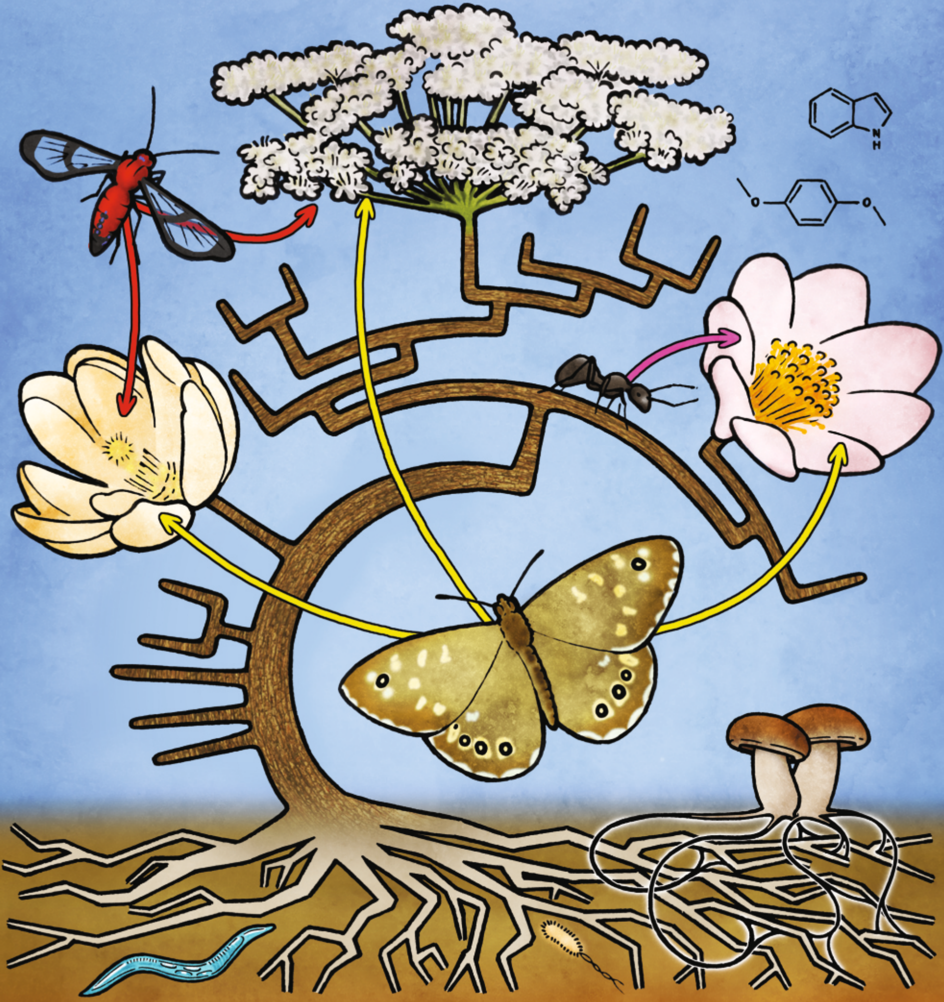
43rd New Phytologist Symposium

Interaction networks and trait evolution



1–4 July 2019
Zürich, Switzerland

New Phytologist Trust

Programme, abstracts and participants

43rd New Phytologist Symposium

Interaction networks and trait evolution

University of Zürich, Switzerland

1–4 July 2019

Scientific Organising Committee

Florian P. Schiestl *(University of Zürich, Switzerland)*
Jordi Bascompte *(University of Zürich, Switzerland)*

New Phytologist Organisation

Freja Kärrman-Bailey *(Events and Promotion Coordinator)*
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Acknowledgements

The 43rd New Phytologist Symposium is funded by the New Phytologist Trust
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The New Phytologist Trust is a non-profit-making organisation dedicated to the promotion of plant science. It owns and produces the international journals *New Phytologist* and *Plants, People, Planet*. The Trust receives income through its publication activities and any excess revenue from publication of the journals is put straight back into supporting plant science. This is achieved by funding a wide range of activities: the organisation and sponsorship of symposia, workshops and meetings; numerous grant schemes; sponsorship of various awards for early-stage career scientists including the Tansley Medal; and ensuring that research published in the journal is as widely and openly available as possible, as such, all of our Tansley series reviews and Forum articles are immediately available to access free of charge upon publication. All of these actions have a common goal to promote emerging areas of plant science and to encourage continued progress and innovation in the field.

Programme, abstracts and participant list compiled by Freja Kärrman-Bailey
'Interaction networks and trait evolution' logo by
Andy Crayston, Promotional Gods, Lancaster, UK

Contact email: *np-symposia@lancaster.ac.uk*

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Information for Delegates

Symposium location

The 43rd New Phytologist Symposium will be held in the KOL-F-118 lecture theatre in the main University building (KOL), University of Zürich, Rämistrasse 71. Telephone: 11 11.ł 634

Directions and a map can be found at the back of this abstract book.

Catering

Lunches, coffee breaks and poster sessions will all be held in the North Atrium (Lichthof Nord) of the main University building. Wine and canapés will be served during the poster session on the Monday evening.

The symposium dinner will be held at the Hotel Uto Kulm on the Uetliberg Mountain on Tuesday evening. The dinner is for all speakers and delegates and is included in your registration fee. We will be taking the 19:35 train from Zürich HB to Uetliberg. We plan on walking to Zürich HB from the University, leaving at 19:00. There are also tram and taxi services between the University and the station.

If you have special dietary requirements please do make yourself known to the catering staff or ask Helen / Freja from the New Phytologist Trust. All our requirements have been provided to the catering team and they will have meals prepared accordingly.

Posters

Posters should be prepared so that they are no larger than A0 size, portrait orientation (118cm high X 84cm wide). Posters should be put up during registration (09:00 – 11:00 on the 1st of July) and will be displayed for the duration of the meeting. Delegates are welcome to view posters during coffee and lunch breaks, but there will be dedicated poster sessions at 16:00 – 18:30 on the Monday and 16:50 – 18:50 on the Tuesday. Please stand by your poster for these parts of the sessions (we appreciate that you will also want to view and discuss other posters). Please note that there will be prizes for the best poster presentations. Posters will be assessed by your peers (the other delegates) and the posters that gain the most votes will receive prizes. A scoring sheet is included in your delegate pack. Please fill out and return this sheet to the registration desk by 09:00 Wednesday 3rd July.

Internet access

Free Wi-Fi will be provided throughout the venue.

Social media

We encourage all attendees to join in discussions on social media sites. Follow @NewPhyt on Twitter and fb.com/NewPhytologist on Facebook for updates before, during and after the meeting. Please use the hashtag #43NPS in all of your tweets.

Photography

Photography will take place at the 43rd NPS.
The resulting photographs will be used by the New Phytologist Trust for the purpose of promoting its activities, and may be published on the New Phytologist Trust's website and social media channels.
If you do not wish to appear in the photographs, please speak to one of the organisers.

Code of conduct

The New Phytologist Trust celebrates diversity and we expect participants in our meetings to be respectful, considerate and supportive of each other, to offer constructive critiques and embrace the variety of opinions on offer. The 43rd NPS is an opportunity to share, develop and broaden our viewpoints within a safe and inclusive setting, and we hope that you will enjoy the meeting. If you have any concerns or suggestions, please speak to one of the organisers.

Contact

The main contact for the symposium is Freja Kärrman-Bailey, email: np-symposia@lancaster.ac.uk, tel: +44 7948 190 448. In a serious emergency, please call the emergency services on 112.

Meeting Programme

Updated 26 June

Monday 1 July

9:00–11:00	Registration and arrivals
11:00–11:15	Welcome from the organisers
Session 1 **11:15–16:45**	**Chair: Marilia Gaiarsa**
11:15–12:00	S1.1 **Judith Bronstein** Context-dependent interaction outcomes in the assembly and evolution of mutualistic networks
12:00–12:45	S1.2 **Miguel Verdú** Plant facilitation networks and trait evolution
12:45–14:00	Lunch
14:00–14:45	S1.3 **Florian Schiestl** An experimental approach to multi-species interactions and their evolutionary outcomes
14:45–15:05	Selected poster talk – **Gitanjali Yadav** Phytochemical Networks of Invasive Species provide evidence for Novel Weapons Hypothesis
15:05–15:25	Selected poster talk – **Irina Birskis-Barros** Trait convergence and diversity in species-rich interactions: habitat use and heterogeneity affect coevolution of mimetic species
15:25–16:00	Break
16:00–18:30	Poster session

Tuesday 2 July	
Session 2 **9:00–12:30**	**Chair: Jiancai Li**
9:00–9:45	S2.1 **John Thompson** Complex trait evolution in small and large networks of coevolving species
9:45–10:05	Selected poster talk – **Karin Gross** Polyploidy and floral evolution in a geographic mosaic of specialised and generalized pollinators
10:05–10:25	Selected poster talk – **Paulo Guimaraes** Indirect effects and the coevolutionary dynamics in mutualistic networks
10:25–10:50	Break
10:50–11:35	S2.2 **Anton Pauw** Long-legged bees make adaptive leaps: linking adaptation to coevolution in a plant–pollinator network
11:35–12:20	S2.3 **Marcelo Aizen** What does the phylogenetic structure of interaction webs tell us about coevolution?
12:20–13:30	Lunch
Session 3 **13:30–16:50**	**Chair: Adrienne Godschalx**
13:30–14:15	S3.1 **Pedro Jordano** Individual traits and the architecture of multiplex ecological networks
14:15–14:35	Selected poster talk – **Matthew Barbour** Extinction of a consumer guild constrains the adaptive landscape of an insect herbivore
14:35–14:55	Selected poster talk – **Carina Baskett** Quantifying importance of pollinators as selective agents on flower color in a subspecies hybrid zone

14:55–15:20	Break
15:20–16:05	S3.2 **José María Gómez Reyes** Floral trait evolution in generalized pollination systems
16:05–16:50	S3.3 **Shoko Sakai** Different pathways for specialization under pollination dilemma
16:50–18:50	Poster session
19:00	Those attending the symposium dinner will assemble by the entrance to the main University building before walking as a group to Zürich HB station in order to take the train to Uetliberg
20:10	Symposium Dinner at Hotel Uto Kulm
Wednesday 3 July	
Session 4 **9:00–12:30**	**Chair: Daniel Bastias**
9:00–9:45	S4.1 **Jordi Bascompte** Effects of climate change on the taxonomic, trait, and phylogenetic diversity of pollination networks
9:45–10:05	Selected poster talk – **Bernat Bramon Mora** Untangling the seasonal dynamics of plant–pollinator communities
10:05–10:25	Selected poster talk – **Katherine Eisen** Emission rates of species-specific volatiles change across communities of *Clarkia* species: Evidence for character displacement in floral scent
10:25–11:00	Break
11:00–11:45	S4.2 **Diane Campbell** Natural selection of trait associations shaped by sequential interactions with pollinators and seed predators
11:45–12:30	S4.3 **Toby Kiers** Networks as organisms and physical structures

12:30–14:00	Lunch
Session 5 **14:00–16:45**	**Chair: Carine Emer**
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15:05–15:25	Selected poster talk – **Erik Poelman** Keystone herbivores and the evolution of plant defense
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16:00–16:45	S5.2 **Catherine Graham** Ecological strategies that govern plant–hummingbird interactions
16:45–17:00	Symposium close

Thursday 4 July

Field trip to Gumen

We will be assembling at Zürich HB station at 7:10. The train to Braunwald will leave Zürich just after 7:30. We will then take a cable car from Braunwald up to Gumen. Trains run back to Zürich from Braunwald every hour. More information about the field trip will be available at the symposium.

Speaker Abstracts

S=speaker abstract, P=poster abstract

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Campbell, Diane	**S4.2**
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Verdú, Miguel	**S1.2**

Speaker Abstracts

Session 1

Chair: Marilia Gaiarsa

Context-dependent interaction outcomes in the assembly and evolution of mutualistic networks

S1.1

JUDITH L. BRONSTEIN

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Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ, USA

11:15–12:00

Networks thinking has sparked new interest in species interactions, and has given us valuable new tools with which to explore them. To what extent, though, do network approaches capture the natural history of species interactions? I will focus particularly on mutualisms, the study of which has been revolutionized by network analysis. I begin with a quick overview of mutualism ecology. I will then highlight (a) features of recent mutualism network models that seem to accurately capture these interactions, and that are leading to exciting insights; (b) model features that are quite distant from the reality of mutualism, and that might thus lead us to inaccurate predictions about how these interactions function and evolve; and (c) mutualism characteristics that are not yet captured in network models, but that would exciting to study. My focus throughout this talk will be on the phenomenon of context-dependency: interaction outcomes vary in space, as well as over both ecological and evolutionary time scales. I will look at a range of attempts to capture this essential biological feature of interactions. I will present no data, but lots of ideas for further exploration. My goal is to stimulate empirical–theoretical synthesis at this exciting research frontier, particularly with regard to the poorly understood evolutionary dimension of context-dependency.

Plant facilitation networks and trait evolution

S1.2

MIGUEL VERDÚ

12:00–12:45

ymottiar@mail.ubc.ca

Centro de Investigaciones sobre Desertificación (CSIC-Universidad de Valencia), Valencia, Spain

The beginnings of the 21st century witnessed a burst of studies representing ecological interactions as complex networks. Plant facilitation, an important ecological interaction shaping plant communities worldwide, started to be studied under this new framework in 2008. One decade later, we review the advances we have experienced on plant facilitation networks. Plant facilitation networks were initially conceived as the result of the evolutionary history of plant species under the assumption that divergent evolution of traits favors the establishment of facilitative interactions. To test this hypothesis, phylogenetic distances have been used as a proxy of trait divergence between species but, surprisingly, phenotypic distances have been seldom used to explain the structure of plant facilitation networks. Knowing whether trait evolution leaves a signal in facilitation networks is the first step to understand how these networks may shape selection. Incipient evidence on the role of facilitation as a selective strength exists, paving the road to connect facilitation network studies with selection analysis.

