup>; Serra P. E.<sup>2</sup>; Fuster Bejarano F.<sup>2</sup>; Gutierrez R.<sup>2</sup>; Galloni M.<sup>1</sup>; Traveset A.<sup>2</sup>

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The Biodiversity Strategy for 2030 and the Nature Restoration Law require EU Member States to strengthen biodiversity monitoring and restore degraded ecosystems. In line with these, we conducted a plant–pollinator network assessment from March to June 2023 in two areas within

the Es Trenc–Salobrar de Campos Natural Park (Mallorca, Spain): a human-impacted and a relatively undisturbed site. Pollinators were surveyed every two weeks along a mobile transect, collected with hand-nets, and identified to species level. Floral resources were evaluated using twelve randomly placed 1-m<sup>2</sup> plots per area per monitoring day. We recorded more than 1,500 insect individuals belonging to 120 species, including 20 bee species classified as Data Deficient, Nearly Threatened, or Endangered in the European IUCN Red List. Floral surveys documented over 1,300 flowering units from more than 50 plant species, including the endangered *Helianthemum caput-felis*. Network-level metrics indicated that the less disturbed site exhibited higher ecological robustness and lower connectance compared with the anthropized area, suggesting a more stable and resilient plant–pollinator system. These findings will be shared with the park authorities to help inform evidence-based conservation actions aimed at supporting plant and pollinator communities, contributing to reducing the information gap in the Mediterranean Basin.

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### **How reliable are pollinator population trends? An interplay between duration, variability, and autocorrelation**

**Presenting:** Julia G. de Aledo

**Authors:** Julia G. de Aledo; François Duchenne; Ignasi Bartomeus

Pollinators are susceptible to anthropogenic influences including climate change, habitat loss, and agricultural intensification. While pollinators are key in providing ecosystem services, supporting ~85% of wild flowering plant species, detecting population changes remains a challenge. Existing models leave a gap in understanding fast-lived insect dynamics. In the currently available data, there is an over-representation of recent and short time series. Our goal is to evaluate the degree of robustness the available data can offer to assess trends. To do so, we analyze how statistical power and the probability of false positives are affected by key factors: duration, slope, stochasticity, and temporal autocorrelation. Additionally, we aim to explore how these trends are compatible with the expectations of stable populations by developing a null-model approach. We found a 20% probability of detecting false positives with the available pollinator data. We propose practical thresholds (more than 10 years) for an acceptable statistical power (75%) to ensure trend inferences are robust enough. However, rigorous evaluation of trends leads to a mismatch between the need of long-term monitoring programs and the emergency of taking conservation actions. To shorten this distance, we provide a framework to test the compatibility of short observed changes with expected ecological stability of a reference population. This framework will introduce a complementary index to help understand the observed trends.

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## **Beetles (Coleoptera) are more than just inefficient mess-and-soil pollinators**

**Presenting:** David Peris

**Authors:** David Peris

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Beetles (Coleoptera) are often characterized as inefficient or incidental “mess- and-soil” pollinators: flower visitors that pollinate flowers while damaging them. However, growing evidence reveals their substantial and ancient role in the evolution of plant pollination systems. An estimated 20% of about 400,000 species of beetles (Coleoptera) are flower visitors. Cantharophilous plants exhibit traits—such as robust floral structures, thermogenesis, and strong, often spicy or fruity scents, protogynous flowers—specifically suited to beetle visitation. Beyond their contributions to basal angiosperms, beetles also participate in the pollination of economically significant crops. But more importantly, as one of the earliest insect lineages to interact with flowering plants, beetles have driven key floral adaptations through their diverse feeding behaviors, sensory ecology, and morphological variation. These findings highlight the complexity of beetle–flower mutualisms and underscore the importance of reevaluating beetles not as inefficient pollinators, but as key evolutionary agents that have shaped modern pollination ecology.

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## **Real world open pollinator communities shapes plant–pollinator networks across land-use gradients**

**Presenting:** Nerea Montes Pérez

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Over recent decades, agricultural intensification and habitat fragmentation have become major drivers of declines and local extinctions. Understanding how these pressures affect ecological dynamics is particularly crucial for plant–pollinator interaction networks, which sustain the essential ecosystem service of pollination. Previous research has shown that land- use intensification reduces plant and pollinator abundance and diversity, often favouring generalist species. Yet most of these studies typically treat communities as closed systems where species cannot be replaced after disturbance. This assumption may underestimate the capacity of ecological communities to persist and buffer environmental change. Here, we investigate how plant and pollinator abundance, species richness and key network properties shift along an agricultural

gradient and compare these responses to expectations under a hypothetical closed-community scenario. We sampled plant–pollinator networks over one season across 30 sites spanning a land-use gradient in the Doñana Protected Area. Our study provides a framework to disentangle how community turnover and network reconfiguration contribute to the resilience of pollination systems in human-modified landscapes.

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### **Effects of forest structural heterogeneity on hoverfly diversity and pollination potential.**

**Presenting:** Clàudia Massó Estaje

**Authors:** Clàudia Massó Estaje, Anne Chao, Jörg Müller, Alice Claßen, Ingolf Steffan-Dewenter

Habitat homogenization from intensive forest management has reduced pollinator diversity, threatening forest regeneration and plant reproduction. Experimental evidence on how forest structural heterogeneity influences pollinator communities at the landscape scale, however, remains scarce. We tested whether enhancing structural heterogeneity through deadwood enrichment and canopy gap creation (Enhancement of Structural Beta Complexity, ESBC) promotes hoverfly diversity, key pollinators in temperate forests, and whether this effect is driven by local ( ) diversity or species turnover ( diversity). Our large-scale forest experiment across 11 regions in Germany compared paired small forest landscapes (ESBC vs. control), comprising 234 patches sampled with pan traps across three seasons. Using incidence-based Hill numbers, we quantified taxonomic, functional, and phylogenetic diversity (TD, FD, PD) at , , and scales. Structurally heterogeneous landscapes supported higher -diversity across all biodiversity dimensions, particularly for taxonomic richness, suggesting that rare hoverfly species benefit most. Most diversity gains were driven by rather than components. Our findings provide experimental evidence that enhancing forest structural heterogeneity can restore multi-dimensional pollinator diversity, reinforcing its potential to sustain floral visitation networks and counteract biotic homogenization.

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### **Alpine & Montane Ecology**

#### **Reproductive strategies in plants of temperate and tropical alpine orobomes**

**Presenting:** Alptekin Koc

**Authors:** Alptekin Koc

**Affiliation:** Dept. of Botany, Charles University, Czech Republic

Pollinator composition varies considerably between tropical and temperate alpine areas. Due to the continuous vegetation period in the tropical alpine and them on average existing at higher altitudes than temperate alpine regions, their invertebrate pollinator density is far lower and mostly consists of flies. For temperate alpine habitats during the summer, their pollinator density is higher with a more varied pool of available pollinators than for the tropical counterpart. The question is: How do plants cope with these conditions? Plants do not always depend on pollinators for their sexual reproduction. They can also be completely autonomous by being selfers or even apomicts. With the differences in pollinators in mind, it would be assumable that there could be more autonomous species present in the tropical alpine compared to the temperate alpine. I investigated this aspect by doing pollination experiments of different treatments in the field in the tropical Andes and the temperate alpine Rocky Mountains. The resulting seed sets I used to determine if pollinators are essential for the local plant species reproduction and if they are pollen limited. The results can help with establishing focused conservational efforts for certain pollinator groups in these unique habitats.

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### **Altitudinal variation in floral allometry and its relationship with pollinators along an altitudinal gradient of the tropical Andes of Bolivia**

**Presenting:** Andrés Romero-Bravo

**Authors:** Andrés Romero-Bravo<sup>1</sup>; Øystein H. Opedal<sup>1</sup>; and Sissi Lozada-Gobilard<sup>1,2</sup>

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Flower traits are shaped by breeding systems and the biotic and abiotic factors defining the pollinator environment and may thus vary along environmental gradients. Environmental variation along altitudinal gradients is often associated with changes in plant and animal diversity, making such gradients ideal systems to study variation in flower traits and their relationship with pollinators. We measured flower traits related to advertisement and pollinator fit in 60 plant species and recorded their legitimate pollinators along an altitudinal gradient (400–4400 m) in the tropical Andes of Bolivia. Flower traits included flower size (advertisement), entrance diameter, flower length and anther-stigma distance (fit). We tested the intra-floral modularity hypothesis which predicts that traits regulating fit tend to be more canalized than those involved in advertising. Specifically, we asked whether canalization varies along the studied altitudinal gradient and across different groups of pollinators. To do so, we compared the allometric relationships of advertisement vs fit traits. Preliminary results show that fit traits are indeed more canalized without any significant change along the environmental gradient or pollinator groups, although bee-pollinated flowers seem to be more canalized than those relying on other pollinator groups, especially birds.

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## **Comparison between the pollinator communities of tropical and temperate alpine environment of the New World.**

**Presenting:** Helena Pijálková

**Authors:** Helena Pijálková<sup>1</sup>; Tadeáš Ryšan<sup>1</sup>; Lucie Holzbachová<sup>2</sup>; Jakub Štenc<sup>1,2,3</sup>; Alptekin Koc<sup>3</sup>; Shannon Serpa<sup>1</sup>; Nyika Campbell<sup>4</sup>; Petr Sklenář<sup>2</sup>; Álvaro Barragán<sup>5</sup>; Sisimak Duchicela<sup>4</sup>; Jiří Hadrava<sup>1</sup>

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Our present study compares two areas belonging to the Cordillera mountain range. Our aim is to provide an insight into the composition of pollinators, and which predictors might affect the seasonal variability in the pollinator communities. The alpine environment hosts many kinds of flowers, many of which rely on insect pollinators. Yet pollinators of alpine environments remain historically understudied, especially in the tropics. In the tropical Andes, highest altitudes are cold and windy, with temperatures at night falling below 0 °C. However, these conditions remain relatively stable throughout the year, with most prominent changes being driven by the seasonal differences in precipitation (rainy vs. dry season). In contrast, temperate alpine environment of Colorado Rocky Mountains has very short vegetational season, of about three months, when the biota must reproduce rather quickly. During this time of the year, the temperatures often exceed 15 °C. Due to these differences, we can expect both alpine environments to have very different pollinator communities. Both areas were dominated by the Diptera, however the changes in insect composition throughout the seasons differs greatly between the two areas, as a consequence of seasonal fluctuations in climate conditions and availability of floral sources.