The role of pathogens in driving host evolution and population dynamics in the wild

ANNA-LIISA LAINE[1,2], LAYLA HÖCKERSTEDT[2], ELINA NUMMINEN[2], HANNA SUSI[2], SUVI SALLINEN[2]

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Pathogens are prevalent across all ecosystems. An individual’s reproductive success and survival will depend on its ability to resist infection, yet natural populations have been shown to support considerable diversity in resistance traits. Theory predicts that under pathogen-imposed selection variation in resistance is maintained by allocation costs with susceptible individuals having higher fitness in the absence of disease. Thus far empirical evidence supporting pathogen imposed selection and costs of resistance as mechanisms that maintain resistance variation have remained sparse and mixed. Moreover, studies have not considered how spatial structure and diversity of pathogens attacking the same hosts may shape resistance traits. Here, we aim to understand how host evolutionary potential and pathogen imposed selection vary across the landscape and what the consequences are for resistance trait variation and host population dynamics. For this purpose, we’ve analyzed resistance trait variation, as well as long-term data on host population size and disease prevalence in the *Plantago lanceolata* populations in the Åland Islands, SW Finland. The results show that the strength of pathogen imposed selection varies across the landscape, in a spatially structured manner, with direct consequences for how trait diversity is distributed. The results highlight the importance of studying host–pathogen dynamics across multiple populations to truly understand what the consequences of infection are for the host.

An experimental approach to multi-species interactions and their evolutionary outcomes

S1.3

FLORIAN P. SCHIESTL

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Department Systematic and Evolutionary Botany, University of Zürich, Zollikerstrasse 107, CH-8008 Zürich

14:00–14:45

Biotic interactors drive plant evolution in various ways, however, we know little about how the composition of interacting partners determine evolutionary trajectories. In my group we have used experimental evolution with fast cycling *Brassica rapa* plants to investigate the effects of different specific pollinators, combinations of pollinators (simulated generalized pollination) as well as combined pollinators and herbivores on plant-trait evolution. We showed that as early as after 9 generations, plants pollinated by bumblebees had evolved taller size and more fragrant flowers with increased UV reflection, whereas plants with hoverfly pollination became shorter, had reduced emission of some floral volatiles, but increased fitness through augmented autonomous self-pollination. Plants with both bumblebee- and hoverfly pollination resembled bumblebee-pollinated plants in having little spontaneous selfing and tall size, but were more similar to hoverfly-pollinated plants in having low floral scent emission. Plants that evolved with bumblebees and herbivores were constraint in the evolution of attractive flowers, and evolved more spontaneous selfing and reduced herkogamy. Our results highlight non-additive effects of different interactors and suggest that the effects of suits of interacting organisms cannot necessarily be predicted by the average effect of individual interactors. For a better understanding of such “non-additive evolution”, experimental manipulation of interaction networks and their effect on phenotypic selection and subsequent adaptive evolution should provide a valuable tool in the future.

Session 2

Chair: Jiancai Li

Complex trait evolution in small and large networks of coevolving species

S2.1

JOHN N. THOMPSON

9:00–9:45

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Department of Ecology and Evolutionary Biology, University of California, Santa Cruz, USA

Diversification of coevolving interactions, rather than extreme reciprocal specialization of pairs of species, may be the more common result of the coevolutionary process. The interactions between saxifragaceous plants and their pollinating and non-pollinating prodoxid moths illustrate how coevolution may shape the diversification of species networks, populations, and traits over large geographic areas. In these interactions, a combination of direct and indirect selection on traits has favoured diversification of pairwise interactions into multispecies networks. These networks have further diversified as the structure and strength of reciprocal selection on species has diverged among populations, ecosystems, and regions. The result has been geographic mosaics in the traits, ecological outcomes, and genetic architecture of the coevolving species. The mosaics have formed more often through selection on trait correlations than on the evolution of novel traits. These studies have shown that coevolution shapes the evolution of species networks, population networks, and trait correlations in subtle ways that may often require a combination of phylogenetic, geographic, ecological, and genetic analyses to identify.

Long-legged bees make adaptive leaps: linking adaptation to coevolution in a plant–pollinator network

S2.2

ANTON PAUW[1], BELINDA KAHNT[2], MICHAEL KUHLMANN[3,4], DENIS MICHEZ[5], GRAHAM A. MONTGOMERY[6], ELIZABETH MURRAY[6], BRYAN N. DANFORTH[6]

10:50–11:35

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[1]Department of Botany and Zoology, Stellenbosch University, Matieland 7602, South Africa; [2]Institute for Biology/General Zoology, Martin Luther University, Halle-Wittenberg, Hoher Rd. 8, D-06120 Halle (Saale), Germany; [3]Zoological Museum, Kiel University, Hegewischstr. 3, D-24105 Kiel, Germany; [4]Dept. of Life Sciences, Natural History Museum, Cromwell Rd., London SW7 5BD, U.K.; [5]Laboratoire de Zoologie, Research institute of Biosciences, University of Mons, Place du Parc 23, 7000 Mons, Belgium; [6]Department of Entomology, 3124 Comstock Hall, Cornell University, Ithaca, NY 14853-2601, U.S.A.

The idea that traits are adapted to their environment has seldom been tested in the context of ecological networks of interacting species. In this talk we explore a way of testing for adaptation, and ultimately coadaptation, using an ecological network of interacting species with known traits, and a phylogenetic hypothesis of relatedness. To qualify as an adaptation, a trait needs to have originated in response to a particular selective environment. Here we test whether leg length in South African oil-collecting bees (*Rediviva spp.*) evolves in response to the selective environment imposed by floral spur length. To quantify the selective environment, we drew a large network of the interactions between *Rediviva* species and oil-secreting plant species. The selective environment of each bee species was summarized as the average spur length of the interacting plant species weighted by interaction frequency. Using phylogenetically independent contrasts, we calculated divergence

in selective environment and evolutionary divergence in leg length between sister species (and sister clades) of *Rediviva*. We found that change in the selective environment explained 80% of evolutionary change in leg length, with change in body size contributing an additional 6% of uniquely explained variance. The result is one of four proposed steps in testing for plant–pollinator coevolution.

Past coevolution can leave its imprint in the cophylogenetic structure of extant pollination webs

S2.3

MARCELO AIZEN[1], LAWRENCE HARDER [2]

11:35–12:20

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Past coevolution can shape the cophylogenetic structure of pollination webs, even though interactions between specialists and strict co-speciation are rare. In fact, in most pollination webs specialists interact differentially with generalists, and generalists with both specialists and other generalists. Regarding this interaction structure, one possibility is that robust and strong symmetric interactions between generalists underlie a web's cophylogenetic backbone. Alternatively, if coevolution were highly asymmetric, interactions between generalist and specialist partners should establish the cophylogenetic structure of a pollination web. We evaluated these alternatives by "mapping" the interactions with the strongest cophylogenetic congruence for a metaweb comprising 1169 interactions between 96 plant and 171 pollinator taxa from 12 Pampean "sierras" differing in size. The most cophylogentically congruent interactions involved bee-specialized plants, mostly rosids and malvids plus a few monocots, and generalist bees from diverse families. This pattern is consistent with asymmetric dependence and ancient coevolution, whereby pollinators imposed stronger selection on plants than vice versa. In addition, some of the most congruent interactions involved associations between native and alien partners (e.g. *Apis mellifera*), further supporting the influence of basic matching traits inherited from very old ancestors on many contemporary ecological interactions. Overall, the number of plant–pollinator interactions varied negatively with habitat size; however, no consistent relation was evident for the subset of highly congruent plant–bee cophylogenetic interactions. Therefore, this long-coevolved interaction type can be relatively robust to disturbance despite species turnover. The historical imprinting of coevolution in the cophylogenetic

structure of a pollination web thus facilitates integration of alien species into native interaction networks, and may promote overall functional resilience under environmental change. More generally, this study reveals that past asymmetric coevolution can leave its mark in the cophylogenetic structure of extant pollination webs.

Session 3

Chair: Adrienne Godschalx

The architecture of multiplex ecological networks

S3.1

PEDRO JORDANO

13:30–14:15

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Interspecific ecological interactions in nature build up from encounters between individual partners, including variable outcomes as the result of overlying multiple forms of interaction. For example, multiplex ecological networks of plant–animal interactions emerge from the juxtaposition of the different interaction types, e.g., mycorrhizal symbioses, herbivory on leaves, roots, flowers, and fruits, pollination, and seed dispersal mutualisms, facilitation, and competitive interactions for shared partners. In contrast to other multilayer networks, multiplexed networks link a given set of nodes with their partners (e.g., plants, and animal mutualists and antagonists) through multiple interactions, i.e., the sequential stages of reproduction including layers of pollination, herbivory, seed dispersal, and establishment. The result of multiplexed interactions is, ultimately, the final effects on fitness of the interacting partners, yet we are far from understanding how these complex networks are intertwined.

Characterizing and sampling multiplexed networks means assessing the interaction modes that correspond to each interaction type. These can be thought of as interaction vectors, each including the outcomes of interaction of each plant species with each partner species, with connections among distinct layers of interaction types along the plant's life history. I discuss these multi-faceted forms of interaction, emphasizing the use of multiplex networks to explore trait correlations of individual–based interaction forms for different processes (e.g., pollination, herbivory, seed dispersal). Multi-species, multiplexed interaction networks are just the result of assembling the distinct interaction modes represented across individuals and species in a given community. Multiplexed networks allow biologically-realistic representations and analysis of the extraordinary diversity of interactions in real-world assemblages and how they relate to trait variation among partners. I review case studies illustrating the use of multiplex networks to assess individual-based and multi-specific networks of plant–animal mutualisms.

Floral trait evolution in generalized pollination systems

S3.2

JOSÉ M GÓMEZ

15:20–16:05

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Generalist plants interact with constellations of pollinators varying in their frequency of interaction and fitness impact. These heterogeneous groups of organisms are themselves networks that define the pollination niches of plants. The composition, topology and architecture of these pollination networks vary spatially, temporally and across organization levels: within individuals phenologically, among individuals of the same population, among nearby populations, among geographical regions, among related species and macroevolutionarily among phylogenetically-distant species. How generalist plants evolve in response to pollinators in this fractal context is yet an interrogant. Here, using as model system plant species of the Brassicaceae family, I explore the role played by pollination networks in the micro- and macroevolution of generalist plants. At microevolutionary level, several attributes of individual-based pollination networks favor the occurrence of significant selection on plant phenotype and promote the maintenance of a fine-scale genetic structure. But not only organisms may be agent of selection. The whole individual network itself can constitute as selective pressures, with some network metrics becoming part of the extended interactive phenotype of generalist plants. Because the inherent spatial variability of individual networks, generalist systems can easily prompt the existence of selection geographic mosaics and landscape-scale local adaptations. Scaling up, spatial variation in network attributes may trigger pollinator-mediated ecological speciation or, on the contrary, foster the occurrence of hybrid zones. At the macroevolutionary level, the lability of clade-oriented networks may cause the occurrence of pollinator-mediated phenotypic diversification. All this evidence suggests that the patterns of plant evolution in generalist scenarios are more complex than previously thought. Their study from a network perspective provides us with a richer and sounder picture of the role that pollinators play in the evolution of generalist plants.

Different specialization pathways under pollination dilemma

S3.3

SHOKO SAKAI

16:05–16:50

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Center for Ecological Research Kyoto University, Japan

Specialization for pollination by a particular group of pollinators was once considered to be common in flowering plants. By specializing to different pollinator groups, plants can reduce pollinator overlaps and competition for pollinators. However, community-wide studies in the last two decades showed that such pollinator segregation is much weaker than was previously considered, and have cast doubt on the importance of competition for pollinators to shape plant–pollinator interactions.

To examine whether competition alone is sufficient to drive pollinator segregation, we constructed a simple game theoretical model, in which plants are players and control their interaction with pollinators. The model shows that pollinator segregation is unstable unless potentially shared pollinators are highly abundant. The prisoner's dilemma payoff structure prevents the plants from taking the mutually beneficial strategy of pollinator segregation. This suggests that weak pollinator segregation observed may not result from insignificance of competition but rather because of the pollination dilemma. Specialist and generalist plants can coexist, but specialist plants still suffer from competition because they are pollinated by generalist pollinators.

Pollination by exclusive pollinators has been reported in different nursery or deceit pollination systems. However, because community-wide studies focus on flower visitors exploiting nectar or pollen, nursery and deceit pollination systems may be underrepresented in community-wide studies. In nursery and deceit pollination systems, plants suffer little from competition for pollinators. Repeated evolution of such pollination systems in different plant lineages indicates that competition is a significant factor to shape plant–pollinator interactions.

In the studies of pollination, specialization has often evaluated only by the range of animal groups that the plant interacts. However, specialist plants are highly variable in the degree of pollinator overlaps with other plant species. We may have to pay more attention to the variation in the potential for competition among specialized pollination systems.

Session 4

Chair: Daniel Bastias

Effects of climate change on the taxonomic, trait, and phylogenetic diversity of pollination networks

S4.1

JORDI BASCOMPTE 9:00–9:45

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Species extinctions induced by climate change may trigger coextinction cascades, thus driving extinct many more species than originally predicted by models of climate change. Recent work on pollination networks shows a significant variability across these networks in the predicted rate of plant extinction. This variability is even higher when considering the subsequent coextinction rates. While geographic location best predicts the probability of a plant species to be driven extinct by climate change, the local network of interactions best predicts subsequent coextinctions. Importantly, incorporating species interactions not only increases the pool of species most likely being driven extinct. It also changes the way extant species are selected from the evolutionary and functional trees with potential implications for the functioning and robustness of the resulting communities.

Natural selection of trait associations shaped by sequential interactions with pollinators and seed predators

S4.2

DIANE CAMPBELL[1,2], HEATHER BRIGGS[1,2], MASCHA BISCHOFF[2,3], ROBERT RAGUSO[4]

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[1]Department of Ecology and Evolutionary Biology, University of California, Irvine, CA, USA; [2]Rocky Mountain Biological Laboratory, Crested Butte, CO, USA; [3]Plant Chemical Ecology, Technical University Darmstadt, Germany; [4]Department of Neurobiology and Behavior, Cornell University, Ithaca, NY, USA

Organismal traits are often subject to natural selection via interactions with multiple species. Floral traits in particular can evolve in response to selection by herbivores as well as pollinators. Furthermore, selection due to interactions with multiple species is not necessarily predictable from examining pairwise interactions. Emergent properties may be especially likely when a plant interacts with other species during multiple episodes of its lifecycle. In theory, directional selection during two sequential episodes, such as during pollination and subsequent seed dispersal, can generate correlational selection for a specific combination of traits that passes both selective filters. If two selective agents, such as a pollinator and a seed predator, select on the same trait in opposite directions, stabilizing or disruptive selection may also result. We outline some predictions for the form of selection in several simple interaction webs for a plant, either representing a single pollinator or two pollinators, and in isolation or with the addition of a seed predator. These predictions were tested using a decade-long field experiment with common gardens of plants in the montane genus *Ipomopsis* and adjacent natural populations. Gardens were planted with seeds of two species and their first and second generation hybrids to expand the range of trait variation, and in sites that differed in whether pollination was primarily by hummingbirds or also included hawkmoths. We examined a suite of floral traits including corolla shape, petal color, nectar production, and emission of volatile organic compounds (e.g. alpha-pinene

and indole). Female fitness (seeds) was broken down into fitness during pollination (seeds initiated) and seed predation (proportion of seeds that escaped predation by flies). Correlational selection was detected for some pairs of traits, even in the simplest interaction web. We discuss a variety of mechanisms that can explain adaptive trait combinations in nature.

Trade networks over space and time

S4.3

TOBY KIERS

11:45–12:30

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The arbuscular mycorrhizal symbiosis is characterized by complex underground networks of plants and fungi trading resources. Trade networks allows individuals to exchange commodities they can provide at low cost, for resources that are otherwise impossible, or more difficult, to access. While it has been shown that both fungal and plant individuals are able to preferentially allocate resources to higher quality partners, the trade dynamics governing these underground markets are unknown. My lab develops tools to visualize, track and quantify symbiotic trade in networks over space and time. Our newest research tool utilizes high resolution imaging to track quantum-dot tagged nutrients across complex networks and into host roots. Ultimately, we are interested in predicting how and when networks of trade are favored to evolve.

Session 5

Chair: Carine Emer

What is the boundary of an ecological network?

S5.1

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14:00–14:45

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Species and their interactions are being influenced by global environmental changes, through a number of known mechanisms. The processes through which ecological networks are degraded can mirror those through which they assemble, and understanding network assembly processes and the ways in which these processes can be disrupted may help us to predict future degradation of networks. In particular, network assembly mechanisms such as trait matching may not apply to all species equally, and environmental gradients can alter these mechanisms via changes in species composition. Environmental filtering of species traits, combined with the connection of traits to both interactions and species' functional roles, provides us with a road map for understanding how the environment influences emergent properties of ecosystems. However, assembly and disassembly processes can make network architecture difficult to define, by causing it to vary through time and space. Moreover delineation of the spatial and temporal boundaries of a network can be arbitrary, yet it is necessary for understanding the scale over which environmental changes may influence ecosystems. Again, species' traits can govern their role in connecting together metacommunities and allowing the propagation of disturbances across what ecologists traditionally view as habitat boundaries. Thus, a response-effect-interaction trait framework is needed to capture how the species that win or lose in different environments assemble into networks and meta-networks, and how the architecture of these networks contributes to ecosystem functioning and stability.

Different mechanisms govern ecological strategies of interacting plants and hummingbirds

S5.2

CATHERINE GRAHAM[1], BEN WEINSTEIN[2], BORIS TINOCO[3], HOLGAR BECK[4], JOHN CLARK[5], MATHIEU PERRET[6]

16:00–16:45

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Species interactions, such as a pollinator visiting a given plant species, form the architecture of biodiversity, yet we lack a unifying theory of why and how they vary. Many studies in network ecology identify emergent patterns using measures of network structure. However, this approach may not detect the ecological processes that result in these emergent patterns. We present three case studies that both refine and challenge how we think about plant–animal interactions using Andean hummingbirds and their nectar resources. First, we show that trait-matching influences hummingbird visitation flower patterns regardless of the availability of flowers in the landscape across time, suggesting hummingbird specialization may promote co-occurrence in diverse Andean assemblages. Second, we explore if a plant's ecological strategy is different from that of a hummingbird. We find that plants in the family Gesneriaceae flower concurrently and attract similar hummingbird visitors, indicating that facilitation as important mechanism shaping flower communities in tropical hummingbird visited assemblages. Third, we use flower exclusion experiments to manipulate the hummingbird resource landscape and show dramatic changes in hummingbird abundance and foraging behavior. Combined these case studies highlight that the mechanisms influencing hummingbird and plants in hummingbird–plant interactions may vary across time and space.

Poster Abstracts

P=poster abstract. S=speaker abstract. Bold=presenting author

Poster Abstracts

Poster abstracts are ordered alphabetically by presenting author (underlined).

P1

Diversity of food habits of cleaners and the network structure of cleaning interactions among birds and large mammals

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Cleaning interactions are interactions in which cleaners benefit from the hosts by feeding on parasites, injured tissues or blood. In tropical ecosystems, birds often act as cleaners of large mammals. Here we investigated the drivers shaping the organization of networks formed by cleaning birds and mammals. Specifically, we hypothesize that these interactions are often opportunistic and, as a consequence, we expect diet generalism is associated with the role of bird species in cleaner-host networks. We used a cleaner-host network from Brazilian openlands to explore the relationship between diet generalism and cleaning behavior. We first contrast the diet diversity of cleaner species with their closed related species. For 7 of 8 bird families, cleaners show higher diet diversity than non-cleaning species. We then explored if generalist bird species are the central species of the cleaner-host network. The results show that there is no correlation between the degree of species centrality in the networks and their diet diversity. We suggest that generalism allow opportunist species to engage in cleaning interactions but the importance of a cleaner species is affected by other attributes, such as abundance and behavioral adaptations.

P2 Skull morphological (co)variation determines species role in bats mutualistic networks

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In mutualistic networks, some species are more important than others to network structure, implying that these species may also assume central roles for the ecology and evolutionary dynamics of mutualistic interactions. A fundamental problem to solve is to understand which factors affect the species network role. In this sense, morphology affects the way individuals from different species interact and may shape the centrality of a given species in the network. If so, we should expect that higher intrapopulation variation in combination of traits across individuals would lead to central species that are able to interact with multiple partners. Here we studied the relationship between intrapopulation morphological (co)variation patterns and centrality of bat species in mutualistic networks. We analyzed 10 pollination and 9 seed dispersal networks describing the interactions between bats and plants. Then, we calculated two measures of centrality (closeness and degree) for the bats species. We used as morphological descriptor the skull mean square correlation, which describes the total degree of association among traits using approximately 20 species that occur in these networks. Our results show no correlation between centrality measures and bats skull mean square correlation in pollination networks. We found a negative correlation between skull mean square correlation and species centrality in seed dispersal networks. We hypothesize the central role of some bats in seed dispersal networks is at least partially shaped by the morphological variation within bat species, which in turn allow individuals to interact with disparate set of potential partners.

P3 The aromatic trait from crops to tree plants

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The aroma contributed by 2-acetyl-1-pyrroline (2AP) is an economically important trait in several crops including aromatic rice and soybean. The gene conferring this trait had firstly been identified in rice (*OsBADH2*) by a positional cloning and in soybean (*GmAMADH2*) by a similarity search approach. The lack of function of the gene is reported contributing to the 2AP biosynthesis in these two crops. To expand our knowledge and provide insights into the common role of *BADH2* in plant evolution, more plant species will need to be investigated. In this study, we identified the aromatic gene in other crops, i.e., winter melon, luffa and in tree plants, i.e., coconut and pomelo. Without a complete genome reference, we identified the gene based on the *de novo* assemblies of transcriptomic data. RNA-seq libraries from non-aromatic and aromatic plants were constructed and sequenced using Illumina's HiSeq2500 system. The candidate gene, *AMADH2*, was characterized and compared between non-aromatic and aromatic varieties. Sequence variations identified in the coding regions of *AMADH2* in these plants all suggested the possible role leading to the loss of enzymatic activity of the *AMADH2*. Our results confirmed that plants share the orthologous gene and a similar mechanism governing the aromatic trait.

P4

Local adaption in a wild cabbage (*Brassica incana*) to different biotic and abiotic factors

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The family of Brassicacea is one of the most diverse and abundant in nature, and has an important economical relevance. Besides the different cultivated varieties there are also many wild species that are phylogenetically very close to cultivated varieties of cabbage. One of these wild cabbages is *Brassica incana*, a plant that grows on costal cliffs in the Mediterranean area, particularly in Southern Italy. An interesting characteristic of this plant is that it grows on different soil types, from calcareous (limestone) to volcanic soils (tuff). Naturally, these populations also experience different biotic factors, such as pollinators and herbivores. In our work we investigate the effects of these different factors on various plant traits and local adaptation. We observed trait differences between the populations growing on different soil types, but our results also suggest possible interactions between biotic and abiotic factors. For instance, the nectar amount found in flowers of populations growing on limestone was significantly higher compared to the populations growing on tuff soils, indicating possible interaction between the soil substrate and pollinator community. Further analyses are currently underway and will be presented on the poster.

P5 Genetic correlations between traits influence the results of arms race in antagonistic interactions

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A central problem to evolutionary biology is to understand the contribution of selection and the genetic architecture in shaping evolutionary dynamics. Here we combined a quantitative genetics framework with a coevolutionary model to explore how genetic architecture (genetic correlations) among traits influence coevolutionary dynamics in species pairs. We found that genetic correlations influence coevolution, shaping the rate to which traits respond to selection and influencing the resulting phenotypic patterns. With no correlation between traits the coevolutionary race reaches equilibrium characterized by some level of trait mismatching between parasites and hosts. Including genetic correlation alters this equilibrium, with two possible outcomes: either the equilibrium host–parasite trait mismatching decreases in comparison with the no correlation scenario, benefiting the parasite, or it increases, benefiting the host. The initial multivariate distance between species determines whether the host or parasite is benefited. Our results suggest that genetic correlations are important in antagonistic coevolution. Moreover, because most species are geographically structured, our results suggest that genetic correlations might create a mosaic of outcomes across space, in which there are some populations where the winner of the arms race is the host and populations where the winner is the parasite.

P6 Extinction of a consumer guild constrains the adaptive landscape of an insect herbivore

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Global change is altering the structure of ecological networks; however, we are currently in a poor position to predict how these altered communities will affect the evolutionary potential of remaining populations. Theory on adaptive landscapes provides a framework for predicting how selection constrains phenotypic evolution, but often treats the community context of evolving populations as a “black box”. Here, we integrate ecological networks and adaptive landscapes to examine how changes in food-web structure shape evolutionary constraints. We conducted a field experiment that manipulated whether a guild of larval parasitoids were able to impose selection on an insect herbivore. We then measured herbivore survival as a function of three key phenotypic traits. We found that more traits were under selection when we excluded interactions with larval parasitoids. The adaptive landscape was more neutral in the intact food web because different parasitoid guilds impose different selection pressures, minimizing relative fitness differences among phenotypes. Our results suggest that the loss of trophic interactions can impose greater constraints on phenotypic evolution. This indicates that the simplification of ecological communities may constrain the adaptive potential of remaining populations to future environmental change.

P7

Use of visual and olfactory cues of flowers by insect pollinators

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Understanding how pollinating insects exploit visual and olfactory cues associated with flower traits it is important to elucidate the co-evolutionary dynamic on plant–pollinator interactions. Pollination can induce changes in flower-associated cues, thereby influencing the behaviour of flower visitors. We investigated the main cues exploited by the syrphid fly *Episyrphus balteatus* and the butterfly *Pieris brassicae* when visiting flowers of *Brassica nigra* plants. We studied the pollinator behavioural responses and pollination-induced changes in flower volatile emission. Pollinator preference was investigated by offering visual and olfactory cues simultaneously as well as separately in two-choice bioassays. We assessed whether pollen provides cues used by pollinating insects. The pollinators showed a strong bias for visual cues over olfactory cues. *Pieris brassicae* only perceive pollination-induced changes when visual and olfactory cues are offered simultaneously. Neither pollinator used pollen as a cue for finding flowers, however the syrphid fly can discriminate between old and new flowers when pollen was available. Collectively, our data show that different pollinators exploit different visual and olfactory traits when searching for nectar or pollen of flowers of *B. nigra* plants.

P8

Quantifying importance of pollinators as selective agents on flower color in a subspecies hybrid zone

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Quantifying natural selection is commonplace, but identifying the selective agents is a major challenge in evolutionary ecology. Hybrid zones provide an opportunity to identify traits experiencing selection in the face of gene flow. Several lines of evidence indicate strong selection on flower color in a hybrid zone of two *Antirrhinum majus* subspecies in the Spanish Pyrenees, but the selective agents are unknown. Divergent flower color of the subspecies is determined by three major genes, two of which are tightly linked. Pollinators (bumblebees) do not differ across the hybrid zone. We tested the hypothesis that pollinator foraging patterns contribute to maintaining the subspecies boundary through either frequency-dependent visitation or selection against hybrids. Over three flowering seasons, we assayed pollinator visitation on hundreds of plants by tagging flowers with plastic discs that reliably fall when the flower is visited. We tested for frequency-dependent visitation using data on flower color of conspecifics neighboring the focal plants. We also tested whether hybrid phenotypes experience lower visitation than parental phenotypes. Ultimately, we can ask whether pollination foraging patterns are likely contributing to a significant fraction of natural selection on flower color in the hybrid zone.

P9 Endosymbiotic bacteria of plant-associated fungi: friends or foes?

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Many bacteria form symbiotic associations with plant-associated fungi. The effects of these symbionts on host fitness usually depends on symbiont or host genotypes and environmental conditions. However, bacterial endosymbionts, i.e. those living within fungal cells, may positively regulate host performance as their survival is heavily dependent on host fitness. A meta-analysis of published results was conducted to evaluate this hypothesis. In addition, the biology of bacterial endosymbionts of fungi was reviewed, with the focus on functional aspects of bacterial–fungal symbiosis. Our analysis supports the hypothesis that endosymbiotic bacteria of fungi are beneficial symbionts. Ecological scenarios, where the presence of beneficial bacterial endosymbionts of fungi could be compromised, are also discussed.

P10 Exploring the interaction functional space across an elevation gradient.

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Functional Diversity (FD) provides insight into the functionality of process. Currently, FD analysis is based on the species traits. However, the functionality of a given process depends on the combined traits of all interacting species, even if they belong to different taxonomic group. We present a framework to analyze the Interaction Functional Space (IFS) and explore the link between networks assembles with process functionality. We analyzed the bird pollination process along an elevation gradient in the Andes using Weinstein et.al's(2017) dataset. The communities showed species and interactions turnover. High turnover suggests a rearrangement of interactions. To construct the IFS we designated each interaction as the entity under analysis and built the functional space based on the process relevant traits. We correlated elevation with IFS amplitude. We observed a reduction of IFS with elevation, suggesting a filter in the process functionality at higher elevations. We measured how the available trait space at each site (all possible interactions trait space) is filled by the trait space of the observed interactions. At mid-elevations, the IFS are more filled than at both gradient extremes, suggesting possibility for new combinations. Our approach allows analyzing the interaction networks beyond topology and link networks with processes.