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## **Bee sampling methods along a tropical elevational gradient**

**Presenting:** Pedro Alonso-Alonso

**Authors:** Pedro Alonso-Alonso

**Affiliation:** Department of Animal Ecology and Tropical Biology, Biocenter, University of Würzburg, Würzburg, Germany.

Despite their relevance as pollinators, bees (Hymenoptera: Anthophila) are not frequently sampled in the wet tropics, where bee research is mostly taxonomical, leaving ecology often aside. In the Neotropics, two groups have got most of the attention, Euglossini and Meliponini, due to their abundance, but also because ecologists know how to catch them. Most methods for collecting bees have been tested in temperate ecosystems and applied in tropical forests without testing their efficiency. We studied bees along an elevational gradient in SE Peru, in the tropical Andes aiming to understand the environmental drivers behind their diversity and abundance patterns. During 11 months of fieldwork, we completed 3 rounds of sampling in 26 locations. We covered the whole gradient from the open Polylepis woodland at 3500 m asl to the lush amazonian Terra firme forests at 230 m asl. To optimize the bee sampling we used multiple methods, catching bees actively during transect-walks and attracting them with scents and also passively using different kinds of traps. Here we discuss the success of the different methods used to collect bees in the different kinds of forests found in the elevational gradient of the eastern slope of the tropical Andes.

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### Comparison of Mountain Pollination in Ecuador and the Colorado Rocky Mountains

**Presenting:** Tadeáš Ryšan

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Mountain ecosystems impose environmental constraints, including temperature fluctuations, steep topography, and variable resource availability. Despite these challenges, they support communities with remarkably high biodiversity and a high degree of endemism. Adaptation to environmental adversity is a key driver of this diversity: species that persist in mountains must develop a range of physiological and ecological traits, from generalism to narrow specialism. But how do these environmental constraints influence the pollination relationships between plants and their pollinators? Do pollinator networks in tropical paramo, which have relatively stable climates but complex topography, tend to be more diverse and specialized than those in temperate mountains with shorter growing seasons, or is the opposite true? In our research, we investigated flowering plant and pollinator communities throughout the flowering season using pollination transects at Pichincha Volcano in Ecuador and Niwot Ridge, Colorado, USA. Our goal was to determine how pollinator networks are structured and how they are influenced by the unique environmental challenges of high-mountain ecosystems. Using the pollination

snapshot method, we recorded several thousand interactions over the entire growing season. exposing to different environments, so it can be triggered by both biotic and abiotic factors. A typical plastic response in plants occurs in response to herbivore attack with the induction of defenses, but the role of the herbivores as modulators of the plastic response of the plant to abiotic conditions has been seldom studied. In this study, we experimentally explore the effect of damage by florivores and folivores on the occurrence and intensity of floral phenotypic plasticity of *Moricandia arvensis* (Brassicaceae) under two contrasting abiotic conditions. In nature, this mustard species blooms in two contrasting environments, facing mild and wet conditions during spring, and hot and dry during summer. In response to these environmental changes, the same individual is plastic for floral traits. Our preliminary results show that plants attacked by each type of herbivores retain the capacity to flower during summer conditions, expressing plasticity for floral traits. These herbivores limit the plastic response of the plant to the abiotic conditions. This study highlights the complex interaction between biotic and abiotic stressors and their combined effect for the evolution of plasticity in *M. arvensis*.

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## Global Change: Climate, Pollution & Long-term Trends

### Resilience and Recovery of Floral and Nectar Traits under Acute Heat Stress

**Presenting:** Alba Edwards

**Authors:** Alba Edwards; Lucy Unwin; Maria Clara Castellanos

**Affiliation:** University of Sussex.

Climate change is driving more intense and prolonged heatwaves, imposing acutely stressful conditions on organisms and ecosystem interactions. During heatwaves, flowering plants exhibit weakened physiological function and disrupted reproductive development. Thermal stress can further diminish the production of floral nectar, which is essential to pollinator attraction. As a consequence, heat-associated reproductive losses can have significant consequences for both wild and crop plants, which are vital for maintaining ecological stability and ensuring food security. In this study, I investigated the impacts of simulated heatwaves on floral and nectar traits in the common bean (*Phaseolus vulgaris*). Results here indicate that heatwaves can significantly alter flower and nectar production in the species. Exposure to an extreme 2-day heatwave (daytime 33°C) caused significant reductions in floral output, flower size, nectar volume and sugar concentration, with the latter of these traits expressing slow and incomplete recovery. These findings highlight how even short-lived severe heat events can negatively modify floral nectar traits, with prolonged effects. Future studies should adopt field-focused approaches to address the outcomes of these diminished floral resources on pollinator foraging, to more intricately determine the consequences of acute heatwaves on plant reproductive success.

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### **Dedusting herbarium stigmas to uncover historical changes in plant–pollinator interactions**

**Presenting:** Macarena Marín Rodulfo

**Authors:** Macarena Marín-Rodulfo<sup>1</sup>; Ana Teresa Romero<sup>1</sup>; Angela Cano García<sup>1</sup>; Carmen Quesada<sup>2</sup>; Rocío Pérez-Barrales<sup>1</sup>

**Affiliation:** <sup>1</sup> Department of Botany, Faculty of Sciences, University of Granada, Granada, Spain. <sup>2</sup> Herbarium of the University of Granada, Granada, Spain.

Herbarium collections have become invaluable archives for understanding ecological and evolutionary processes through time. In this study, we explore a novel use of herbarium material to analysing pollination interactions by examining pollen grains on stigmas in specimens of two *Linum* species with contrasting pollination systems, the generalised *L. narbonense* and the specialised *L. suffruticosum* s.l., collected across the Iberian Peninsula since 1899 to 2022. We sampled flowers from sheets from major Spanish herbaria (MA, BC, VAL, SEV, GDA) and store them in alcohol 50% to hydrate stigmas. Then, stigmas were mounted in fuchsin-stained glycerine jelly for microscopic observation and observed under x10 magnification to identify pollen grains to determine intraspecific pollen and heterospecific pollen at the family or morphotype level. Statistical analyses (GLMMs) using biodiversity indices reveal patterns of variation in pollen transfer and community composition through time and space and confirmed the magnitude of pollination specialization of the species under study. This study provides unprecedented insights into the historical dynamics of pollination interactions, as well as methodological basis for future studies using herbaria to investigate biotic interactions, contributing to the broader understanding of pollination ecology.

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### **Monitoring Biodiversity in the Genomics Era: Using herbaria to assess genetic diversity trends across time**

**Presenting:** Melissa Viveiros Moniz

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Climate change is having far-reaching consequences on all living beings, altering ecosystems, habitats, and biodiversity worldwide. Species distributions are shifting, with alpine plant species being particularly threatened. Traditional monitoring based on individual counts produce delayed signals of biodiversity loss and overlook the fact that genetic diversity is the fundamental basis for evolutionary processes. Here, we draw attention to the use of genetic diversity in monitoring schemes to anticipate negative trends in biodiversity by applying two fundamental methodologies: genomics and the use of herbarium specimens. Genomic approaches provide a vast amount of data without requiring previous knowledge of the organism, making them suitable for non-model species. Meanwhile, herbaria serve as excellent sources of plant material for comparative studies across time with their chronologically recorded collection data. Building on these approaches, we investigated temporal patterns of genetic diversity in endemic alpine plant species from Sierra Nevada, a region highly vulnerable to climate change. By combining next-generation sequencing with genomic analyses, we were able to estimate genetic diversity metrics for each taxon and track changes over time. Our study highlights the potential of combining genomics and historical collections to inform conservation strategies in the face of rapid environmental change.

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### **Butterfly responses to weather anomalies depend on local adaptation and range position**

**Presenting:** Yolanda Melero

**Authors:** Yolanda Melero; Luke C. Evans; Mikko Kuussaari; Reto Schmucki; Constantí Stefanescu; David B. Roy; Tom H. Oliver

Intra-specific variation in responses to climate change that can be linked to adaptation to the local conditions. Likewise, species are expected to be more resilient at the centre of their distribution, but this pattern may be not general. Using long term monitoring data for 34 species across six European bioclimatic regions, we showed that species responses to climatic anomalies vary with local adaptation and position in the distributional range. While climatic anomalies negatively affected all population changes of species locally adapted, populations of non-locally adapted species were positively or negatively affected, depending on their location and direction of the anomalies. As a result, population trends of locally adapted species showed stable abundances over time at the trailing margin, but steep declines at the leading; while the rest showed a steeper decline at the trailing. Our results urge for contextualised forecasting and management, incorporating information on species adaptations and location.

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## **Three decades of butterfly–plant interaction turnover explained by climate and species loss**

**Presenting:** Pau Colom

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Understanding the mechanisms behind interaction turnover over long-term periods is essential to predict how ecological networks respond to global change. We used a high-resolution dataset of butterfly–plant interactions spanning 13–29 years in seven Mediterranean communities to assess how climate fluctuations and community shifts shape interaction turnover and its components—species turnover and rewiring. Early in the time series, rewiring explained most interaction turnover, but its influence declined as species loss reduced the pool of shared partners between years. Consequently, species turnover became increasingly dominant, even though communities shifted toward butterfly species with generalist traits that promote rewiring. Nevertheless, rewiring intensified in years with stronger temperature fluctuations, when populations experienced greater shifts in phenology and abundance and were more likely to rewire. In the context of biodiversity loss, species turnover increasingly governs interaction dynamics, while the short-term flexibility provided by rewiring may collapse as communities become impoverished.

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## **Vulnerability of Oromediterranean pastures to ozone pollution and atmospheric nitrogen deposition: experimental approaches for analysing impacts on atmosphere-plant-insect interactions**

**Presenting:** Sara Campos Saelices

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Increased tropospheric ozone ( $O_3$ ) and atmospheric nitrogen (N) deposition are two environmental problems affecting high-mountain Mediterranean pastures. When both factors are

considered, the critical thresholds defined for vegetation protection are exceeded in the area, constituting important stress factors for these communities. While few experimental O<sub>3</sub>-effects on the vegetative growth of species of these plant communities have been observed, its impact on flowering-related variables and reproductive capacity has been demonstrated. N-deposition can also affect pasture communities by altering their structure and species composition, as well as by modulating their O<sub>3</sub>-response. This thesis project presents an experimental design to investigate how an Oromediterranean pasture community, consisting of seven representative species, responds to the interaction between O<sub>3</sub> x N, considering four O<sub>3</sub>-levels, ranging from pre-industrial background values to those predicted throughout this century; and two N-levels, reproducing the ranges in the area. The experimental assay will be carried out at the CIEMAT Open Chamber Facility. The effects on variables related to growth and physiology will be analysed, especially those related to plant-pollinator relationship. Floral characteristics relating to pre- and post-pollination will be analysed, as well as pollination and floral-visitation rates. The effects on life expectancy and insect growth will be analysed using experimental pollinators.