P11 Indirect effects on plant fitness mediated by pollinators and propagated within networks

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Studies of indirect effects within ecological networks remain most restricted to antagonisms, although pollinator-mediated competition/facilitation are widespread in plant communities. Incorporating fitness estimates and plant traits into networks is necessary to identify the direction of pollinator-mediated indirect effects. We estimated the extent to which a plant species affects (‘influencing degree’) and is affected (‘influenced degree’) through shared pollinators within a pollination network from a dune community. We related such “indirect roles” to fitness (seeds/flower) and floral traits for 23 species and assessed their motif positions within networks to identify indirect pathways. We expected positive effects for attractive species while negative to less attractive ones, suggesting competition. Plants with higher influencing degree showed higher fitness whereas those with higher influenced degree were less fit. Influencing plants likely benefited from concentrating pollinator visitation and usurping them from influenced species, consistent with competition. The most influencing plants showed larger flowers, longer flowering and were generalists within motifs, while influenced species showed few and zygomorphic flowers, occupying peripheral positions or being embedded in well-connected motifs. Thus, indirect effects propagated from attractive and generalized to less attractive and specialized species. Overall, results showed how pollinator-mediated indirect effects on fitness translate into competition processes within communities.

P12 The evolution of competitive ability in phytoplankton

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Competition for limiting resources is one of the most fundamental ecological interactions, and has long been considered a key driver of biodiversity patterns. Species' minimum resource requirements, their R*, are key traits that link individual physiological demands to the outcome of competition. Until recently, evolution was seen as a slow, varying constraint on species traits, rather than a dynamic feedback mediating shifts in abundance and the outcome of species interactions. A key question remains unanswered -- to what extent are species’ competitive traits able to evolve over ecological time scales? To address this knowledge gap, we tested the hypothesis that competitive traits of phytoplankton are able to adapt in response to selection under resource limitation. Alternatively, there may be limits to adaptive trait evolution; for example if resource requirements for different essential resources (i.e. nitrogen or phosphorus) are genetically or physiologically correlated. To identify potential constraints on evolved competitive trait variation, we grew five populations of *Chlamydomonas reinhardtii* for ~ 300 generations under seven different environmental conditions. We quantified the minimum resource requirements of the ancestral and descendant populations and the potential for rapid adaptation to alter the outcome of competition.

P13

Trait convergence and diversity in species-rich interactions: habitat use and heterogeneity affect coevolution of mimetic species

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Understanding the evolutionary process generating and maintaining trait patterns in species-rich communities is a central problem to evolutionary ecology. One example of trait pattern at community level is the coexistence of distinct groups of unpalatable species with different warning signals, the mimicry rings. The coexistence of different mimicry rings seems paradoxical because selection among unpalatable species should favor convergence to a single warning pattern. Habitat heterogeneity associated with the use of distinct habitats may promote mimicry ring diversity. We combined mathematical modeling and numerical simulations to explore how habitat heterogeneity and habitat use by mimetic species influence the formation of mimicry rings. Our results suggest that mimicry rings may evolve rapidly due to distinct, habitat-related selection pressures or by reciprocal selection imposed by mimetic species that share similar habitats. We show that when habitat and mimicry are strong sources of selection, evolution of multiple rings takes longer to emerge due to conflicting selective pressures. Moreover, habitat generalist species decrease the distinctiveness of mimicry rings and even a few generalists can prevent the evolution of multiple mimicry rings. These results may explain why co-occurring mimicry rings only evolve in groups of animals that tend towards habitat specialism, such as butterflies.

P14 Untangling the seasonal dynamics of plant–pollinator communities

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A major goal in ecology is to understand the way communities vary over time. Unfortunately, we are still searching for the best approach to untangle the complexity of changes in populations and the interactions between them. Often, ecologists study the dynamics of diverse communities via sophisticated mathematical models. An alternative approach that has yet to be fully explored is to exhaustively compare the structure of these communities—i.e. their network of interactions—along ecological gradients or within time series. By comparing networks within a changing environment, one can understand how the roles of different species vary and change under different pressures. Here, we apply a novel network-comparison technique—network alignment—as a way to study ecological communities and shed light on their underlying dynamics. We compared the structure of plant–pollinator networks over time, and in doing so untangled the mechanisms by which species' positions vary within these networks. Specifically, we identified groups of roles that are consistently preserved over time, and showcased how species rapidly switch positions across such groups. We expect that these results will provide deeper understanding of the dynamics of plant–pollinator networks as well as potentially inform predictions regarding the effects of perturbations and environmental variability.

P15 Variation in herbivore pressure and defence investment among plant populations at different elevations

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Elevational gradients can offer important insights into how plants adapt to rapidly changing environments. However, the relative roles of abiotic and biotic selective factors in shaping variation in relevant ecological traits along elevation gradients is still not well understood. To this end, we combined field surveys and greenhouse experiments to screen multiple populations of a perennial alpine plant, *Arabis alpina* (Brassicaceae), from low, intermediate and high elevations for genetic divergence in traits related to defence against herbivores. Rates of herbivore damage declined with increasing elevation in the field, and plants from low elevations were generally less palatable for specialist herbivores than those from higher elevations. Elevational clines were also observed in several glucosinolate defence compounds, and leaf herbivory more strongly induced total glucosinolates in high-elevation plants than those from low elevations. However, populations from similar elevations also diverged in many of these defence-related traits, which suggests that the observed elevational trends in defence traits are being shaped by multiple ecological factors. Ongoing work is measuring constitutive and induced chemical defences across a broader range of populations from different elevations in order to identify those abiotic factors and biotic interactions driving variation in defence investment.

P16 Macroevolutionary imprints on the assembly of frugivory networks

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Biological interactions are a key aspect of ecological communities. Current interaction network structures are snapshots of dynamic processes of community assembly. Thus, assessing the temporal dynamics of ecological networks or the deep time mechanisms related to the assembly of those networks are key to better understand biodiversity changes in broader time scales. However, knowledge on the macroevolutionary patterns behind the assembly of these networks is still scarce. Here we show that more central species in frugivory networks belong to lineages with higher macroevolutionary stability.

More specifically, we found a non-linear negative relationship between centrality measures and two metrics of macroevolutionary stability that is modulated by precipitation seasonality. For networks of temperate latitudes (contrasted to tropical ones) this relationship is particularly stronger. Our results demonstrate how network structure may be linked to macroevolutionary patterns resulting on more stable lineages playing key roles in seed dispersal. We also suggest that plant phenology may be an important factor shaping these relations. To our knowledge this study is the first to show a macroevolutionary imprints on the assembly of frugivory networks.

P17

Detection of fungal enzymes and plant enzymes associated with oil palm tree, infected by *Ganoderma boninense*

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Ganoderma boninense, a causal pathogen of basal stem rot disease, lead to a major loss of oil palm in leading palm oil producing countries in Southeast Asia. The fungus degrade host cell walls by producing lignocellulosic enzymes before mycelial invasion and finally fungal fruiting bodies are formed. In this study, *Ganoderma*-infected oil palm trees from 19 orchards in Southern Thailand were selected. All enzyme activity measurements were done by spectrophotometric method. The lignocellulosic enzymes including, lignin peroxidase (LiP), Manganese peroxidase (MnP), laccase, cellulase and xylanase were detected from rhizosphere soil suspension in phosphate buffer pH 7.0. The enzyme activities (U/g soil) were LiP (0.004 – 0.104), MnP (0 – 0.005), laccase (0.0003 – 0.024), cellulase (0 – 0.397) and xylanase (0.288 – 0.569). While, the defense responses of oil palm were induced by the fungal mycelia. Chitinase and β-1,3-glucanase, the main pathogenesis-related (PR) proteins, were found from root extracts of 0.334 – 0.985 and 0.043 – 0.598 U/g root, respectively. Moreover, the plant defenses-related enzyme activities (U/g root) including, polyphenol oxidase (0.093 – 0.492), peroxidase (0.005 – 0.110) and phenylalanine ammonia lyase (0 – 0.007) were also found from the root of oil palm, when the trees were attacked by *Ganoderma*.

P18

Similar functional roles despite high species and interaction turnover in seed-dispersal networks

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We studied plant–bird seed-dispersal networks across South America and tested whether changes in species composition lead to corresponding changes in the composition of species’ functional roles, using two approaches. First, we compared changes in species composition with changes in the composition of species interactions, species’ functional traits, and species’ functional roles. The networks showed an almost complete turnover in species composition and interactions but differed less in their composition of functional traits and functional roles. Second, we identified bird species with similar functional roles across all networks by combining all networks into a metanetwork and then sorting bird species into modules based on the similarity in the plant species they consumed, (i) only considering the species ID of the plants and (ii) also considering the functional traits of the plants. Modularity analysis informed by species ID could not detect species with similar functional roles in the different networks, whereas the analysis informed by species traits identified groups of bird species with similar functional roles across all networks. Comparison of species communities and interaction networks informed by species traits provide more insight into the similarity of species communities and the functional roles of species than comparisons based only on species identities.

P19 Plant species that can disperse further tend to interact with a greater number of mycorrhizal fungi

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Dispersal is a crucial opportunity in the plant life cycle to enhance fitness, allowing it to escape local antagonists and density-dependent competition. As plant propagules arrive to new habitats, recruitment may be limited by the availability of compatible symbiotic partners. We hypothesized that plant species with longer dispersal distances would interact with a greater number of mycorrhizal symbionts. We collated 30 plant–mycorrhizal networks from published studies and calculated normalized degree for each plant species. We then collated a range plant traits related to dispersal. For seed plants, we predicted species' maximum dispersal distances based on these traits using the dispeRsal function in R. We used phylogenetically-informed analyses based on MCMCglmm to investigate normalized degree as a function of plant traits and dispersal distances. Preliminary results indicate significantly higher normalised degree among fruit-dispersed than seed- or spore-dispersed species in closed-canopy forests, whereas seed-dispersed species that rely on wind achieved highest normalised degree in early successional sites. Final analyses will be presented at the Symposium, should they concur, we could conclude that better dispersers interact with more mycorrhizal partners; which may be due either to their wider fundamental niches, or because they arrive first, thus having more time to acquire interaction partners.

P20 Are plant–pollinator networks robust tophenological shifts?

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Pollinators play an important role in terrestrial ecosystems by providing key ecosystem functions and services to wild plants and crops, respectively. The sustainable provision of such ecosystem functions and services requires diverse pollinator communities, with both high functional complementarity and redundancy. Despite the fact that climate warming has been linked to pollinators phenological shifts, how this process could affect pollinator assemblages remains unexplored. By using dynamic models and real data to parametrize it, we investigate the plant–pollinator networks robustness to plants and pollinators phenological shifts. Preliminary results show that the robustness of pollination networks highly depends on the competition pressures and on responses heterogeneity more than the averaged mismatch between plant and pollinator phenological shifts. This work is in progress and we are currently taking in account the fact that these phenological shifts are not randomly distributed among species but depend on evolutionary history and seasonal earliness. Such patterns could lead to change a lot taxonomic and functional diversity distribution along the season. If the temporal organization of plant- pollinator network is often neglected, it seems that networks at the beginning of the season and networks at the end are functionally different, and that play a big role in species persistence.

P21

Emission rates of species-specific volatiles change across communities of *Clarkia* species: Evidence for character displacement in floral scent

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One evolutionary outcome of pollinator sharing among co-occurring plants is character displacement, where the traits of one or more species differ in sympatry versus allopatry. Although floral scent can mediate pollinator attraction and constancy, previous studies have neglected the potential for character displacement in floral scent. We conducted a greenhouse common garden experiment to investigate whether the emission rates of floral volatiles varied in two species of *Clarkia* (Onagraceae) across communities that contain one, two, or four *Clarkia* species. Floral volatile samples were collected using a dynamic headspace method and analyzed using GC-MS. Species and community types were separated by the first two axes of a constrained correspondence analysis, which explained 29 percent of the total variation in floral scent. Of the 23 compounds that were significantly correlated with these axes, nine showed patterns consistent with character displacement. Two compounds produced primarily by *C. unguiculata* and two compounds produced primarily by *C. cylindrica* were emitted in higher amounts in sympatry. Emissions of five additional compounds (primarily monoterpenes emitted by *C. unguiculata*) were lower in communities with four *Clarkia* species. Taken together, these results suggest that changes in the emission of species-specific volatiles may result from character displacement in sympatric communities.

P22

Alien plant and pollinator species configure the seasonal dynamics of mutualistic networks

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Alien species can drastically disrupt ecological processes such as those involving plant–pollinator interactions, performing central roles that may affect the structure of native pollination networks. However, most studies to date have focused on a single trophic level of alien species, evaluating either the impacts of an alien pollinator or an alien plant species, and have neglected their effects on the seasonal dynamics of mutualistic networks. Here we investigated how alien plant and pollinator species structure consecutive temporal networks, and how these species affect the beta-diversity of interactions across a summer season. Our study system is located in the South Island of New Zealand, where 68% of the sampled plant species and 14% of the pollinator species that interact with them are alien. Alien pollinator species exhibited higher interaction degree, specialization, and strength than their native counterparts, while alien plant species showed the opposite pattern. We found that invader complexes (in which alien species interact significantly more with each other than with native species) were established across the season and interactions involving alien plant species were the main connectors of the temporal networks. Both alien plant and pollinator species increased total interaction turnover through the summer season by promoting interaction rewiring in the case of alien plants, and by increasing species turnover in the case of alien pollinators. Combined, the effects of invaders may affect the persistence of interactions performed exclusively by native species and suggest a state shift towards alien-dominated communities, with uncertain consequences for ecosystem functioning.

P23 Reproductive isolation in a beetle–plant pollination network

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In pollination networks, where a pool of pollinators is shared by closely related and co-flowering plant species, reproductive barriers are crucial to reduce pollinator competition and pollen loss due to interspecific pollen flow. Interspecific differences in floral traits such as scent, timing of flowering and functional morphology probably shape pollinator specificity in such networks. We investigated a Neotropical pollination network with more than 20 co-flowering Araceae and six nocturnal scarab beetle pollinators. These beetles spend ca. 24 hours in an inflorescence chamber and must leave before it closes. Our multidisciplinary approach included pollinator and flowering cycle observations, scent analyses, thermogenic measurements and behavioral assays. While most of our study plants emit similar scent bouquets containing widespread compounds, the scents of a few species comprise unique compounds that attract two specific beetle species not found on other plants. The other four beetle species are generalists that visit most study plants including those with specific compounds. Despite the beetles being guided by olfactory cues, differences in floral scent composition alone are insufficient for reproductive isolation. Our results show that temporal differences in the synchronization between scent release, heat production and inflorescence closing time likely drive reproductive isolation of the studied 'nocturnal' network.

P24

Decoupling functional and phylogenetic diversity and their contribution to plant community assembly using floral, clonal and leaf traits in a wide range of Central European habitat types

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Ecological differences among species – and communities – can be determined by evaluating functional and phylogenetic differences. However, these two measures are not independent from each other, but rather complementary. In this study our aim was to evaluate the effect of phylogeny on functional trait variability in plant assemblages by testing how community assembly patterns are expressed by functional and phylogenetic diversities across different Central European habitat types. We have used a recently proposed method (de Bello et al. 2017 *Methods in Ecology and Evolution*), which enables us to statistically decouple functional and phylogenetic dissimilarities. This approach is suitable for the detection and "magnification" of functional differences between evolutionary close species. We used different groups of functional traits (leaf, floral and reproductive, clonal and bud bank) compiled from databases (LEDA, Biolflor, CloPla, respectively), as well as vegetation relevées from ca. 30 habitat types across the Czech Republic. Our results showed differences between non-decoupled and decoupled functional diversity in the different habitat types, which indicates different degrees of overdispersion in the functional traits within and between closely related species. These relationships were also affected by environmental gardients, suggesting that benign vs. harsh environments have different phylogenetic constraints on the functional traits of plant species.

P25

Evolutionary insights on plants' response to arbuscular mycorrhizal fungi: the role of phylogenetic relatedness and climatic niche

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The symbiosis between plants and arbuscular mycorrhizal fungi (AMF) alleviates plants stress caused by harsh biotic or abiotic environmental condition, balancing the trade-off between growth and defence investments and facilitating the rapid spread and diversification of land plants across a wide range of habitats. The plant genus *Plantago* has a worldwide distribution, and species occurrence span across greatly contrasting climatic regions. Here we grew 30 species of *Plantago* plants with or without an artificial AMF community. We measured a whole set of plant traits related to growth and defence to disentangle the importance of phylogenetic conservatorism or climate-driven-adaptation in plant response to AMF. Overall, *Plantago* species functional niche was affected by AMF in a species-specific fashion, but dependent on the phylogenetic relatedness and climatic niche for specific traits. Less defended species displayed stronger positive response when colonized by AMF suggesting a compensatory effect of AMF for species that were more vulnerable to herbivores, and the intensity of the response was driven by the phylogenetic relationship. Ours preliminary results sheds light on the evolution of plant-AMF symbiosis revealing a phylogenetic conservatorism component in dictating plant response to AMF with a minor influence of the climatic niche.

P26

The molecular mechanisms of new character origination: A study on the elaboration of *Nigella* petals

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Understanding how and why new characters originated is a key to understanding the nature of evolution. Petals of *Nigella* (Ranunculaceae) species, due to successive origination of quite a few new characters, are very complex and elaborate in shape, structure and color patterning, and can be an excellent system for studying new character origination. By conducting high-resolution spatiotemporal comparative transcriptomic analyses on five representative species, we found that the overall expression patterns of most genes are similar among different species at early developmental stages but diverged significantly at later stages, which is consistent with the increasingly larger morphological variations during petal development. We also found that co-expression modules among the five species are largely conserved. Since the unconserved modules or genes are likely to be correlated with the origination of new characters, we then focused on identification of genes that have distinct expression patterns. Candidate genes for stalk elongation (*ARF3*), trichomes development (*GL1*, *GL2*, *GL3* and *TT8*) and pseudonectary formation (*SHN1*) were identified and the expression of genes related to trichomes development were confirmed. Our results not only provide new insights into the molecular mechanisms of elaborate petals, but also highlight the molecular basis of evolutionary innovation and the primary cause of biodiversity formation.

P27

How are complex networks structured in tropical forests?

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The structural description of mutualistic interactions disentangle how plants and animals are organized and allows inferences to be made about the robustness of the interactions, heterogeneity in specificity degrees and ultimately the consequences of functional lost for ecosystem functioning. Ecological and evolutionary outcomes are the product of a complex of interacting processes, in which each frugivorous group is only a small part. A persisting challenge in the analysis of mega-diversified mutualistic networks is the lack of studies encompassing all major higher taxa of frugivores coexisting in conserved habitats, the major goal of this study. Here we identified the role played by each group in shaping ecosystem dynamics using an integrative approach that considers each taxon as an important part of a complex system, rather than sole actors. We described how seed dispersal interactions are structured in two hyper-diverse pristine tropical communities within the largest remnant of the Atlantic forest in Brazil, a tropical biodiversity hotspot, using a network approach. We present data for about 135 frugivorous species in 30 families belonging to the most important frugivore groups in the tropics - ungulates, primates, birds, bats and small mammals - dispersing seeds of more than 310 species in 73 families of plants.

FAPESP *#2018/06634-5*

P28 Interaction flexibility predicts pollinator population dynamics

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Global change alters communities and may disrupt ecological interactions, resulting in the loss of ecosystem services. As communities respond to global changes, species may either go extinct or form novel interactions. Due to the lack of long-term interaction datasets, it is still unclear how, and if, species are flexible in their interaction patterns. Using the longest contemporary species-level temporal dataset on mutualistic networks, we apply a novel network approach to explore how species traits affect interaction flexibility at different network scales. We introduce three measures of interaction flexibility, explore which traits enable species to be flexible, and show how interaction flexibility predicts species occupancy in the landscape. Abundance, specialization, and phenological breadth affected interaction flexibility at different scales, suggesting that different mechanisms may be acting at different network scales. We provide the first empirical evidence that interaction flexibility increases site occupancy across a highly modified landscape. Interaction flexibility, therefore, is one potential mechanism for communities to maintain function given changes in community composition. By demonstrating the relationship between interaction flexibility and species' persistence in the landscape our results may help anticipate species' vulnerability to extinction, and the subsequent loss of interactions and ecosystem services.

P29 From structure to function in interaction networks: well-connected frugivores are better seed dispersers

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Interaction networks are frequently heterogeneous, modular and nested. It is well known that these patterns emerge from differences between species in their contributions to network organization. However, we are still far from understanding whether topologically relevant species are the most important in ecological or evolutionary terms. We answer this question by focusing on the local interaction networks of frugivorous vertebrates and fleshy-fruited plants in two Colombian tropical dry forests. We estimated frugivore contribution to network structure by integrating measurements of degree, contribution to modularity and contribution to nestedness. We represented frugivore functionality as seed disperser effectiveness, an integrative measure of the quantitative and qualitative effects of animals on plant recruitment. Effectiveness was estimated from frugivore abundance together with morphological (e.g. body size) and behavioural (e.g. seed handling, habitat use) traits assumed to directly impact seed fate. We found that contribution to network structure and seed disperser effectiveness were positively correlated across species in both forests, indicating that topologically relevant frugivores were the most effective seed dispersers. The reason of this correlation is that the occurrence of frugivore–plant interactions depends on the set of animal features (abundance and matching traits) which later condition effectiveness of seed dispersal.

P30 Herbivore-mediated negative frequency-dependent selection underlies a trichome dimorphism in nature

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Negative frequency-dependent selection (NFDS) governs a diverse array of traits ranging from human handedness to plant defenses. NFDS has been confirmed through modelling, experimental approaches, and genetic analyses. We investigate if NFDS is acting upon natural populations by analyzing field data from over 30 populations of dimorphic *Datura wrightii*. These plants either possess glandular or non-glandular trichomes, making the leaves sticky or velvety respectively, and the ratio of these morphs varies substantially between populations. We found that the change in morph frequency over a 20-year period was negatively correlated with starting frequency and that neither morph became fixed in any population over this period – suggesting that NFDS acted to maintain the observed dimorphism. Furthermore, we found that both current morph frequencies and morph-frequency changes over time were significantly correlated with the damage inflicted by two herbivores: *Lema daturaphila* and *Tupiochoris notatus*. The latter is a specialist on the sticky morph and damage by this herbivore was greatest when the sticky morph was relatively common. The reverse was true for *L. daturaphila*, such that damage increased with the frequency of the velvety morph. These findings suggest that these herbivores may mediate NFDS on the observed trichome dimorphism.

P31

High fungal overlap between mutualistic and antagonistic interactions in arbuscular mycorrhizal networks

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In the arbuscular mycorrhizal (AM) symbiosis, plants generally supply carbon to their associated Glomeromycotina fungi, which in turn provide the plants with mineral nutrients and water from the soil. A plant typically associates simultaneously with multiple AM fungi, and each AM fungus often associates with multiple plants, creating complex underground networks. However, some AM interactions are antagonistic: achlorophyllous mycoheterotrophic plants exploit AM fungi for nutrients and carbon. Yet, little is known about the fungal preferences of antagonistic plants in relation to the mutualists. Using DNA metabarcoding, we reconstructed an AM network from a tropical rainforest in French Guiana with a total of 33 plants, of which five mycoheterotrophs, including 693 mutualistic, 239 antagonistic interactions and 89 shared fungi. To test whether antagonistic plants have similar fungal preferences than mutualistic plants, we searched for motifs indicative of simultaneous links of mutualistic and antagonistic plants to each fungus individually. We found that mutualistic and antagonistic plants are simultaneously linked to the same fungi more often than expected by chance. This demonstrates that mycoheterotrophic plants preferentially exploit AM fungi that are mutualistically well-connected to other plants. We hypothesize that these fungi provide the most reliable source of nutrients to sustain antagonistic interactions.

P32

Bat-flower visiting network in the Pantanal wetland, Brazil: does pollen essential amino acids drive the diversity of plant-visiting bats

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Pollen-feeding behavior by phytophagous bats has intrigued researchers from decades. The goal of this study is to describe the role of chiropterophilous plant species on shaping the structure of bat-pollination networks in the Pantanal Wetland, Brazil. Because phytophagous bats supplement their diet by feeding on amino acid-rich resources, such as pollen grains and given that pollen grains from different plant species differ in their amino acids composition and concentration, we hypothesize that phytophagous bat species would prefer to visit plant species which pollen grains show the most rewarding composition of essential amino acids. Therefore, amino acid-rich plant species would be the main components of the structure of bat-pollination networks. Our results showed significant correlation between amino acid-rich plant species and the diversity of plant-visiting bats; pollen from *Bauhinia ungulata* shows the higher proportions and composition of essential amino acids, notably Tryptophan. Thus, *B. ungulata* pollen grains can be considered as a key amino acid resources for the maintenance of *plant-visiting* assemblages *in the Pantanal Wetland.* Flower-visiting by insectivorous/carnivorous neotropical bats can be more common than expected, especially in disturbed environments or regions with a prolonged dry season as in the Pantanal wetland, where there is an irregular supply of preys.

P33

Polyploidy and floral evolution in a geographic mosaic of specialised and generalised pollinators

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Floral traits are amazingly diverse also within species. Mutations are one of the processes ultimately causing diversification. Whole-genome duplications (polyploidization) are the most dramatic form of mutation. Polyploidy is widespread in flowering plants. However, little is known how polyploidy affects diversification of complex floral traits such as floral scent as well as pollinator communities. Here, we study the origin of floral scent diversity through polyploidization in the woodland star (*Lithophragma bolanderi*, Saxifragaceae). This species exhibits an incomparably high variation in floral traits and is composed of multiple cytotypes. It is pollinated by the highly specialised seed parasite *Greya politella* but also by generalised pollinators. We collected seeds from natural populations throughout the distribution range of *L. bolanderi*, grew them in a greenhouse common garden environment and measured floral scent, floral morphological traits, and genome size. We found three major ploidy types: diploids, tetraploids, and hexaploids. We present data on the covariation of complex floral traits with the geographical distribution of ploidy types and how this is linked to the geographic mosaic of specialised and generalised pollinators found in *L. bolanderi*. These results provide insights into the ultimate cause of the diversification of floral traits within species.

P34

Indirect effects and the coevolutionary dynamics in mutualistic networks

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A major challenge in evolutionary biology is to understand how ecological interactions shape coevolution in species-rich systems that often form ecological networks. We investigate the problem of coevolution in species-rich networks by integrating empirical data on mutualistic networks, coevolutionary models, and tools derived from network science. In mutualistic networks, the consequences of selection imposed by mutualistic partners may cascade across the network, leading to indirect effects. These indirect effects reorganize the adaptive landscape, favoring slow but continuous trait evolution. Moreover, our analyses indicate that indirect effects among non-interacting species are likely to drive much of the trait evolution of mutualistic networks whenever mutualisms are a significant source of selection. We then generalize our approach to explore coevolution in networks across multiple sites. Our results show that indirect effects may interact with patterns of gene flow across metacommunities, leading to the emergence of trait patterns at the level of the landscape. Finally, we generalize our approach to describe of coevolution of multiple traits in mutualistic networks. Our results suggest that indirect effects may interact with the genetic architecture of traits, changing the pace of coevolution and shaping spatial variation in the outcomes of coevolutionary process. To sum up, we hypothesize that network structure may shape coevolution in species-rich mutualisms, driving the evolution of complex phenotypes within and across ecological communities.

P35 Phylogenetic constraints or convergent adaptation? Leaf thermal tolerance of native and exotic Zingiberales in a tropical lowland forest

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Two consequences of global warming in the next century are a reduction of photosynthetic rates and an associated increase in plant mortality. Using native and exotic Zingiberales in a tropical rain forest as our study system, we addressed the following questions: is thermal tolerance of Zingiberales associated with their habitat (primary, secondary forests or old pastures)?, geographic origin (native or exotic species)? or is photosynthetic thermal tolerance constrained by their evolutionary history? Using chlorophyll fluorescence, we determined photosynthetic thermal tolerance in 32 native and 7 exotic Zingiberales species in a tropical rain forest in Costa Rica, Central America.

Using a molecular phylogeny, we evaluated phylogenetic clustering and overdispersion of thermal tolerance species from secondary forests and open areas tolerate higher temperatures than species in old growth forests (F= 1.49, DF = 2, *P*=0.24). Exotic species are more tolerant to high temperatures than native species (F=0.12, DF= 1, *P*=0.73). Plant families differ in their tolerances to high temperatures (F= 6.14, DF= 5, *P*= 0). However, thermal tolerance of closely related species does not deviate from thermal tolerances expected at random (λ= 0.22). It is possible that plant species typical of warmer habitats, as well as exotic species are preadapted to future temperatures.