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## Applied Pollination Ecology

**Do spontaneous ground covers conserve wild pollinators and enhance crop pollination in apple orchards from northern Spain?**

**Presenting:** Ángel Plata Sánchez

**Authors:** Ángel Plata<sup>1</sup>; Teresa Moran-López<sup>1</sup>; Marcos Miñarro<sup>2</sup>; Daniel García<sup>1</sup>

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Promoting non-crop habitats in agroecosystems, such as ground cover vegetation within crops, may enhance pollinator abundance and diversity by providing resources that crops lack. These habitats may support broad pollinator conservation and supply pollinators that spill over to crops during bloom, enhancing pollination. However, they may also compete with crops for pollinators. Spill-over and retention can operate simultaneously, making them difficult to distinguish through approaches based on species occurrence. Apple orchards offer a valuable model for evaluating these processes, as apple yield depends on both pollinator abundance and diversity. In northern Spain, climatic conditions allow spontaneous ground cover vegetation to persist most of the year with minimal management, offering a cost-efficient opportunity

for growers to promote ground covers. However, it remains unclear whether such ground covers effectively conserve wild pollinators and enhance apple pollination. Here, we characterize flower and pollinator communities in spontaneous ground covers of twenty-six Asturian apple orchards before, during, and after apple bloom, and compare them with pollinators visiting apple flowers. We then assess how flower abundance and diversity in ground covers shape pollinator communities both within the covers and on apple trees. Finally, we discuss approaches to infer whether ground covers drive pollinator spill-over and/or retention.

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### **Widespread pollination deficits in pear (*Pyrus communis L.*) orchards: the role of pollinators, landscape context and pesticide risk**

**Presenting:** Lucia Lenzi

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European pear (*Pyrus communis L.*) is an important entomophilous crop, and most varieties are self- incompatible, therefore strongly dependent on insect pollinators. However, harsh conditions during bloom and low sugar content of nectar often lead to low pollinator visitation rates, causing shortfalls in production. Our aim was to assess pollination services, detect pollination deficits in pear orchards and analyze the effects of local factors (pesticide load, orchard management) and landscape factors (“pollinator-friendly” cover) on pollinators and pollination services. Our results confirm the dependence of fruit set on pollination (mean 37%). We also report significant pollination deficits across pear orchards (mean 31%), and low pollination service (mean 17%). Most flower visitors were honeybees and Diptera Muscidae, while wild bees were the least abundant group. However, “pollinator-friendly” cover (1.5 km) positively influenced wild bees’ visitation rate. Pollinators had no effect on pollination deficit, but higher bumblebee visits negatively affected seed set. Pear flowers were contaminated with at least four pesticides, and pesticide risk had a negative effect on fruit set. Our results indicate insufficient pollination services in pear orchards and raise concerns about the management of pollination provision, highlighting the importance of semi-natural areas to boost wild bee visits and reduce pesticide pressure on pollinators.

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## **Assessing nesting patterns of *Osmia* spp. in almond orchards across contrasting landscape contexts**

**Presenting:** Gabriel Arbona Taberner

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The decline of wild pollinators threatens crop production, emphasizing the need to diversify pollination services beyond the managed honeybee. Solitary *Osmia* bees are promising alternative pollinators for early flowering crops due to their high foraging efficiency, ease of management, and the possibility of synchronizing their emergence with crop bloom. This study aimed to obtain *Osmia* cocoons from wild populations inhabiting almond orchards across Mallorca, representing contrasting landscape contexts, to examine the structural and ecological characteristics of their nests. Nesting aids made of natural reed bundles (300 cavities per site) were installed in 15 orchards. After the flight season, reeds were dissected and nest traits recorded. Nests and cocoons with distinct morphologies were detected. In total, 180 nests and 492 *Osmia* cocoons were obtained, with mixed-context orchards showing the highest occupation. Most nests were built in 6-mm reeds, though typically less than half of the cavity length was used. Nests with fewer than seven cells exhibited less consistent patterns in cell size and cocoon weight. Statistical analyses revealed that nest features and the presence of cleptoparasitic larvae had stronger effects on cocoon presence than landscape variables. These results provide key insights for optimizing *Osmia*-based pollination in almond orchards.

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## **Urban Pollination Ecology**

### **Thermal buffering ability of butterflies across urban and natural environments**

**Presenting:** Ashley Tejeda Meneses

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Urbanization alters microclimates, potentially affecting pollinator activity and plant–pollinator interactions. We examined whether the thermoregulation of butterflies, key pollinators in Mediterranean ecosystems, is affected by urbanization. Specifically, we test if urban populations exhibit enhanced thermal buffering ability compared to natural ones, and whether this capacity predicts species persistence in cities. We conducted field surveys in urban parks and surrounding natural areas in Barcelona, recording air and thoracic temperature of butterflies, to quantify thermal buffering ability across species and populations. We did this during their flight period in the bioclimatic region (March–October) over two years. Preliminary analyses suggest inter- and intraspecific differences in thermal buffering. Some species show enhanced thermoregulation in urban areas, while others appear more vulnerable to urban heat. Variation between populations of the same species also indicates possible local adaptation or plasticity. Our results indicate that behavioral thermoregulation is a crucial mechanism for coping with urban heat islands and a key filter determining which butterfly species can thrive in them. Such information can help prioritize conservation actions and guide the management of urban green spaces. Understanding these patterns helps predict changes in pollination dynamics under urban warming, as butterfly activity influences floral visitation and plant reproduction.

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### **Integrating conservation and public engagement through pollinator gardens: lessons from the Botanical Garden of Bologna**

**Presenting:** Marta Barberis

**Authors:** Marta Barberis<sup>1</sup>; Fortunato Fulvio Bitonto<sup>1</sup>; Nicola Herrmann Lothar<sup>2</sup>; Ioannis Mondin<sup>1</sup>; Costanza Viglianisi<sup>1</sup>; Mariacristina Laureti<sup>1</sup>; Martina Capacci<sup>1</sup>; Silvia Del Vecchio<sup>1</sup>; Umberto Mossetti<sup>2</sup>; Laura Bortolotti<sup>3</sup>; Annalisa Managlia<sup>2</sup>; Marta Galloni<sup>1</sup>

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Pollinators play a crucial role in maintaining biodiversity and ensuring the productivity of natural and agricultural ecosystems. However, over the past decades, they have been declining due to habitat loss, pesticide use, and climate change. The implementation of pollinator gardens represents an effective action for restoring urban green spaces while raising public awareness about the topic. An example is represented by the Pollinator Garden established at the Botanical Garden of Bologna as part of the LIFE 4 Pollinators project (LIFE18 GIE/IT/000755).

It includes nearly 80 nectar-rich species selected to ensure continuous floral resources throughout the seasons, organized in flowerbeds representative of the main floral morphologies (*sensu* Faegri and Van der Pijl). During the first two years following establishment, flower- insect interactions were monitored weekly from March to December by walking a transect running along the perimeter of each flowerbed. The no. of recorded interactions was 6868, observed during 78 monitoring days. Alongside, the total number of pollination units per plant was counted, for a total no. exceeding 124,000. Comparison of network indices revealed increased connectance, links per species, and nestedness. Here, we present the results obtained from network analysis, the concept beyond design, as well as challenges and opportunities encountered.

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## Citizen Science

### Easy pollinator learning with PreguntadoR

**Presenting:** Esther Funes-Ligero

**Authors:** Esther Funes-Ligero; Mohamed Abdelaziz; A. Jesús Muñoz-Pajares

**Affiliation:** Department of Genetics, Universidad de Granada.

Learning how to identify pollinators is often hard for students. This key skill usually requires lot of time from teachers and repeated trips outside. To fix this problem in learning taxonomy, we created PreguntadoR, a special app built entirely with R for interactive learning. PreguntadoR takes the tough job of learning insect body parts and makes it quick and fun. We designed it to give users a structured, but very adaptable, place to gain both basic and advanced knowledge. The app uses game-like features with its different settings and personalized exercises. When users practice with specific tasks, they see the important visual signs and classification groups they need for correct identification over and over. This system makes sure the key differences in shapes stay in their memory fast. So, PreguntadoR serves as a strong digital helper for teachers, supporting classes and independent study, and opens up the complex world of pollinator taxonomy for everyone.

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## Using Citizen Science to Expand Plant-Animal Interaction Data in the Pyrenees

**Presenting:** Oriane Hidalgo

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Plant-animal mutualisms have strongly shaped the evolutionary trajectories of both lineages, yet research often centers on conspicuous pollination systems (e.g., orchids) and narrow spatio-temporal scales (e.g., single-site daytime monitoring). This bias is acute in the megadiverse, globally distributed family Asteraceae, perceived as generalist. In this context, citizen-science platforms could offer a complementary source of observations, though their usefulness for interaction ecology needs careful evaluation. Here, we assess the value of citizen-science records for studying interactions between Asteraceae and invertebrates (inc. Insecta, Arachnida and Gastropoda) in the Pyrenees. We built a curated dataset combining iNaturalist observations with targeted field sampling at monitored sites, currently encompassing c. 14,000 records of plant-animal interactions. We describe the taxonomic composition and spatial distribution of the dataset, and identify common sources of bias. We also illustrate practical applications, including generating reference lists of invertebrate species for training automated identification tools, and constructing plant-animal interaction networks. Our results show that reviewed citizen-science observations, when complemented with focused fieldwork, can substantially increase the amount and diversity of interaction data available. This integrated approach provides an efficient way to improve biodiversity monitoring and to support plant-focused analyses of interaction networks at multiple scales.

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## Pollination, herbivory, microbiota and pathogens

### Developing Functional Profiles for Wild and Managed Pollinator Gut Microbiomes

**Presenting:** Christian Gostout

**Authors:** Christian Gostout<sup>1</sup>; Luis J. Chueca<sup>1</sup>; Xabier Salgado-Irazabal<sup>1</sup>; Estefanía Tobajas<sup>1</sup>; Jennifer Rose<sup>1</sup>; Brais Hermosilla<sup>1</sup>; Montserrat Muriana<sup>1</sup>; Celia Baigorri; Jon Poza; Ainhoa Magrach<sup>1,2</sup>

**Affiliation:** <sup>1</sup> BC3 Basque Centre for Climate Change, Leioa, Spain. <sup>2</sup> IKERBASQUE, Basque Foundation for Science, Bilbao, Spain.