P36 Leaf lobation acts as a deterrent against a leaf-processing herbivore

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Plant leaves are diverse in shape, but their roles in nature are largely unknown. Here, we have explored whether leaf shape deters leaf-processing by an herbivorous weevil. Plants in the genus *Isodon* (Lamiaceae) host a specialized leaf-rolling weevil *Apoderus praecellens* that processes a whole leaf into a leaf roll to serve as food and shelter for larvae in Japan. Because leaf processing imposes sequential complex behaviors on females, we hypothesized that the unusually lobed leaves of *I. umbrosus* var. *hakusanensis* may serve as an inhibition against them from processing leaves. Under both natural and laboratory conditions, females preferred *I. trichocarpus*, a close relative with non-lobed leaves, over *I. umbrosus*, despite larvae developing equally well on both hosts. Modifying *I. trichocarpus* leaves to mimic the shape of lobed *I. umbrosus* leaves also discouraged leaf rolling. Video recording showed that leaf processing often terminated before the leaves damaged because weevils failed to properly inspect on lobed *I. umbrosus*. These results demonstrate that leaf shape mechanically deters plant use by *A. praecellens*. Leaf shape may be a hidden factor that affects the interactions between plants and leaf-processing herbivores.

P37 Predation risk influences food-web structure by constraining species diet choice

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The foraging behaviour of consumers determines their diet, and therefore also the emergent food-web structure. Optimal foraging theory (OFT) has previously been applied to predict food-web structure through the consumer-centric consideration of diet choice. However, the resource-centric viewpoint, where species must adjust their behaviour based on reducing the risk of being found by their predators, has not been considered. We develop a mathematical model that merges metabolic theory with OFT to incorporate the effect of predation risk on diet choice to assemble food webs. This “predation-risk-compromise” (PR) model better predicts the nestedness and modularity of empirical food webs relative to the classical optimal foraging model. Specifically, compared to optimal foraging alone, the PR diet-choice mechanism leads to more-nested but less-modular webs by broadening the diet of consumers at intermediate trophic levels. We conclude that predation risk likely imposes a significant constraint on food- web structure in the real world, and needs to be considered in future work.

P38

Strawberry functional trait variation: linking above and below ground species interactions

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Herbivores, pollinators, and mycorrhizae interact to shape plant fitness via direct and indirect effects on plant physiology, chemistry, and development. Floral scent plays a key role in pollinator attraction and can be affected by herbivores and mycorrhizae. Little is known, however, about mechanisms underlying chemically-mediated effects on above and belowground species interaction networks. Our research aims to examines the influence of herbivory and arbuscular mycorrhizal fungi on functional traits of wild and cultivated strawberries (*Fragaria virginiana* and *F. x ananassa*) in a field study. We hypothesize that herbivory will negatively influence plant physiology, growth, and floral volatile emissions, thus reducing pollinator attraction and strawberry productivity. We predict, however, that mycorrhizal associations will modulate these effects. Results to date demonstrate that greater flower number positively influences pollinator visitation and total strawberry productivity. Flower number, however, is negatively associated with flower and fruit size. Preliminary data show that plant physiological response to herbivory depends on genotype. For both photosynthesis and stomatal conductance, we found a significant herbivory x cultivar interaction effect over three days post-defoliation. This project is on-going and we anticipate future results will provide further insight into ways biotic interactions can shape plant functional traits.

P39

Tropical herbivore diet tracks host-plant phylogeny instead of chemical defences across guilds

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Herbivore guilds acquire resources in varying ways. Therefore, different guilds are expected to have different specialisation when on the same host. We use a unique plant–herbivore interaction dataset to address the following: Do herbivores specialize in phylogenetically restricted or chemically similar host ranges? How do phylogenetic and chemical specialisation vary for guilds sharing host species? Is the specialization of faunas from different plants evolutionarily conserved? Is this congruent for phylogenetic and chemical specialization? Interactions were recorded for 1083 herbivore species from 10 guilds and 122 plant species in Papua New-Guinea. A phylogeny and a profile for phenolic compounds were constructed for all plants. There were differences among guilds in the correlation between chemical and phylogenetic specialization. Specialization of faunas from different plant species was very different across the plant phylogeny when phylogenetic or chemical specialization was considered. While phylogenetic specialization was very conserved and negatively correlated with the evolutionary distinctness of plants, chemical specialization had the opposite pattern. This is caused mainly by herbivores being restricted to plant lineages, even when plant clades show a very large variability in chemical compounds. This suggests herbivores track other traits besides defenses for plant selection and many of these traits are phylogenetically conserved.

P40 Apple Genetic Resources Evaluation based on Phenotypic Traits in Republic of Korea

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Since most apple breeding is based on selection from progenies produced by crossing parents, to select those with desirable traits for breeding is very important. The phenotypic traits of 105 apple genetic resources were investigated more than 3 years to evaluate the availability for breeding programs. Eight morphological (e.g. leaf blade, fruit shape, fruit skin color) and phenological characteristics (e.g. blooming and ripening date) were investigated. Fruit quality-related traits (e.g. fruit size, soluble solids content, fruit firmness and titratable acidity) were also evaluated. The majority of the fruits had conic (48%) and obloid (37%) shapes. Most of varieties showed a yellow green ground color (78%) and blushed by a red (54%) in fruit skin. Full blooming occurred between April 10 and May 16. Fruit ripening time showed from July 16 of 'Hunter Melba' to October 31 of 'Kyoko' spanning 104 days. The average fruit weight, firmness, soluble solids content and titratable acidity were 233g, 3.11kg/8mmø, 13.36^{o}Brix, and 0.67% respectively. Regarding statistical correlation analysis among the characteristics, the most significant correlation coefficients were for ripening time and fruit size, soluble solids content, and titratable acidity. This information about apple genetic resources will be useful for future apple breeding programs.

P41 Comparison of RNA-Seq in transcriptome profiling of peach (*Prunus persica*) cultivars

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In order to compare transcription profiles of peach cultivars that are differentially flesh color expressed, three cDNA libraries were constructed. Differences of gene expression red-, yellow- and white-fleshed peach cultivar were investigated by next-generation sequencing (NGS). Expressed sequence tags (ESTs) of clones from the red-, yellow- and white-fleshed peach cultivars were selected for nucleotide sequence determination and homology searches. The levels of transcripts coding for proteins involved in pathogenesis related proteins, temperature stress, protein degradation, sorbitol metabolism were significantly higher in white-fleshed peach cultivar than in red- and yellow-fleshed peach cultivar. On the other hand, the up-regulation of proteins involved in anthocyanin and flavanol biosynthesis and ethylene synthesis were observed in red- and yellow-fleshed peach cultivar. Dihydroflavonol 4-reductase was preferentially expressed in the red-fleshed peach cultivar, agreeing with the accumulation of anthocyanin and expression of other previously identified genes for anthocyanin biosynthesis. We applied high resolution melting (HRM) analysis to peach single nucleotide polymorphism (SNP) discovery based on the predicted SNP information derived from the peach EST database. These SNP markers could be useful for marker assisted breeding in peach and provide a good reference for relevant research on molecular mechanisms of color variation in peach cultivars.

P42 ABCG subfamily proteins in plants coevolved with ABCGs of pathogens

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ABCG subfamily proteins of the ABC transporter family are highly enriched in terrestrial plants. To understand why the ABCG subfamily proteins proliferated extensively during the evolution of the green plant lineage, we constructed phylogenetic trees from a broad range of eukaryotic organisms. We found that ABCG proteins were massively duplicated in land plants and in oomycetes, a group of agronomically important plant pathogens, but not in other organisms. We further observed that ABCGs in land plants and oomycetes appeared to have a common origin and their expansion closely mirrored that of each other. Thus, many genes involved in host–pathogen interactions were positioned in comparable phylogenetic positions, prompting us to hypothesize that plant and pathogen ABCGs coevolved. Indeed, *AtABCG31* expression was activated following infection with *H. arabidopsidis,* and disrupting *AtABCG31* led to increased susceptibility to *H. arabidopsidis*. Homology models of AtABCG31 and HpaP802307 were compatible with the notion that they may have a related structure and thus substrate specificity. Taken together, our results suggest that ABCG genes in plants and their oomycete pathogens coevolved as drug pumps in an arms race to extrude toxic chemicals secreted by each other.

P43

Escaping autotoxicity by evolving a specialized metabolite pathway in wild tobacco

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Plants produce an extreme diversity of specialized metabolites of significant agricultural and medical values. Elucidating mechanisms contributing to this diversity can broaden our understanding of how complex traits evolve and guide metabolic engineering in plants. While external ecological stresses, which are often combated by specialized metabolites in plants, have received much attention in understanding the evolution of plant metabolites, the role and mechanisms of autotoxicity, an intrinsic factor caused by cellular and metabolic processes in plants, are little understood. Here, using coyote tobacco as a model system, we investigated the evolution of diterpene glycosides, a group of defensive compounds produced in some Solanaceae plants, including genus of *Nicotiana, capsicum and lycium*. Silencing several components of diterpene glycosides biosynthesis pathway lead to autotoxicity and plant sterile. Phylogenic analysis shows that downstream detoxifying catalytic activities were already exist before the divergence between *Solanum* and *Nicotiana*, whereas the signature of positive selection on enzyme catalytic activity was only detected among *Nicotiana* species. In addition, the evolution of strong substrate affinity in a branchpoint enzyme facilitated the metabolic flow switched from an ancient indirect-defensive homoterpene pathway to current direct-defensive diterpene glycosides pathway. These results support the retrograde hypothesis for evolution of metabolic pathways and exemplify the sophisticated evolutionary assembly strategy of new metabolite pathway via escaping autotoxicity.

P44 Trait-based assembly of ecological networks, and their resistance to climate change

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Species interactions play a fundamental role in the structure and dynamic of plant communities and can mediate the response of plant species to climate change. Thus, it is crucial to understand the assembly of plant community networks and their resistance to climate change. Here, we aimed at developing a new framework that combines functional traits with network theory, and we show its application to alpine plant communities. First, we found that dominant, stress-tolerant plants characterised by low specific leaf area and small height were the most important species for supporting the cohesiveness of a plant community network. Whereas, water- and nutrient-demanding plants characterised by competitive traits were the least connected species within the network.

Second, we found that the resistance of plant community networks to climate change depends on specific drivers. In particular, stress-tolerant species with high leaf dry matter content and low specific leaf area increased network resistance against biodiversity loss in scenarios of increasing drought and temperature but accelerated local species extinction in scenario of increasing nitrogen input.

These results provide a mechanistic understanding of the role played by plant networks in driving the assembly of plant communities and modulating their response to climate change.

P45

Predicting the outcome of plant-mediated herbivore interactions from frequency observations in the field

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Plant mediated interactions between herbivores are crucial in shaping plant associated communities, and are increasingly put forward as key drivers in evolution of plant defence strategies. Sequential attack by herbivores is hypothesised to include a measure of predictability, where development of secondary attackers can be inhibited by induced defences or facilitated due to crosstalk between defence pathways. Support for predictability of the ecological outcome is however far from unanimous.

We performed a greenhouse experiment evaluating the outcome of pairwise interactions between 10 herbivore species mediated by the annual plant *Brassica nigra.* To interpret these results in an ecological framework we related the outcome of pairwise interactions to data on frequency of these interactions collected during three years of field observations. We found that subsequent herbivore performance was not predicted by induced responses, but by the identity of the subsequent herbivore. Interestingly, strong ecological effects (positive or negative) were exclusively observed in interactions that were uncommon under field conditions, while more common interactions were less variable in their outcome and associated with increased resistance to the subsequent herbivore. This study suggests that induced plant responses in *Brassica nigra* are adaptive in a community context of multi-herbivore attack.

P46 Identifying keystone plant resources for Neotropical frugivores in the light of a new network framework

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The identification of keystone plant resources (KPR) for animal frugivores is a central issue for management and restoration of tropical ecosystems. Despite the recent theoretical advances regarding interaction networks, we still lack studies translating these interaction patterns into basis for conservation planning. Here we aimed to identify the KPR families for avian frugivores occurring in 38 interaction networks across Neotropical region. We first elected the potential KPR species from families that combined higher scores of centrality indices in the networks. Then, we performed species removal simulations to compare changes in network descriptors (nestedness, modularity and niche overlap) between random removal simulations (null models) and removal of species within families elected as potential KPR. Species from Melastomataceae, Urticaceae, Moraceae, Rubiaceae, Araliaceae, Lauraceae, Meliaceae and Burseraceae families arose as potential KPR among 108 plant families recorded on networks. Melastomataceae, Urticaceae and Burseraceae removal simulations led to remarkable changes in nestedness and niche overlap, suggesting plants within this taxon as important components for maintaining the structure of fruit–frugivore interaction networks across the Neotropics. Our study propose a new objective network framework for identifying keystone interactors. We suggest that families elected as KPR in our study should be used in Neotropical restoration programs.

P47

Climate change effects on the ecology and evolution of an alpine plant–pollinator interaction network

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The alpine areas of Australia are highly restricted regions of high endemicity that are particularly at risk due to climate change. Recent studies have found a reduction in snow cover and a significant increase in mean maximum temperature in these areas. The shrinking of alpine ecosystems can generate rapid ecological and evolutionary changes that can alter the structure and composition of local communities. However, it remains largely unknown how plant and pollinator communities are being affected by these events. In this study we assessed the effects of climate change on an Australian alpine community after a period three decades. We examined variations in plant–pollinator network structure and community composition, as well as shifts in plant and pollinator functional trait diversity using contemporary and historical data. We report an increase of the presence of shrubs and invasive weeds, as well as an increase in the abundance of non-native pollinators, specifically *Apis mellifera.* Our results highlight some of the rapid changes that have been observed in Australian alpine plant–pollinator communities over the last three decades, and discuss the implications for conservation of these threatened areas.

P48 Weaver 2.0: A Next-Generation IBM to simulate eco-evolutionary dynamics in food webs

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Studying microevolution within food webs entails understanding a number of interdependent networks: genetic, trait, interaction and spatial, as well as how several mechanistic models are coupled. In addition, the multidimensional nature of the phenotypes and the associated genetically-based trait distributions lead to complex selective pressures that propagate through the network, driven by direct and indirect interactions as well as indirect genetic effects, all of which vary across space. Weaver 1.0 (Moya-Laraño *et al.* 2014 *Adv. Ecol. Res.* 50: 75-143) was a first attempt to grasp all of the above complexity in a simulation platform for soil food webs that linked space and eco-evolutionary dynamics in food webs. Here, we present an extensive update of Weaver (2.0) which has been fully parameterized for beech forest food webs. Among the novelties, this version includes different reproductive modes (parthenogenesis, haplodiploidy), realistic genetically-variable individual growth curves, indeterminate growth, accommodation of the full range of terrestrial temperature and water availabilities, as well as predator preferences and prey switching. We will present some examples to highlight the unprecedented level of detail allowed by Weaver in evolutionary simulations of food webs. Other food webs are currently being parameterized to work with this platform.

P49

The dimensions of diet breadth: what does it mean to be a generalist?

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Diet breadth has been linked to an array of ecological and evolutionary processes including speciation and extinction, response to environmental change, and multi-trophic interactions. In this regard, dietary specialists have been of keen interest due to the strong phylogenetic linkages between consumer and diet, with less understood about the complex interactions associated with dietary generalists. This represents a significant void in that generalists are ecologically pervasive and inherently drive connectance within ecological networks. We report on a large-scale, historic dataset of highly generalized tree-caterpillar network in temperate forests of Canada and examine the relationships between diet breadth, ecological traits, and network structure. In doing so, we take a multi-facetted approach to characterize polyphagy within Lepidoptera at broad spatial scales.

P50

Impact of *Streptomyces* sp. AH04 on bacterial community and the promotion of *Brassica alboglabra* growth in the plant–parasitic nematode infested soil

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The impact of *Streptomyces* sp. AH04 on rhizosphere bacterial community and the growth of *Brassica alboglabra* planted in plant-parasitic nematode infested soil were assessed. Two months after planting, total bacterial communities DNA was extracted from the uninoculated rhizosphere soils and the inoculated rhizosphere soils. Denaturing Gradient Gel Electrophoresis (DGGE) fingerprints of PCR-amplified 16S rDNA were obtained from bacterial communities. PCR-DGGE analysis revealed that the strain was capable of surviving and proliferating in the nematode infested soils throughout the entire 60 days of a cultivation period as well as friendly to bacterial community. The strain significantly increased biomass, shoot and root length by 45%, 12% and 37%, respectively. Inoculation of the strain significantly increased plant elements including total N, P, Ca and Fe (14%, 5%, 20 % and 42%, respectively). Altogether, its beneficial characteristics suggested that *Streptomyces* sp. AH04 could be a potential actinomycetes for being integrated in the plant management program.

P51

Impact of temperature on host–parasitoid webs: high and low elevation food webs reveal dissimilar responses to global warming scenarios.

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Understanding how and why complex networks of species interactions respond to environmental changes is a key goal in community ecology. We investigated how the structure and dynamics of a coevolved, tropical *Drosophila*–parasitoid food web responded to increased temperatures through trait and density mediated processes. Specifically, we wanted to examine whether high and low elevation food webs revealed similar structural and dynamic changes when exposed to warming temperatures. We predicted that, due to local adaptation to lower average temperatures, high elevation food webs should display a greater shift in their structure and reveal less stable dynamics (e.g., more species extinctions) over the course the experiment. To test out hypothesis, we assembled high and low elevation *Drosophila*–parasitoid food webs in the lab at three different temperatures (20, 24, and 28C) and sampled repeatedly over a 3-month period. Our preliminary results revealed that parasitism rates were lower in higher temperature treatments and the network structure of lower elevation food webs were less impacted by increased temperatures. We observed shifts in *Drosophila* pupal size over time, but did not find an association with parasitism rates. These results offer a unique insight into how specialized, tropical food webs might respond to warming temperatures.

P52

Using phylogenetic specificity symmetry to compare bipartite networks of lichens, endophytes and mycorrhizae

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In network analyses, specificity and the symmetry of specialization have been proposed to be drivers of species abundance and geographic range, whole-network stability, modularity, and coevolutionary dynamics. In several systems, symbiont switches and host range have been shown to be phylogenetically constrained. However, network ecology has yet to incorporate phylogenetic information when measuring specificity and specialization symmetry. Several diversity indices now include phylogenetic information and have been used extensively in studies of host–parasite interactions to assess host-specificity.

However, these tools only map specificity onto the phylogenies of one partner. We use existing metrics of phylogenetic alpha diversity to estimate species level and whole-network specificity and specificity symmetry in an interaction network between lichen-forming fungi and their *Nostoc* symbionts, as well as endolichenic fungi and ectomycorrhizal fungi and their respective hosts. We compare these results with estimates from currently available network specificity metrics.

P53

Constraints upon cheating emergence in mutualistic networks: evidence in the mycorrhizal symbiosis

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While multiple-partner mutualisms are widespread and essential in ecosystems, cheating species often exploit mutualistic interactions and threat their stability. The persistence of mutualisms relies on constraints upon cheating emergences: cheaters can be constrained by interaction mechanisms preventing cheating (*interaction constraints*) or by phylogenetic conservatisms of interactions (*phylogenetic constraints*). By investigating the structure of the large-scale interaction network (>15,000 interactions) and the phylogenetic distribution of cheaters, we provide an integrative framework to evaluate the strength of the constraints upon cheaters in the mycorrhizal mutualistic symbiosis, linking land plants to arbuscular mycorrhizal fungi, where non-photosynthetic plants (*mycoheterotrophs*) repeatedly evolved. Unlike mutualistic autotrophic plants, cheating plants appeared narrowly specialized toward some closely-related specialist fungi. This shows that (i) cheaters are specifically isolated into modules by interaction constraints, and (ii) mycoheterotrophic lineages convergently interacted with 'cheating-susceptible' fungal partners, breaking any phylogenetic conservatism.

Beyond mycorrhizal systems, our approach highlights that cheating emergences in multiple-partners mutualisms are strongly limited by interaction constraints, likely ensuring the overall persistence of mutualisms.

P54 Intraspecific variation in floral scent in the perennial herb *Arabis alpine*

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Floral scent is an important trait in shaping plant–insect interactions. Several factors may contribute to inter- and intraspecific variation in the composition and emission rate of floral scent, including selection form pollinators and herbivores, environmental conditions, biochemical constraints and genetic drift. In a greenhouse experiment, we have investigated intraspecific variation in floral scent among multiple European populations of the arctic-alpine perennial herb *Arabis alpina* that vary in mating system.

Self-compatible populations in Scandinavia, Spain and France had a lower scent emission rate and largely different scent composition, as compared to self-incompatible populations in Italy and Greece. Furthermore, floral scent composition varied substantially among self-incompatible populations, with populations at relatively close geographical proximity displaying large differences in scent composition. Overall, our results suggests that the dependence of pollinators for fertilization is important in shaping intraspecific floral scent variation between populations of different mating system. Additional population-level variation among self-incompatible populations could include adaptations to local pollinator communities or potentially result from different phylogeographic histories for different populations. On a broader level, our results provide an example of the potential of multiple factors to cause extensive intraspecific variation in the floral phenotype of a geographically widespread plant.

P55

The structure of trophic networks along elevation

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Environmental clines represent a natural laboratory to explore how species interactions respond to environmental changes, but comparing ecological networks along natural gradients remains a minority of network studies. Using the plant–orthoptera study system, we aim at identifying variations of structural properties for bipartite networks along the elevation gradient. We selected 48 study sites distributed along six elevation transects in the Swiss Alps and reconstructed interaction networks using DNA metabarcoding applied on insect faeces. We compared the slopes of the observed metrics *vs.* elevation to those drawn from a metaweb of random interactions. The method allows to determine whether the metrics are robust to the variation of underlying network sizes and highlights the independent contribution of the changes in topology and interaction strength along elevation. We show that at high elevation, networks are more connected and insect diet breadths tend to be broader. In the context of climate change, increased migration and extinction rates may shift species composition and interaction within trophic networks. Beyond the study of network structure, trait-matching analyses would permit a mechanistic understanding of species interactions toward predictive abilities.

P56 Keystone herbivores and the evolution of plant defense

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Plants need to defend themselves against a diverse and dynamic herbivore community. Such communities may be shaped by keystone herbivores that through their feeding alter the plant phenotype as well as the likelihood of attack by other herbivores. Not only may these herbivores have a large effect on the interaction network structure and insect assembly on individual plants, these effects of keystone herbivores may have associated fitness consequences for the plant. In a field study on *Brassica nigra* and its insect community, we identified that caterpillars of *Pieris rapae* may qualify as keystone herbivore. Induced responses to feeding by *P. rapae*, but not to the aphid *Brevicoryne brassicae*, caused plants to be colonized earlier and more frequently by other insect herbivores and the indirect effect of *P. rapae* herbivory on community assembly negatively affected plant fitness. Thereby, *P. rapae* may be considered a dominant agent of selection on plant defense traits by its large indirect effect on plant fitness that overarches its direct effect on plant fitness. Merging the keystone herbivore concept with plant fitness and trait selection frameworks will provide an approach to identify which herbivores drive selection in complex multispecies interactions.

P57

Interaction flexibility and pyrodiversity increase pollinator population resistance

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Understanding the landscape and species characteristics that promote population and community resistance is essential for predicting the impacts of global change. Focusing on plant–pollinator communities, I examine how landscapes with diverse fire histories, or high pyrodiversity, shape interaction networks, and the resulting impacts on community and population resistance. I find that before an extreme drought, pyrodiversity promotes the functional complementarity and redundancy of interactions, though this does not translate to higher resistance to co-extinction cascades. In addition, pyrodiversity acts in synergy with interaction flexibility to enable species to respond to changes in community composition. Specifically, pollinators that are more able to shift their partners and network role are better able to take advantage of the heterogeneity generated by pyrodiversity – buffering pollinator populations against changes their plant partners' abundances. This study provides one of the first empirical tests of the importance of ecological network structure in determining community and population resistance to a perturbation.

P58 Functional genomics for understanding trait evolution in forest tree-environment contexts

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Genomics can provide many fascinating insights into the traces of evolution on plant genomes in the form of genetic variation that, over the millennia, proved beneficial for the plant's survival and fitness upon recurrent exposure to parasitizing organisms present within the plant's local environment. Moreover, adaptation to local climate also left the respective traces of genetic variation along the genome, usually detected as strong signals in association genetics. Here, we discuss different cases of such signal detections in the context of long-lived forest tree–environment interactions that is: 1) herbivory by *Pissodes strobi* (Coleoptera) in spruce and the issue of growth and host defenses trade-offs (Porth, 2018), 2) different host utilization by the polyphagous *Lymantria dispar* (Lepidoptera) on naïve vs. exposed conifer species comparing differences in hosts' inherent defensive foliage metabolites with the insect's unique enzymatic detoxification potential (Keeling, 2019), and finally 3) the role of genome-wide gene copy number variations in a widely distributed North American *Populus* species that we linked to adaptive selection for resistance to disease in the south and to abiotic stress in the north of its distribution (Prunier, 2019). In sum, we investigated three different systems to elucidate traits' variation that coevolved under diverse environmental circumstances.

P59

Interaction networks of plants and ectomycorrhizal fungi in Mediterranean mixed pine-oak forests

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Ectomycorrhizal fungi (EcMF) are a highly-diverse and widespread fungal guild that associates mostly with roots of woody plants. The interaction networks between EcMF and host plants can mediate important ecological processes in plant communities, such as species coexistence. However, the characterization of these networks along different forest ecosystems, and particularly in the Mediterranean ones, remains yet scarce. We aimed to determine the structure of plant–EcMF interaction networks in Mediterranean mixed forests, and to analyze whether the host plant identity and spatial-temporal factors could shape these networks. We used high-throughput sequencing to characterize root-tip EcMF of eight plant species sampled in autumn and spring in two mixed pine-oak forests of Southeastern Spain. The frequency of interactions between plants and EcMF taxa were calculated, which helped to define different network parameters (modularity, nestedness, betweenness). Plant species affected the structure of the interaction networks in each forest, and the seasonality did also influence it, but into a much lower extent. This work highlights that host plant identity together with spatial-temporal factors are key drivers of plant–EcMF interaction networks in Mediterranean mixed forests. This knowledge might give new insights on the underlying mechanisms that regulate the structure and dynamics of plant communities.

P60 Rhizobial biogeography in rooibos (*Aspalathus linearis*): functional benefits in nutrient-poor soils

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Rhizobia establish mutualistic symbioses with legumes, providing fixed atmospheric N_2 in exchange for photosynthates. These functions are particularly important in habitats with low nutrient availability such as the arid Cape Floristic Region of South Africa. Rooibos is an endemic legume shrub from this region, growing in acidic and extremely poor soils in terms of available N, P, micronutrients, and water. The coexistence of cultivated and wild rooibos populations allows addressing two important questions: 1) Do cultivated and wild rooibos populations host distinct rhizobial assemblages? 2) If so, can we use this rhizobial diversity to improve the N nutrition and growth of rooibos? During 8 months we raised rooibos seedlings from a commercial cultivar in cultivated, wild, and 1:1 mixes of both soils collected across its distribution range. We recorded plant biomass and nutrient accumulation, and described the rhizobial nodule communities colonizing rooibos roots through sequencing of functional (nodA) and taxonomic markers (gyrB). The strongest predictor of rhizobial community structure was the geographical origin of the soil, while the rhizobial communities from cultivated and wild rooibos were marginally distinct. Yet, wild and mixed soils from a particular area increased plant growth compared to the other soils. We further identified candidate rhizobial strains only found in that geographical area that might be driving such functional benefits. Our results suggest the geographical origin of rhizobia can drive the functional benefits from this mutualism in rooibos.

P61

Interactions with pollinators and herbivores drive real-time plant evolution

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Pollinators can impose strong selection on floral traits, however, herbivory by insects can be an important selection factor as well. Nevertheless, our understanding of how floral traits evolve under different pollinator and/or herbivory scenarios is still limited. Using an experimental evolution approach, we investigated floral and mating system evolutionary changes in *Brassica rapa* subjected to four treatments: bumblebee-pollination (*Bombus terrestris*) and hand-pollination, with and without herbivory (*Pieris brassica* larvae); each treatment was replicated three times, each comprising 36 plants for a total of 8 generations. With this full factorial design, we evaluated the impact of bumblebee-pollination (P), herbivory (H) and their interaction (H x P). We found that plants under selection by bee-pollinators evolved increased floral attractiveness, mainly due to a higher emission of the volatile compounds benzaldehyde, benzyl nitrile and *p*-anisaldehyde. On the other hand, plants that underwent herbivory evolved increased chemical defenses (concentrations of glucosinolates in leaves). Plants under selection of both, bee-pollinators and herbivores simultaneously evolved higher degrees of autonomous selfing and reduced spatial separation of sexual organs (herkogamy). In conclusion, our experimental evolution approach was successful in addressing fundamental questions regarding adaptive floral evolution under different pollination and herbivory scenarios.

P62

Settling on leaves or flowers: Herbivore feeding site determines the outcome of indirect interactions between herbivores and pollinators

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For antagonistic and mutualistic community members, indirect interactions can impact community structure and trait evolution, influencing eco-evolutionary dynamics. In nature, antagonistic and mutualistic networks are intertwined, but how trait variation in herbivore species affects plant interactions with mutualists has seldom been explored. We investigated the effect of trait variation in feeding behavior of plant antagonists (herbivorous insects) on the visitation by plant mutualists (pollinators) on flowering *Brassica nigra* plants. We placed herbivores on either leaves or flowers, recorded the responses of two pollinator species when visiting flowers, and measured herbivore preference and performance. Our results show that trait variation in antagonist feeding behavior has profound impact on the outcome of antagonist–mutualist interactions. Herbivores feeding on flowers had consistent positive effects on pollinator visitation, whereas herbivores feeding on leaves did not. Herbivores themselves preferred to feed on specific feeding sites, which determined herbivore performance. Our study contributes to the growing appreciation of the role of indirect interactions in the ecology and evolution of communities, and identifies that antagonist trait variation is important in determining the linkage between antagonistic and mutualistic networks.