The gut microbiome of wild pollinators plays an important role in pollinator health and resilience. The composition of pollinator gut microbiota has been characterized using metabarcoding, and more recently, metagenomic approaches for a limited number of species, especially commercially used pollinators. These approaches have allowed the observation of changes in the composition of the gut microbiome in response to certain environmental factors, but the implications of these changes for gene expression and metabolic pathways, and in turn, pollinator health, are virtually unknown. We move beyond studies focused on the composition of gut microbiomes to focus on their functions using metatranscriptomic analyses of RNA extracted from the gut of the wild pollinator, *Bombus pascuorum*, and the managed species, *Apis mellifera*. We show that taxonomic profiles can be used to make initial inferences of function, and that metatranscriptomics can confirm functional expression. Across 122 specimens, we detected an overrepresentation of gene expression transcripts linked to specific metabolic pathways, including the breakdown of sugars and complex polysaccharides. Our study expands microbiome functional studies to wild pollinators, and creates new commentary on their interactions with managed species. We present an initial perspective on our study approach and outlook, including a look at preliminary results.

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### Pathogen Transmission Through the Bee–Flower Network in Urban Ecosystems

**Presenting:** Giovanni Cilia

**Authors:** Giovanni Cilia<sup>1</sup>; Dario Scalambra<sup>1,2</sup>; Rosa Ranalli<sup>3</sup>; Laura Zavatta<sup>4</sup>; Marta Galloni<sup>2</sup>

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Urban environments, with their concentrated floral resources and complex pollinator communities, create plant–pollinator–pathogen networks that can facilitate pathogen transmission. This study investigated these interactions in two urban parks in Northern Italy by sampling wild bee females, their pollen loads, and the last visited flowers (377 samples per matrix, April–September 2024). Molecular analyses revealed that pathogens were deeply surrounded within the network structure: DWV (45.2%) and Nosema ceranae (41.3%) circulated across bees, flowers, and pollen, confirming the bidirectional movement of pathogens through shared floral resources. DWV reached 73.3% prevalence in bees and loads of  $3.6 \times 10^{12}$  copies, while

*N. ceranae* was most common on flowers (41.5%) and in pollen (38.7%), indicating that flowers act as persistent environmental reservoirs. Seasonal patterns showed increased prevalence in bees during warm periods but stable pathogen abundance in flowers and pollen, suggesting continuous environmental contamination even when bee infection levels fluctuate. Pollen identification reconstructed individual foraging networks, revealing that bees visiting a richer diversity of plant species had lower probabilities of pathogen presence and co-infection. Overall, these findings demonstrate that urban plant–pollinator networks function as tightly interconnected systems for pathogen exchange, highlighting the need to integrate pollinator health into urban ecological planning.

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### **Unmasking microbial associations behind insect-attractant scents in the mucilage droplets of sticky carnivorous plants**

**Presenting:** Celia Vaca Benito

**Authors:** Celia Vaca-Benito<sup>1</sup>; María Salces-Castellano<sup>1</sup>; Ceferino Carrera<sup>2,3</sup>; Irene Punta<sup>3</sup>; Belén Floriano<sup>4</sup>; Fernando Ojeda<sup>1</sup>

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Nectar-dwelling microbes modify the floral scents that attract insect pollinators <sup>1,2</sup>. Similar to floral nectar, the mucilage droplets on the leaf-traps of sticky carnivorous plants (e.g., *Drosera*, *Drosocephyllum*) emit olfactory signals – often mimicking floral or fruit scents – to lure prey insects <sup>3</sup>. Although bacteria and fungi have been documented in the mucilage of sundews (*Drosera* spp.) <sup>4</sup>, the microbiome of *Drosocephyllum lusitanicum* has not been examined, nor has the potential contribution of these microbes to leaf-trap scent. We investigated the mucilage microbiomes of *Drosocephyllum lusitanicum* (nine populations) and two *Drosera* species, *D. intermedia* (six populations) and *D. rotundifolia* (three populations), using metabarcoding of the 16S rRNA gene (bacteria) and the ITS region (fungi). We also characterized their volatilomes (volatile organic compound profiles) using direct thermal desorption–gas chromatography/mass spectrometry (TD-GC/MS) <sup>5</sup>. To assess links between scent profiles and microbial communities, we applied co-inertia analyses comparing PCoA ordinations of the bacterial and fungal datasets with those of the volatilome across all 18 populations. We found a significant common structure between the microbiome and the volatilome for fungi, but not

for bacteria, suggesting that fungi may play a more prominent role in shaping the luring scent of the mucilage droplets in sticky carnivorous plants.

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### How do herbivores modulate floral phenotypic plasticity to abiotic conditions?

**Presenting:** Violeta Quiroga Álvarez

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Phenotypic plasticity is the ability of a genotype of producing alternative phenotypes when exposing to different environments, so it can be triggered by both biotic and abiotic factors. A typical plastic response in plants occurs in response to herbivore attack with the induction of defenses, but the role of the herbivores as modulators of the plastic response of the plant to abiotic conditions has been seldom studied. In this study, we experimentally explore the effect of damage by florivores and folivores on the occurrence and intensity of floral phenotypic plasticity of *Moricandia arvensis* (Brassicaceae) under two contrasting abiotic conditions. In nature, this mustard species blooms in two contrasting environments, facing mild and wet conditions during spring, and hot and dry during summer. In response to these environmental changes, the same individual is plastic for floral traits. Our preliminary results show that plants attacked by each type of herbivores retain the capacity to flower during summer conditions, expressing plasticity for floral traits. These herbivores limit the plastic response of the plant to the abiotic conditions. This study highlights the complex interaction between biotic and abiotic stressors and their combined effect for the evolution of plasticity in *M. arvensis*.

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## Poster presentations

### Plant Traits, Floral Biology, & Pollination Mechanisms

#### **Pollination and Breeding System of *Succisella carvalhoana* (Caprifoliaceae): a Morphologically Generalist, but Complex and Critically Endangered species**

**Presenting:** Afonso Petronilho

**Authors:** Afonso Petronilho; Sílvia Castro; João Farminhão

**Affiliation:** Centre for Functional Ecology, Associate Laboratory TERRA, Department of Life Sciences, University of Coimbra, Coimbra, Portugal

*Succisella carvalhoana* (Mariz) Baksay (Caprifoliaceae, Dipsacoideae) is a Critically Endangered species, endemic to marshy areas of the Beira Litoral region in central Portugal. Its highly restricted distribution makes conservation a priority, yet its reproductive biology remains entirely unknown. This study presents the first investigation into its floral biology, breeding system, and pollination ecology. We report a strong case of inflorescence-level di-chogamy. All florets within a capitulum open sequentially, first in a male phase characterised by prominently protruding stamens, followed by a synchronous shift to the female phase. This transition is accompanied by additional differences, such as a significant increase in nectar production during the female phase. This mechanism prevents self-pollination, resulting in a pollinator-dependent system with significant pollen limitation. The generalist floral morphology attracts a diverse array of pollinators, although with novel and varied behaviours. The recent discovery of a new population, representing a potential distinct ecotype with different corolla colours and contrasting pollinator communities, suggests local adaptation to divergent conditions. Our findings reveal a surprisingly complex breeding system for a morphologically generalist species that promotes outcrossing and challenges some generally accepted patterns. Understanding these mechanisms is crucial for developing effective in-situ and ex-situ conservation strategies to prevent its extinction.

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#### **Phenotypic variation and functional expression in endemic and threatened species of the genus *Petrocoptis* A. Braun ex Endl.: implications for the conservation of rupicolous plants**

**Presenting:** Angie Paola Carvajal Muñoz

**Authors:** Angie Carvajal-Muñoz<sup>1</sup>; F. Javier Jiménez-López<sup>1</sup>; Stela Vlajos-Gómez<sup>1</sup>; Luis Navarro-Echeverría<sup>2</sup>; Carlos Lara-Romero<sup>1</sup>; Martí March-Salas<sup>1</sup>

**Affiliation:** <sup>1</sup> Rey Juan Carlos University, Department of Biology and Geology, Physics and Inorganic Chemistry. <sup>2</sup> University of Vigo, Department of Plant Biology and Soil Science.

Rupicolous plants inhabit extremely restrictive microenvironments that generate isolated populations with low genetic diversity. Understanding whether phenotypic diversification has a genetic or environmental origin, as well as the mechanisms that regulate it, is key to predicting their future responses. This study focuses on the genus *Petrocoptis*, whose reproductive systems could modulate its phenotypic variation. We evaluated the origin of such variation in size, reproductive, and leaf traits among species, reproductive systems, and populations of *P. grandiflora* using linear mixed models. We found significant differences among species in all assessed traits. Three species showed late flowering, greater reproductive allocation, and larger diameter, likely in response to relatively more favorable conditions. In general, autogamous species exhibited higher values of reproductive allocation and diameter, as well as a greater coefficient of variation for traits, reflecting a possible effect of the reproductive strategy on phenotypic variation. Populations of *P. grandiflora* differed in flowering peak, reproductive height, diameter, and leaf thickness, associated with microclimatic variation. The persistence of these intra- and interspecific divergences under common garden conditions indicates a heritable genetic basis, which may be compatible with possible local adaptation processes.

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### **Variation Barcodes: a new tool to monitor the loss of genetic diversity in flora caused by climate change**

**Presenting:** Cristina Montoya de Haro

**Authors:** Cristina Montoya de Haro<sup>1</sup>; Mireia Bustos Aibar<sup>1,2</sup>; Mohamed Abdelaziz<sup>1</sup>; Antonio Jesús Muñoz Pajares<sup>1</sup>

**Affiliation:** <sup>1</sup> BioChange Network, Department of Genetics, University of Granada – Spain <sup>2</sup> Aragon Health Research Institute [Zaragoza] – Spain

Climate change is driving the disappearance of taxa at rates comparable to major mass extinctions. In this scenario, monitoring the loss of genetic diversity is essential to enable timely action and preserve biodiversity. For this reason, we propose a novel methodology for such monitoring: Genetic Diversity Barcodes, short DNA regions capable of accurately estimating whole-genome genetic diversity. We identified these regions in 6,536 GenBank genomes belonging to 180 genera that represent all major plant taxa. For each genus, we performed a sequence alignment and calculated genetic diversity using both the complete cpDNA and sliding windows of different sizes (between 150 and 2,400 bp). We assessed the accuracy of these estimates through regressions between both diversity measures, using the R<sup>2</sup> value as an indicator. Our results demonstrate that specific regions of the cpDNA exhibit levels of genetic diversity that reliably reflect whole-genome diversity. The relevance of these regions lies in their potential to make conservation studies based on genetic monitoring much more

affordable, accessible, and efficient, enabling their long-term implementation and improving our ability to respond to biodiversity loss.

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### **Floral preferences with and without spatial context: comparison of different methods of deriving pollinator preferences**

**Presenting:** Eva Matoušková

**Authors:** Eva Matoušková<sup>1</sup>; Jakub Štenc<sup>2,3</sup>; Martin Freudenfield<sup>1</sup>; Lucie Sedláčková<sup>4</sup>; Zdeněk Janovský<sup>5</sup>

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While foraging, pollinators' decisions on which flower to visit next play a crucial role in pollen transfer among flowers, especially in systems with generalist pollinators, such as hoverflies and bumblebees. The decision can be viewed as a composition of flower constancy and flower preference. Flower constancy states that the pollinator stays on the same floral morph as the last visited one. In contrast, flower preference either strengthens or weakens the potential switch to a different flower. There are several methodological approaches for collecting such data. We will compare generalist hoverfly and bumblebee flower visitations from natural observation experiments with different methodological approaches, which simplify the system to two or a few flowers but enable us to look closely at the pollinator decision. One compared method is the 'interviewing-stick' method, where the pollinator is presented with a choice of two flowers. Second example is 'array' where pollinator is presented with an arranged array of flowers in a specific pattern to forage on. Are these methods comparable, and can we make any relevant predictions from data on flower preference and constancy without other factors, such as the spatial distribution of the flowers or overall species distribution in the meadow?

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### **Light and Gravity Interactions in the Control of Flower Orientation**

**Presenting:** Giovanna Aronne

**Authors:** Giovanna Aronne; Aurora Anzivino; Leone Ermes Romano; Luigi Gennaro Izzo

**Affiliation:** Department of Agricultural Sciences, University of Naples Federico II

Flower orientation - the angle between a flower's main axis and the horizontal - is widely deemed to interact with pollinators in terms of flower attraction, foraging behavior, and effective input and output pollen transfer. These hypotheses are currently being demonstrated by experimental evidence that stimulates more in-depth investigations into the biological processes responsible for this phenomenon. Flower orientation depends on internal factors interacting with external factors, especially light and gravity. Previous research proved that light direction drives changes in flower orientation. Here, to disentangle the role of gravity from that of light in flower orientation, we treated flowering plants of *Viola tricolor* and *Cyclamen persicum* with several combinations of light directions and gravity conditions. Gravity was altered by applying space-biology methods generally used to simulate microgravity. Specifically, we compared flower orientation of plants placed on a uniaxial clinostat with light source positioned either above the plant or turned 90° with respect to the plant axis. Results showed that gravity more than light affects final orientation of flowers. Anatomical analyses revealed the occurrence of statoliths in the endodermis cells of the flower pedicel shedding light on the processes regulating gravity sensing and final orientation of flowers.

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### **Form and function: the role of flower morphology on pollen flow in two distylous *Linum* species.**

**Presenting:** Joana Retamero Argemí

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Distyly is a floral polymorphism characterized by the presence of two floral morphs with reciprocal positioning of anthers and stigmas. Darwin's Cross-Pollination Hypothesis states that this arrangement promotes disassortative pollination (i.e. pollen transfer between opposite floral morphs) through the spatial segregation of pollen deposition on the pollinator's body. In this way, the function of distyly requires a specialized pollination system. Here, we evaluated pollen flow patterns in two *Linum* species that differ in their flower architectures and pollination systems. By analyzing stigmatic pollen loads of recipient flowers of *L. narbonense* and *L. suffruticosum* subjected to different pollination environments (plots with pollen donors of the same or the opposite morph), we compared the degree of specialization of their pollination systems, tested the Cross-Pollination Hypothesis, and compared the efficiency between

them. The results provide valuable insights into pollen flow patterns under natural conditions. The two species behaved as expected under Darwin's Hypothesis, but *L. suffruticosum* exhibited a slightly higher cross-pollination efficiency, while *L. narbonense* was less efficient and experienced apparent higher rates of self-pollination. These patterns suggest that floral architecture plays a significant role in intra- and inter-morph pollen transfer patterns as well as self-interference.

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### **Food Security and Pollination: Building a Database on School Meals in Brazil**

**Presenting:** Kayna Agostini

**Authors:** Sara Stefani Domingos<sup>1</sup>; Kayna Agostini<sup>2</sup>

**Affiliation:** <sup>1</sup> Universidade Estadual Paulista Júlio de Mesquita Filho. <sup>2</sup> Universidade Federal de São Carlos.

Pollinators are essential for global agricultural production, contributing to food security and nutritional diversity. Approximately 75% of crops depend on animal pollination, influencing the availability of fruits, vegetables, and oilseeds. In Brazil, the National School Feeding Program (PNAE) plays a fundamental role in ensuring food security for millions of students by providing balanced and diverse meals. This study analyzed 2019 purchase invoice data from PNAE in eight municipalities of São Paulo state.. Food items were classified according to the NOVA processing categories and organized into food groups. (e.g., fruits, vegetables, cereals). To evaluate pollination dependence, each fresh or minimally processed plant-based food item was categorized using the methodology of Klein et al. (2007), which classifies crop dependence into five levels: essential, high, modest, low, or no increase. The most frequently consumed pollination-dependent foods included apple, bean, orange, papaya, tomato, and watermelon, all of which contributed substantially to the nutritional diversity of school meals. The results highlight the importance of pollination services in sustaining the quality and diversity of foods offered through PNAE. They also underscore the need to further investigate how pollinator conservation can support food security policies and strengthen the resilience of school feeding programs.

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### **Protocols' synthesis for addressing questions in Pollination Biology**

**Presenting:** Kayna Agostini

**Authors:** Marina Wolowski<sup>1</sup>, Pedro Joaquim Bergamo<sup>2</sup>, Arthur Domingos de Melo<sup>3</sup>, Kayna Agostini<sup>4</sup>

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Compiling pollination protocols is a necessary effort given the large amount of widespread information and the need for updating methodologies for contemporary studies. This initiative is being developed by the INCT Pollination in Brazil, with the goal of producing a synthesis of standardized protocols for data collection to address both classical and contemporary questions in pollination biology. The synthesis aims to organize methods applied in fieldwork and laboratory, and to consolidate reproducible procedures that encompass different research topics. This effort will support the production of systematized data collection for floral biology research and monitoring plant-pollinator interactions, as well as promoting data alignment with databases such as the Brazilian Network on Plant–Pollinator Interactions (REBIPP). We are developing a dynamic catalog that can be expanded over time, linking research questions to specific protocols and to the descriptors of plant–pollinator interactions available in the REBIPP database. Each topic in the catalog will include descriptions of the most used protocols, a list of references that have been applied or adapted to them, and illustrations to assist users during procedure executions. Each protocol will be curated and authored by a group of specialists, ensuring methodological accuracy and practical guidance for users.

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### Hybridisation, Pollination and Climate Change in Alpine *Gymnadenia* Orchids

**Presenting:** Hannah Gunn

**Authors:** Hannah Gunn, Dr Kelsey J. R. P. Byers, Dr Mikhaela Neequaye, John Innes Centre

Mountain ecosystems contain an elevated level of species richness and endemism and are under threat from accelerated rates of climate warming and more frequent extreme weather events. Responses of different species to global change are idiosyncratic and likely to lead to a disruption of ecological networks. Orchids found on different mountainsides across the Swiss and Italian Alps provide distinct populations that can be used to study local adaptation and spatial variation in plant and pollinator communities. The orchid species *Gymnadenia conopsea* and *Gymnadenia rhellicani*, two species with overlapping ranges in the European Alps, produce F1 hybrids in limited frequencies where they occur in sympatry. Differing morphologies of the parent species make cross-pollination improbable, theoretically the reason for hybrid scarcity, but hybrid parentage is bidirectional and site dependant. This indicates differences in pollinator communities at different sites, possibly dependent on the sites' plant community composition. Climate warming and extreme weather events may impact plant and pollinator survival and ranges. Preliminary results show possible growth in orchid population

size at one site with proportions of parent species and hybrids remaining stable, and no difference in hybrid morphology between sites. Climate projection models show range contractions for *G. rhellicani* across the Alps.

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### **Identifying Patterns of Genetic Diversity Loss in Non-Model Species**

**Presenting:** Lea Ada Palao Picotti

**Authors:** Lea Palao-Picotti; Mohamed Abdelaziz; A. Jesus Muñoz-Pajares

**Affiliation:** BioChange Network, Department of Genetics, University of Granada, Spain

Genetic diversity is essential for population stability and adaptive capacity, and its decline, increasingly considered in conservation strategies, is recognized as an early indicator of population deterioration. However, its detection is limited by the frequent absence of specific reference genomes in many plant groups. This limitation often leads to the use of phylogenetically close references to align individual reads, a practice that can introduce bias and hinder the interpretation of true signals of diversity loss.

In this study, we explore the ability to detect trends of genetic diversity erosion in the absence of a specific reference by combining multiple alternative references with the analysis of populations exhibiting contrasting levels of genetic variability. To this end, we employed references distributed along a gradient of phylogenetic proximity and generated simulated populations with progressively reduced diversity through the controlled removal of pre-existing variants.

This approach allows us to evaluate the impact of reference choice on the detection of genetic erosion and provides criteria for a more consistent interpretation of genetic diversity in species lacking species-specific genomic resources.

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### **Why do we say wild when we want to say feral?**

**Presenting:** Luis J. Chueca

**Authors:** Luis J. Chueca<sup>1</sup>; Ainhoa Magrach<sup>1,2</sup>

**Affiliation:** <sup>1</sup> Basque Centre for Climate Change-BC3, Leioa, Spain. <sup>2</sup> Ikerbasque, Basque Foundation for Science, Bilbao, Spain.

Wild pollinator species are undergoing well-documented declines worldwide, yet relatively few are formally assessed or protected under existing conservation frameworks. Despite the urgent need to address these declines, recent studies have focused on conserving so-called “wild”

honeybee (*Apis mellifera*) populations; a misplaced emphasis which risks overshadowing the conservation needs of the thousands of genuinely wild bee species already facing pressing threats.

Here, we evaluate the assumptions underlying recent claims that unmanaged honeybee colonies represent endangered wildlife populations in Europe. A key conceptual flaw is the definition of “wild” colonies based solely on their occurrence outside a managed hive, rather than on demographic self-sufficiency, or genetic distinctiveness. We show that these assessments rely on geographically limited cavity-occupancy data, ignore immigration from managed hives, and do not account for the extensive gene flow that characterizes European honeybee populations. As a result, demographic inferences based on nest-site turnover cannot be interpreted as evidence of continental decline, nor can unmanaged colonies be treated as self-sustaining, evolutionarily distinct units. We argue that conservation resources should prioritize truly wild species with demonstrated declines and limited human support, rather than feral populations of a heavily managed species in order to develop effective, evidence-based conservation policies.

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### Pollen Transfer: From Stochasticity to Stability

**Presenting:** Martin Freudenfeld

**Authors:** Martin Freudenfeld<sup>1</sup>; Eva Matoušková<sup>1</sup>; Petr Švanda<sup>1</sup>; Jakub Štenc (1, 2, 3)

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**Background:** Pollen transfer is influenced by many factors. Pollen load on the pollinator’s body and the ratio of conspecific and heterospecific pollen changes not only over time, but also influenced by pollen production, surrounding flower abundance, or plant-pollinator interactions. In addition, a relatively large amount of pollen is lost due to pollinator consumption and not every pollinator visit leads to the pollen depositon, which introduces further stochasticity. In the end, only a small fraction of the transferred pollen reaches a conspecific stigma.

**Questions:** What influences path of pollen? What introduces stochasticity into the pollen transfer process? Can such a stochastic process be successful?

**Methods:** We collected data on pollen loads (swabbing pollen from their body), pollen consumed (dissection of the gut) and single visit deposition (SVD) of common pollinators (*Eristalis* and *Helophilus*) of *Succisa pratensis*. In addition, we determined the total deposition on stigmas, the abundance of flowering plants, and plant-pollinator interactions.

**Results and Conclusions:** The individual steps in the pollen transfer and pollen loss (pollen load, consumed pollen and SVD) are highly variable and stochastic. Despite all the stochasticity, relatively stable deposition of conspecific pollen on the stigmas of *Succisa pratensis* occurs.

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### **Effects of climate variability and landscape modifications on the long-term stability of butterfly communities and their pollination interactions**

**Presenting:** Olivia Gardella

Understanding how climate and land-use changes affect pollinators and their interactions with plants is crucial for predicting ecosystem responses to anthropogenic pressures. Yet, the mechanisms underlying the stability of communities and interactions remain poorly understood. We assessed the effects of climate variability (mean and SD of annual temperature) and landscape modifications (% natural areas and landscape heterogeneity within 2-km buffers) on temporal community stability, species synchrony, and variance ratio (community variance/sum of population variances) of butterfly communities and interactions, using 30-year data from seven butterfly communities of the Catalan Butterfly Monitoring Scheme. Stability metrics, along with landscape and climate variables were calculated per site within 5-year windows across data series. We also considered species and interaction diversity as internal properties linked to stability. The percentage of natural habitats in the landscape promoted butterfly community stability, while temperature variability emerged as the main external driver of interaction instability. Furthermore,

landscape heterogeneity reduced interactions' variance ratio, suggesting that heterogeneous landscapes enhance interaction stability by reducing covariances among interactions. Notably, species and interaction stability strongly increased with diversity. Our findings highlight biodiversity's pivotal role in sustaining community stability and ecosystem functions, while cautioning against the destabilizing effects of climate change and land-use pressures.

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### **20 years analysing evolution of snapdragons and relatives (*Antirrhinum* spp.)**

**Presenting:** Pablo Vargas

**Authors:** Pablo Vargas

**Affiliation:** Real Jardín Botánico de Madrid

After 20 years of research (and around twenty scientific publications) on *Antirrhinum* and its relatives (snapdragons), we have provided a modest contribution to advancing our understanding of their complex evolutionary history. In this presentation, I will summarize the most significant findings from our long-term project, encompassing taxonomy, phylogenetics, phylogeography, population genetics, pollination networks, pollinator (bee) behaviour, and species conservation, among other aspects.

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### Pollen transfer efficiency as a function of pollen deposition and removal

**Presenting:** Petr Švanda

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**Background:** Most of the produced pollen grains end up being lost via consumption, heterospecific deposition and falling on the ground. Moreover, different pollinator taxa differ significantly in the ratio of pollen which they remove from anthers and deposit on stigma i.e. pollen transfer efficiency. Pollinator's efficiency shows how many pollen grains did the pollinator lose but it doesn't tell us how or where the pollen grains were lost. For this reason, our goals are not only to determine the pollen transfer efficiency among pollinator taxa visiting *Succisa Pratensis*, but also to trace down the pollen pathway to paternity from production to deposition, including the determination of loss processes during the pollen transport.

**Methods:** We collected data about visitation frequency and the amount of pollen removed and deposited during a single visit of a pollinator. To conclude how much pollen they lose we collect data about pollen production, pollen in the pollinator's gut and on his body. For context and stronger results we also collect the total depositions on stigma and visitation network for all plants interacting with *Succisa Pratensis* through pollinators.

**Results:** Current analyses suggest that the likelihood of single-visit pollen deposition is influenced by the pollinator's sex and foraging behaviour. Furthermore, different pollinator species vary in the amount of pollen deposited on *Succisa pratensis*. The relationship between pollen on the pollinator's bodies, in their guts, and on the stigmas of the plant will be fully analyzed and presented at the time of the conference.

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## **Reconstructing the coastal dune flora of Renaissance using the Aldrovandi herbarium**

**Presenting:** Silvia Del Vecchio

**Authors:** Silvia Del Vecchio<sup>1</sup>; Gabriele Gheza<sup>1</sup>; Juri Nascimbene<sup>1</sup>; Fabrizio Buldrini<sup>1,2</sup>

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Using herbarium data to track shifts in species distributions and losses offers a rare opportunity to monitor biodiversity trends across past centuries. We aimed to reconstruct the coastal dune flora from approximately 400 years ago by analysing species preserved in the Aldrovandi herbarium, a 16th-century collection notable for its precisely documented collection locations. From a database of about 5000 specimens, we selected those collected from the Italian coastal sites. We compared the native-range categories of the species, life forms, and Ecological Indicator Values between the western and eastern coasts, as well as potential data biases. Additionally, we compared the past and current distribution of rare species. We gathered a total of 215 herbarium specimens, corresponding to 131 species. The analyses of native-range categories, life forms, and Ecological Indicator Values were too strongly affected by geographical and taxonomic sampling biases to support meaningful interpretations. By contrast, we were able to document the historical occurrence of currently rare or regionally extinct species, providing information that can help update current knowledge of their past distribution, not only at the regional but also at the national scale. Our research outlines historical dune flora and emphasizes digitization of herbarium specimens for accurate, bias-corrected analyses.

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## **How do biotic and abiotic factors affect color variation in *Digitalis purpurea*?**

**Presenting:** Sissi Lozada Gobilard

**Authors:** Sissi Lozada Gobilard<sup>1,2</sup>; Pamela Espinoza Peñaloza<sup>2</sup>; Zaina Aliwi<sup>1</sup>; Giovanni Pascucci<sup>3</sup>; Øystein Opedal<sup>1</sup>

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Flower color is a key trait influencing plant–pollinator interactions and may also respond to abiotic factors such as soil properties. We investigated association between pollinators, soil nutrients and flower color variation in *Digitalis purpurea* across native-range populations in

Sweden and recently introduced populations in Bolivia. We measured floral traits, floral reflectance of the petals and inner nectar-guide spots, and plant size traits, performed pollinator observations and estimated fruit set, seed production and germination rate; and quantified soil nutrients (N, C, P, K, Fe). Individuals were categorized into violet, pink, and white flower color morphs confirmed by spectral measurements and bee vision modelling, but reflectance of the inner nectar guide spots overlapped across morphs, potentially limiting pollinator discrimination. Bumblebees were the main pollinators in all populations, and while visitation varied among flower color morphs, these differences were population-specific. In the Bolivian populations, violet flowers were predominant (B1: 87%; B2: 70%), with pink (13–17%) and white (0–13%) morphs occurring at lower frequencies, whereas in the Swedish populations the distribution was more even, with violet representing 20–43%, pink 38–69%, and white 11–30% of individuals. Reproductive fitness varied across populations but not consistently among color morphs: the largest native Swedish population had the highest fruit set but the lowest seed set, while germination rates were lower in the introduced Bolivian populations. Soil phosphorus concentration was lower below violet individuals, while other soil variables, plant size, and floral traits did not differ detectably among color morphs. Our results indicate that flower color variation in *D. purpurea* is primarily driven neither by pollinator visitation nor soil conditions. Floral color did not influence pollinator visitation or reproductive success, suggesting that its maintenance may reflect local environmental conditions, selective neutrality, or historical and demographic processes rather than selection.

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## Pollinator Ecology, Networks, Health & Conservation

### A unified framework to study pathogens and pathologies in wild solitary bees

**Presenting:** Ana Pérez Pérez

**Authors:** Ana Pérez-Pérez<sup>2</sup>; Carlos Hernández-Castellano<sup>1,2,3</sup>; María Benito-Murcia<sup>4</sup>; David Risco<sup>4</sup>; Eduardo J. García-Vicente<sup>2</sup>; María Martín-Domínguez<sup>5</sup>; Noelia Hermosilla<sup>2</sup>; Roser Velarde<sup>1</sup>; María Escobar-González<sup>1</sup>; Josep Estruch<sup>1</sup>; Irene Torres-Blas<sup>1</sup>; Emmanuel Serrano<sup>1</sup>

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Bee losses are driven by multiple interacting factors, with pathogens playing crucial roles. In the context of the global decline in wild pollinators, assessing the contribution of pathogens is essential. While *Apis mellifera* benefits from diverse tools to evaluate pathogen presence and impact, our understanding of pathogens in wild solitary bees remains extremely limited. This gap is alarming because animal health studies are fundamental for interpreting wildlife population dynamics and ecosystem functioning. Current research on solitary bees is largely restricted to detecting honeybee pathogens, without addressing the reality of infectious agents and their pathogenicity is lesser unknown. Herein compiled existing knowledge on managed and wild bees and highlighted the urgent need to uncover the full diversity of pathogens affecting solitary species. In this way, a comprehensive framework is proposed, based on previous works and representing parasitology, wildlife biology, and pollinator ecology. This framework integrates complex tools, such as omics, to characterize the complete infectome of wild bees, together with population monitoring at flowering plants and nesting sites. Experimental infections and histopathological analyses will further elucidate disease development and physiological mechanisms. A holistic understanding of solitary bee health is crucial for interpreting the risk of involvement of these species.

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### **Unveiling the functionally rich pollination network of *Angelica pachycarpa* in the Atlantic Islands National Park (NW Spain)**

**Presenting:** Ane Navarro-Ayensa

**Authors:** Ane Navarro-Ayensa<sup>1</sup>; Lea Ada Palao Picotti<sup>1</sup>; Luis Navarro<sup>2</sup>

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Understanding the diversity and functional structure of plant-pollinator interactions is fundamental for evaluating ecosystem functioning and the contribution of individual species to local biodiversity. We characterized the floral-visitor assemblage of *Angelica pachycarpa* (Apiaceae) in the Atlantic Islands National Park (NW Spain) through standardized pollination censuses conducted during spring 2023. A total of 43 visitor species were recorded, spanning 13 functional groups, including flies, beetles, short- and long-tongued bees, bumblebees, hoverflies, wasps, ants, bugs, ant-lions, birds, and lizards. Flies were by far the dominant functional group, followed by ants, beetles, and both bee guilds. Species-level analyses revealed pronounced differences in visitation rates. Notably, our survey provides the first record of the Iberian wall lizard *Podarcis hispanica* and the black redstart (*Phoenicurus ochruros*, a passerine bird) visiting and pollinating flowers of *A. pachycarpa* within the park, highlighting the unexpected breadth of vertebrate participation in this system. Together, these results uncover

a remarkably diverse and functionally rich pollination network, underscoring the ecological significance of *A. pachycarpa* as a key floral resource in these insular landscapes.

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### **Autonomous Low-Cost System for Pollinator Monitoring and Species Identification: Key Obstacles and Challenges**

**Presenting:** Barbora Jelínková

**Authors:** Barbora Jelínková<sup>1</sup>; Karel Petránek<sup>2</sup>; Eva Horčíková<sup>1</sup>

**Affiliation:** <sup>1</sup> Faculty of Environment, Jan Evangelista Purkyně University in Ústí nad Labem, Czech Republic. <sup>2</sup> Faculty of Science, University of Hradec Králové, Czech Republic.

The rapid advancement of machine learning algorithms, combined with the increasing accessibility of low-power single-board computers, offers transformative opportunities for ecological research. While traditional monitoring of plant-pollinator interactions is labor-intensive, costly, and prone to observer bias, these technological innovations allow for the development of automated, non-invasive data collection systems. However, implementing these technologies in field conditions remains a challenge. We present an ongoing project aimed at developing a cost-effective (approx. €400) autonomous monitoring unit. The goal is to construct a device capable of continuous recording, automatic detection, and species-level identification of pollinator presence using commercially available hardware. Here we summarise obstacles in the implementation of such device.

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### **Study of the acute lethal contact doses of oregano essential oil in *Apis mellifera* and *Varroa destructor***

**Presenting:** Eduardo José García Vicente

**Authors:** Eduardo José García-Vicente<sup>1</sup>; María Benito-Murcia<sup>2</sup>; María Martín-Domínguez<sup>3</sup>; Ana Pérez-Pérez<sup>1</sup>; Noelia Hermosilla<sup>1</sup>; Josué Delgado<sup>4</sup>; Juan Manuel Alonso<sup>3</sup>; Salomé Martínez-Morcillo<sup>3</sup>; David Risco<sup>2</sup>

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The mite *Varroa destructor* represents the main problem for honeybees. Synthetic acaricides present various issues, as they are losing effectiveness due to the emergence of resistant mite

populations, and they leave large amounts of residues that accumulate and persist for long periods of time. This latter aspect has a direct negative effect on bees through chronic exposure, and it also predisposes them to the appearance of concomitant infectious and parasitic processes, which deteriorate the general health status, not only of honeybees, but also of their environment, due to the high likelihood of pathogen transmission to other species of wild pollinators. In this study, the effect of oregano essential oil was evaluated as a potential organic acaricidal product, both on the mite and on the bees, in order to determine the doses needed to use it without causing negative effects on the host. In this way, the acute lethal contact doses for both species were determined through laboratory assays, establishing a dose range for oregano essential oil from 1 115 ppm to 12 408 ppm, which would be safe for the bees and effective against *V. destructor*.

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### **Taxonomic, functional and phenological comparison of two western Mediterranean bee communities.**

**Presenting:** Gerard Rigola Coll

**Authors:** Gerard Rigola-Coll<sup>1</sup>; Sergio Osorio-Cañadas<sup>2</sup>; Antonio Burguillos<sup>1</sup>; Anselm Rodrigo<sup>1,3</sup>; Jordi Bosch<sup>1</sup>

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The Mediterranean Basin holds a very high bee (Hymenoptera, Anthophila) diversity. While regional bee faunas are quite well established in Mediterranean countries, we know much less about the composition and richness of local communities. This information is important for bee conservation and to understand the spatial and temporal structure of bee assemblages and their relationships with flowering plants. In this study, we sampled two local (< 5 ha) bee communities separated by 22 km near Barcelona (NE Iberian Peninsula) once a week for one year. We compare the two communities in terms of richness, composition and functional traits (body size, tongue length, sociality, nesting substrates, pollen preferences and nesting phenology). Bee activity occurred year-round at the two sites, including the winter months and the summer drought period, and species richness peaked between May and June. The richer community had a surprisingly high number of species (225), compared to the poorer community (131). Despite this difference, the two communities were similar in taxonomic (distribution of species across genera) and functional composition. We discuss the results obtained in relation to the ecological factors of the two sites and compare them to published results from other bee communities.

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## **Effects of photovoltaic plants on plant–pollinator networks in the province of Badajoz (SW Spain)**

**Presenting:** Gregorio García Sánchez-Ramal

**Authors:** Gregorio García Sánchez-Ramal<sup>1</sup>; José Luis Pérez Bote<sup>2</sup>; José María Maya Manzano<sup>1</sup>; Francisco Javier Valtueña Sánchez<sup>1</sup>; Ana Isabel Ortega Olivencia<sup>1</sup>; Josefa López Martínez<sup>1</sup>; Tomás Rodríguez Riaño<sup>1</sup>

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The rapid expansion of photovoltaic installations to meet growing energy demands may temporarily alter plant–pollinator interactions. In 2024, interaction networks were constructed in two photovoltaic plants and four control habitats (holm oak woodland, streamside, olive grove, and cropland) through direct pollinator censuses and video recordings. Analyses in R using the bipartite package revealed marked differences in network structure and species composition. Holm oak woodland exhibited the highest interaction richness ( $>1,200$  links) and modularity ( $Q = 4.6$ ), whereas cropland was consistently the poorest across all indices. Specialization ( $H_2$ ) peaked in one photovoltaic plant (0.47) and the streamside site (0.65), indicating more selective interactions in these habitats. Nestedness was greatest in the woodland and the second photovoltaic plant ( $NODF = 2.4$ ). Assemblage dissimilarity was high ( $WN = 0.8–1$ ), driven mainly by species turnover ( $ST$ ). Pollinator composition varied substantially: small bees and bees dominated photovoltaic sites and Riverside, while syrphid flies and beetles were more frequent in woodland and cropland. Plant assemblages also shifted, with *Diplotaxis virgata* and *Erodium moschatum* prevailing in photovoltaic areas, contrasting with *Cistus crispus* and *Crepis vesicaria* in natural habitats.

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## **Pollinators of beaver territories: How the return of beavers affects the pollinator spectrum**

**Presenting:** Helena Pijálková

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The European beaver (*Castor fiber*) has been absent from central Europe for many decades. Over the past 40 years, we have observed its return to its original habitats and the consequent effect it had on local river ecosystems. Many insect pollinator species are known to have aquatic or semi-aquatic larvae, while others breed in decaying wood. The aquatic larvae of insects also differ in their requirements for various types of water, including still or flowing water, and water that is either deep or shallow. All of these conditions can be met in beaver territories. The areas cleared out near the beaver dams also provide a suitable environment for many species of flowering plants. The aim of this preliminary project is to investigate the diversity of insect pollinators in the surrounding of beaver territories and the impact of beaver activities on the composition of local pollinator communities and plant-pollinator networks.

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### **Plant-pollinator interactions in relation to post-fire ecological succession**

**Presenting:** Ignasi Lampreave Farran

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In Mediterranean ecosystems wildfires play a key role in the dynamics of biodiversity. However, how plant-pollinator communities assemble after these disturbances are understudied. The main objective was to evaluate how plant-pollinator interactions vary through the post-fire ecological succession, based on the hypothesis that the greatest complexity will be found in the initial and intermediate stages, due to greater floral availability and favorable habitat conditions. We selected eight wildfires with different years of recovery and conducted plant-pollinator surveys. We conducted generalized additive mixed models (GAMM) to relate different variables of plant-pollinator communities and interactions with time after fire. The results show greater flower abundance and richness in the intermediate stages (3–7 years), as well as a slight upward trend in bee abundance. Overall, the intermediate stages of post-fire succession appear to offer more favorable conditions for the complexity of plant-pollinator communities.

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## The resilience of plant-pollinator networks after the disturbance by large wild herbivores

**Presenting:** Júlia Coromina

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Overabundant populations of large herbivores, an increasing pressure in Mediterranean ecosystems, may erode plant–pollinator networks. However, network components’ resilience remain empirically unevaluated. We assessed plant–pollinator networks’ resilience after the disturbance of overabundant red deer (*Cervus elaphus*). The study consisted of hectare-scale enclosures in a Mediterranean scrubland, where plant–pollinator surveys were performed during four years. We simulated two deer overabundance scenarios: high densities (>30 individuals km<sup>-2</sup>), hyper densities (>90 individuals km<sup>-2</sup>) and compared them with a control scenario (no deer). Deer densities decreased during the study, achieving natural densities (10 individuals km<sup>-2</sup>). Most network components declined under both overabundant scenarios. Flowering plant and pollinator communities were generally resilient in the high- but not in the hyper-density treatment. Visitation rate and generality of palatable plants (*C. populifolius*), declined without recovery. Network structure showed contrasting patterns: modularity and robustness were resilient under both treatments, network size only under high-density, and interaction richness showed no recovery. Plant-pollinator network resilience was affected by disturbance intensity: network integrity was generally less resilient in the hyper-density treatment. In large herbivore overabundance scenarios, palatable plants may fail to recover. As such, while some network properties may be readily resilient, the assemblage of interactions may take longer to recover.

## **Long-term climatic and landscape changes shape the functional diversity of butterfly communities**

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Climate and land-use changes are major drivers of insect declines worldwide, but their effects on functional diversity remain poorly understood. Landscape homogenization and rising temperatures are expected to reduce the functional diversity of insect communities. Here, we tested how long-term changes in local landscape heterogeneity and thermal conditions during the reproductive season influenced species richness and functional diversity (richness and divergence) in highly-diverse Mediterranean butterfly communities. For this, we combined functional traits with butterfly records spanning 10-30 years across 88 communities of the Catalan Butterfly Monitoring Scheme (CBMS) in three climatic zones (alpine/subalpine, mesic, and xeric). Species richness and functional diversity indices were highest in the alpine/subalpine region, intermediate in the mesic, and lowest in the xeric region. As expected, species richness, functional richness, and functional divergence significantly decreased over time. Higher landscape homogenization was related to decreases in both species and functional richness. In addition, higher temperatures in the reproductive season were related to declines in species and functional richness in the xeric and mesic regions, but to increases in the alpine/subalpine region, possibly reflecting altitudinal shifts. This study demonstrates that landscape homogenization and rising temperatures modulate the functional diversity of butterfly communities, potentially affecting their stability and functioning.

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## **Insects And The City - Flower availability as a primary driver of urban wild pollinator diversity in sown wildflower meadows**

**Presenting:** Liza Moerman

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Urbanization continues to drive pollinator declines through habitat loss and fragmentation, yet targeted interventions can help transform urban greenspaces into alternative habitats. We focused on urban sown wildflower meadows and studied how local habitat variables (meadow size, meadow age, and flower availability) and the surrounding impervious cover influence the taxonomic diversity of wild pollinators and entomophilous plants. We surveyed wild bees, hoverflies, and flowering plants at 17 sites within the city of Ghent (Belgium) during two sampling rounds, one early summer (June-July) and one late summer (August). Wild bee and hoverfly abundance and species richness increased with increasing flower cover or species richness, while neither impervious cover nor meadow size had a significant effect. Flower cover and flower species richness were unaffected by the proportion of impervious cover, meadow age, and meadow size. Our results show that local habitat quality, particularly flower availability, is a key driver of pollinator diversity in urban wildflower meadows. Even small, well-managed meadows can provide meaningful support for urban pollinator communities. Improving the local habitat quality of urban wildflower meadows could further benefit both plant and pollinator biodiversity, thereby contributing to healthy urban ecosystems, which form the backbone of liveable cities for people and nature.

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### **Unveiling the functionally rich pollination network of *Angelica pachycarpa* in the Atlantic Islands National Park (NW Spain)**

**Presenting:** Luis Navarro

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Understanding the diversity and functional structure of plant-pollinator interactions is fundamental for evaluating ecosystem functioning and the contribution of individual species to local biodiversity. We characterized the floral-visitor assemblage of *Angelica pachycarpa* (Apiaceae) in the Atlantic Islands National Park (NW Spain) through standardized pollination censuses conducted during spring 2023. A total of 43 visitor species were recorded, spanning 13 functional groups, including flies, beetles, short- and long-tongued bees, bumblebees, hoverflies, wasps, ants, bugs, ant-lions, birds, and lizards. Flies were by far the dominant functional group, followed by ants, beetles, and both bee guilds. Species-level analyses revealed pronounced differences in visitation rates. Notably, our survey provides the first record of the Iberian wall lizard *Podarcis hispanica* and the black redstart (*Phoenicurus ochruros*, a passerine bird) visiting and pollinating flowers of *A. pachycarpa* within the park, highlighting the unexpected breadth of vertebrate participation in this system. Together, these results uncover

a remarkably diverse and functionally rich pollination network, underscoring the ecological significance of *A. pachycarpa* as a key floral resource in these insular landscapes.

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### **Proteomic Analysis of Organic Treatments Mechanisms Against Varroa destructor**

**Presenting:** María Benito-Murcia

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Varroa destructor is an external parasite mite of honeybees and one of the main causes of mortality in hives. The most commonly used control methods are synthetic acaricides; however, these treatments can induce resistance in varroa populations and leave residues in wax and honey. Consequently, organic alternatives are being explored. One of the most promising are postbiotics, bioactive products of beneficial lactic acid bacteria from honeybees.

This study tests the mechanism of action of a postbiotic used in bioassays against varroa. A proteomic analysis was performed on varroa mites treated with the postbiotic, its supernatant and a peptide-concentrated fraction from this postbiotic, as well as varroa mites treated with oxalic acid as a positive control and MRS as a negative control.

Overexpression or underexpression was observed in different proteins involved in basic mite functions such as detoxification, movement capacity, essential metabolism, cuticle formation, and calcium regulation. These results show the activity of this postbiotic against varroa and provide a more precise understanding of the pathways that can be targeted to develop a natural and effective treatment for one of the biggest problems in beekeeping today.

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## **Spatio-temporal dynamics of honeybee–pathogen networks: implications for colony health and productivity**

**Presenting:** María Martín Domínguez

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Pollinator declines threaten biodiversity and food security, with honey bees (*Apis mellifera*) suffering widespread losses due to multiple interacting stressors. Pathogens—including Varroa destructor, associated viruses, Nosema ceranae, and emerging pests—form complex antagonistic communities within hives, yet the structure of these interactions remains poorly understood. Understanding spatial and temporal variation in pathogen networks is essential for predicting colony performance.

This study aimed to (1) characterize the ecological network of honeybee colonies and their pathogens, and (2) assess how network structure relates to colony population dynamics and productivity. Fieldwork was conducted in Extremadura (Spain) across five apiaries (2020–2024). Layens hives were randomly selected and monitored twice per season to quantify colony strength, productivity, and pathogen load.

Hive–pathogen interactions showed strong spatial and temporal structuring, with hives often dominated by a single pathogen in specific locations and seasons. This generated distinct network compartments differing in infection levels, population trends, and productivity. Colony declines were mainly driven by overall pathogen load and *V. destructor*, although some low-performing compartments were unrelated to pathogen presence, suggesting additional environmental stressors.

These findings indicate that targeted management of the most vulnerable network compartments could be more effective than broad sanitation strategies.

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## **Bee diversity patterns in urban and adjacent natural ecosystems: high species turnover makes urban parks biodiversity refuges**

**Presenting:** Marina Aguilar

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Bee populations are declining worldwide due to multiple stressors, including land-use changes such as urbanization. However, urban parks are regarded as potential biodiversity refuges, despite to date evidence remains contrasting. In this study, we evaluated the effectiveness of urban parks as refuges for bees -i.e., whether they host more or distinct species than adjacent natural areas-, and whether this function varies across seasons. We characterized bee communities in urban parks and adjacent natural areas in a city of the NE Iberian Peninsula during one year and across the whole activity period of bees. We assessed species richness, the nested structure of bee communities, and the patterns of species distribution over space explaining community differences (nestedness vs turnover). Urban parks hosted lower bee richness than natural areas, but only in the late season. Bee communities of urban parks were not nested subsets of communities from natural areas, as in both seasons more than 30% of species were idiosyncratic to specific sites. Such idiosyncratic species were rare in distribution and abundance. Communities from urban parks differed strongly from those in natural areas, mostly due to species turnover. Thus, in our study system, urban parks are bee diversity refuges throughout the year, hosting distinct communities with many unique species. Improving bee diversity and conservation in cities may rely on enhancing species turnover by establishing a network of urban parks, and on providing effective flowering and nesting resources, especially for idiosyncratic species, to prevent their local extinction.

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### From flowers to parasites: inside the *Hoplitis laevifrons* network

**Presenting:** Rosa Ranalli

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*Hoplitis Klug, 1807* (Megachilidae) is the most species-rich genus within Osmiini, yet its biology remains poorly understood. The subgenus *Pentadentosmia*, including the *laevifrons* species group, is characterized by ground-nesting habits and oligoleptic foraging, but detailed data for *H. laevifrons* (Morawitz, 1872) and its association with the brood parasite *Chrysis rufitarsis* Brullè, 1833 are still lacking. To address this gap, we investigated nesting aggregations of *H. laevifrons* in the Matese Limestone Massif (Central Italy). Pollen morphological analyses were performed on loads collected from the female scopula and from brood-cell provisions to assess floral preferences. Nesting site structure and parasite presence were recorded, and pathogen sharing among *H. laevifrons*, the pollen load, and *C. rufitarsis* was examined using molecular screening. Results indicated strong oligolecty on Fabaceae, mainly *Lotus herbaceus* L. and *Ononis spinosa* L., both abundant near the nesting sites, with only occasional Asteraceae pollen. Pathogen screening revealed the presence of honey bee-associated pathogens in *Hoplitis*, *Chrysis*, and pollen samples, suggesting possible horizontal transmission pathways. Overall, this study enhances understanding of *H. laevifrons* ecology and emphasises the need for integrated behavioural, ecological, and molecular approaches to assess conservation risks faced by solitary bees in Mediterranean ecosystems.

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### **Pollinator networks in a regional Park of Northern Italy: comparison between gypsum natural habitat and quarries within UNESCO World Heritage site**

**Presenting:** Serena Magagnoli

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This study examines the biodiversity and ecological role of pollinators in the Vena del Gesso Romagnola Regional Park, a high-value protected area in Emilia-Romagna, Northern Italy, recently recognized as a UNESCO site. The Park's extensive gypsum formations are the key geological element shaping both the landscape and its associated habitats.

Pollinators play an essential role in ecosystem functioning, supporting the reproduction of more than 75% of major food crops, yet global declines driven by climate change, pesticide use, and habitat loss threaten their populations.

This research aimed to characterize pollinator community and analyze plant–pollinator interactions as a proxy of ecosystem complexity and resilience. The focal groups were Apoidea (Anthophila) and Syrphidae, with additional consideration of butterflies (Papilionoidea). Samplings were conducted at three representative sites: a quarry active until 1980 and now completely renaturalized, a currently active quarry, and a natural gypsum outcrop never subjected to extraction. At each site, standardized transects and Malaise traps were used in grassland and gypsum-outcrop habitats, followed by morphological identification of specimens.

Preliminary bipartite networks (connectance, modularity, nestedness,  $H$ ) revealed that grasslands supported denser, more generalist, and functionally redundant networks sustained by season-long floral continuity; gypsum outcrops acted as ecological filters, yielding more specialized and potentially vulnerable networks dominated by morphologically suited Apoidea, while Syrphidae and Papilionoidea were more sporadic. Site-level differences underscored the influence of landscape context in the community of pollinators.

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