P63

Spatial and species variation in ambrosia and bark beetle communities on *Pterocarpus macrocarpus* Kurz and their associated fungi

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We studied bark and ambrosia beetle communities attacking the important timber tree, *Pterocarpus macrocarpus*, and the associated, possibly pathogenic, fungi, in the Western, Northeastern and Northern regions of Thailand using bait branches. Only a small proportion of the species present in each area (determined by EtOH trapping) actually attacked Pterocarpus, possibly due to abundant gum production. Different species of beetle were dominant in each region. Distinct seasonal changes in the abundance, diversity and species richness of the beetle community were not evident. Associated fungi obtained from living beetles (external surface), and gallery walls, were cultured to isolate and identify fungi. We isolated two distinct fungal strains, each associated with one beetle species, and closely related to *Fusarium solani* f.sp. *robinae* NRRL 22161 and *Fusarium solani* f.sp. *pici* NRRL 22161, respectively. Morphological characters and BOX fingerprint patterns will be used to classify the two isolates, and further work on the fungal associates of other beetle species is in progress.

P64

How does selection asymmetry affect coevolutionary dynamics in mutualistic networks?

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Mutualistic interactions can generate reciprocal selective pressures between interacting partners, which, in turn, may lead to coevolutionary changes. However, the strength of selection imposed between pairwise mutualists may vary, generating asymmetries in the strength of selection each partner imposes. For example, in pollination interactions, the benefit for the plants is to secure its reproduction while for the pollinator the benefit is to obtain resource. Furthermore, the number of partners each species has may play a role in the selective differential imposed to one species. Here, we used a coevolutionary model to explore the consequences of the selection asymmetry to coevolutionary dynamics. We found that highly asymmetrical interactions lead to differences on the amount of evolutionary changes observed in each mutualistic partner. We also found that higher selective asymmetry decreases overall trait convergence in the community but increase trait matching between partners. We are now exploring how network structure might influence this dynamics.

P65 Ecological and evolutionary patterns of symbiotic dinitrogen fixation in plant communities across biomes

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Atmospheric dinitrogen (N_2) fixation by plants (in symbiosis with root bacteria) is the primary source of new nitrogen to land ecosystems. However, the patterns of abundance of plants capable of N_2 fixation are puzzling. This plant functional trait allows plant growth in nitrogen-poor habitats but at a high energetic cost. Therefore, nitrogen fixation should be widespread in nitrogen-limited habitats and restricted in nitrogen-rich conditions where non-fixing neighbors can outcompete fixers. In reality, N_2-fixing plants are abundant in many nitrogen-rich tropical forests, but are often absent or restricted in nitrogen-poor soils (*e.g.*, temperate, Boreal, and Mediterranean forests). We show observations and a theoretical analysis that explain the emergence of symbiotic fixation as an evolutionary stable strategy across climate- and biome-specific differences in the nitrogen cycle. We analyze empirically and theoretically the conditions in which a constant fixation strategy (obligate) prevails, versus conditions in which the prevalent strategy is regulation of nitrogen fixation in response to soil nitrogen availability (facultative). We conclude that biome-scale differences in N_2 fixation can be explained by the interaction between individual plant strategies and climatic constraints on the nitrogen cycle over evolutionary time.

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Different functional mechanisms modulate the structure and evolutionary dynamics of antagonistic and mutualistic networks

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Coevolution plays a key role in assembling and maintaining species interactions. Yet, the processes shaping the structure of networks and driving species evolution remain poorly understood. Functional mechanisms underlying interactions describe the effect of species traits on fitness, being traits both outcomes of coevolutionary dynamics and drivers of the coevolutionary process. To unravel how coevolution by trait matching and trait thresholds (i.e. exploitation barrier) drives the structure and the evolutionary dynamics of antagonistic and mutualistic assemblages, we build an adaptive network model for single-trait evolution. We show that models considering a balance between coevolutionary and environmental selection and strong functional mechanism effect have a better performance than non-coevolutionary trait-based models in predicting empirical network structure, especially in antagonistic systems. Trait matching better explains the structure of antagonistic networks while that of mutualistic networks is better reproduced by exploitation barrier. These functional mechanisms also imply in different coevolutionary dynamics. Trait matching increases the evolutionary stability of antagonistic networks by reducing temporal trait fluctuation, the magnitude of arms races and interaction rewiring. In mutualistic networks it is the exploitation barrier mechanism that increases interaction stability by reducing temporal trait fluctuations and interaction rewiring, but it also increases the magnitude of trait change. Our results help to understand how coevolution shapes the structure and evolutionary dynamics of antagonistic and mutualistic networks.

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Induction defense response in muskmelon plant (*Cucumis melo*) against gummy stem blight by *Trichoderma* sp. PSU-P1

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Gummy stem blight of muskmelon (*Cucumis melo*) caused by *Stagonosporopsis cucurbitacearum* negatively impacted for muskmelon cultivation in Thailand. *Trichoderma* species has been known as effective biological control agent (BCA) against several plant disease pathogens by multifaceted of mechanisms. In this study, induction of plant defense responses in muskmelon seedlings treated with *Trichoderma* sp. PSU-P1 was clarified by evaluation the fungal cell wall degrading enzymes (chitinase and *β*-1,3-glucanase). The results showed activities of chitinase and *β*-1,3-glucanase in muskmelon seedlings treated with *Trichoderma* sp. PSU-P1 were significantly higher than those of control ($p < 0.05$). Furthermore, application of *Trichoderma* sp. PSU-P1 spore suspension was also significantly reduced disease severity index (DSI) of gummy stem blight ($p < 0.05$). The obtained results suggested that *Trichoderma* sp. PSU-P1 efficiently induced cell wall degrading enzyme activities and reduced DSI of gummy stem blight in muskmelon plant caused by *S. cucurbitacearum*.

P68

Slippery petals as a defense against nectar-thieving ants

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The diversity of the floral characters is commonly understood as the result of adaptation to pollinators. Floral antagonists, such as nectar thieves and florivores, also have the potential to exert selection on floral characters, but adaptation against floral antagonists has attracted comparatively little attention. We found that the corollas of *Codonopsis lanceolata* (Campanulaceae) and the tepals of *Fritillaria koidzumiana* (Liliaceae) are slippery to ants; because the flowers of both species have exposed nectaries, slippery perianths mayfunction as a defense against nectar-thieving ants. When wiped with hexane, the perianths lost their slipperiness, and scanning electron microscopy observations indicated that the slippery zones were coated with epicuticular wax crystals. Artificially bridging the slippery zones using non- slippery materials allowed ants to enter flowers more frequently, and experimental introduction of live ants to the *Codonopsis* flowers evicted hornet pollinators and shortened the duration of pollinator visits. Although no significant differences were found in the fruit or seed sets of flowers with and without ants, our findings indicate that slippery perianths ensure proper visitation by legitimate pollinators by filtering out ants.

P69 Temporal variation in abundance of floral visitors modifies the effect of predators on their host plants

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Indirect impacts of predators on plants mediated by floral visitors have been considered as important in assembling ecological interactions. However, studies concerning tritrophic interactions have not yet explored how temporal variations in the floral visitor community may affect these relationships. To evaluate the indirect effects of predators on plant success through time, we studied the impact of a predatory weaver ant, *Oecophylla smaragdina*, on its host plant, *Melastoma malabathricum*, for two years. Our results show that temporal variation in the density of bee community modifies the effects exerted by predators on their host plants. In the first year, the presence of ants on flowers deterred the less effective pollinator, *Nomia* sp., and attracted the most effective, *Xylocopa* sp. However, two years later *Xylocopa* bees visited plants with and without ants similarly. Although *Nomia* bees still foraged mainly at plants without ants, the reduced number of individuals hardly affected resource availability. Consequently, while fruit and seed set were higher at plants with ants in the first year, two years later plants with and without ants had similar reproductive success, indicating the role of temporal variation on the assembly of ecological interactions.

P70 Filling the Spatial and Temporal Gaps in Plant–Pollinator Networks in Europe

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Plant-pollinator networks are useful when studying plant and insect communities in order to assess network stability. These species and interactions are decreasing at an alarming rate because of anthropomorphic and global climate change. Previous studies that have looked at plant–pollinator networks have been conducted mostly in Western Europe in the past 15 years, causing a spatial and temporal data gap. Filling this gap gives us knowledge on the richness of interactions in Europe and how particular systems have changed recently. We investigated four different spatial and temporal networks. We studied networks at different land-use gradients in Romania and Germany, to see how agriculture and grazing affect networks in meadows. Using historic data sets, we re-sampled areas in the Swiss Alps and in Finnish Lapland and compared them to century-old networks to show how the network structure has changed in these vulnerable habitats. These networks help to increase our knowledge in understanding how networks change over space and time in under-represented areas of Europe.

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Fomitiporia (Basidiomycota): updating molecular phylogeny

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Fomitiporia Murill are distributed worldwide and contain approximately 50 taxa plus numerous unidentified species· *Fomitiporia* species are pathogens and saprobes on numerous hardwood genera, for example, *F. mediterranea*, *F. Cupressicola*, *F. torreyae*· There are 81 *Fomitiporia* names listed in Index Fungorum (2019), however, some of them are synonyms and some were transferred to other taxa based on phylogenetic evidence· This study was report about recent molecular data taxonomic background and recommended genetic markers of *Fomitiporia* are provided· Basidiocarp and basidiospore characters can be used to identify this genus· However, due to inconsistency, cystidioles and hymenial setae cannot be used in species identification· Therefore, use of DNA sequence data is crucial· Single gene and multigene phylogenies demonstrated that *Fomitiporia* is a monophyletic group· ITS is recommended genetic marker to identify mushroom to genus level, Multigene analysis (LSU, ITS, TEF1-a, RPB2) is recommended for species level identification· There are 81 species epithets in Index Fungorum· However, 50 are accepted, but sequence data are only available for 46 species·

P72 An unexpected outcome for florivore–plant–pollinator interactions

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Florivores can exert strong selection on flower morphology by changing floral traits that pollinators recognise and use as cues to visit flowers. This can be especially important for hummingbirds, for which visual cues play a fundamental part in their foraging behaviour. Thus, one can expect that damages to corolla might interfere in flower–hummingbird communication by making flowers unrecognizable or less preferred by them. We selected an ornithophilous species to test the hypothesis that damages to floral shape may negatively affect hummingbird visitation and consequently affect plant sexual reproduction. We, experimentally, simulated natural florivory in recently opened flowers and checked if it affected pollen deposition and fruit set. For that, we used GLMM with binomial error distribution. We found no difference regarding the probability of pollen grains being deposited onto the flowers' stigmas ($Z = 0.275$, $p > 0.1$), neither regarding fruit set ($Z = -1,107$, $p > 0.1$) when comparing intact and damaged flowers. Our results showed that the integrity of floral shape was not crucial for hummingbirds to locate flowers. This raises new questions about how hummingbirds perceive and locate flowers. In addition, this finding may shed light on how these complex florivore–flower–pollinator systems have been maintained in nature.

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Complex network and trait patterns arise from simple coevolutionary dynamic between competing species

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Network structural properties contribute to ecosystem stability. In competitive networks, for example, modular structures are thought to contribute strongly to resilience of a community to disturbances. But little is known about how such structures can emerge from eco-evolutionary dynamics and persist for long time periods. We use a simple dynamic model with trait-mediated interaction framework for competitive networks to identify which network structures emerge more commonly and can persist longer. It combines a trait-matching model, which represents niche overlap between competing entities, with Lotka-Volterra system-based dynamics, which follows population, trait and network dynamics of competing species over time. We show that structures with high modularity emerge frequently from arbitrary assemblages. These structures persist longer under the paradigm of weak competition. Traits show divergent patterns in their evolution, but the rates of divergences differ between species because of a strong influence of population dynamics. This results in deviations from the common expectation of evenly spaced species along a trait axis and allows coexistence of large numbers of competing species. Thus, complex network and evolutionary patterns can emerge out of simple eco-evolutionary dynamics between competing species.

P74 The complexity of symbiotic interactions influences the ecological amplitude of the host: a case study in *Stereocaulon* (lichenized Ascomycota)

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Lichens are among the best known, globally distributed symbiotic systems whose ecology is shaped by the requirements of all symbionts forming the holobiont. The lichen genus *Stereocaulon* provides a suitable model to study the ecology of green algal symbionts (i.e., phycobionts) within the lichen symbiosis. We analyzed 282 specimens, collected in diverse habitats worldwide. Phylogenetic analyses revealed a great diversity among the predominant phycobionts. The algal genus *Asterochloris* (Trebouxiophyceae) was recovered in most sampled thalli, but two additional genera, *Vulcanochloris* and *Chloroidium*, were also found. We used variation-partitioning analyses to investigate the effects of climatic conditions, substrate/habitat characteristic, spatial distribution, and mycobionts on phycobiont distribution. Analogically, we examined the effects of climate, substrate/habitat, spatial distribution, and phycobionts on mycobiont distribution. According to our analyses, the distribution of phycobionts is primarily driven by mycobionts and *vice versa*. Specificity and selectivity of both partners, as well as their ecological requirements and the width of their niches vary significantly among the species-level lineages. The species-level lineages, which accept more symbiotic partners, have wider climatic niches. Additionally, the survival of lichens on substrates with high concentrations of heavy metals appears to be supported by their association with toxicity-tolerant phycobionts.

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Real-time plant evolution in a multitrophic community

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Understanding the process of evolution in multitrophic communities represents a fundamental and outstanding challenge in evolutionary biology. In nature, plants are threatened by herbivores and colonized by diverse microorganisms. Accumulating evidence suggests that the plant microbiota changes the host's defense against herbivores and is altered by herbivory. However, it remains unknown to what extent interactions between plants and their microbiota affect the process and trajectory of plant evolution under herbivore pressure.

We aim to close this knowledge gap by investigating the process and mechanism of herbivory-driven plant evolution in real-time outdoors. We will perform "selection and resequence" experiments using the giant duckweed (*Spirodela polyrhiza*), one of the fastest growing plants, as a model system. We will impose herbivory pressure on *S. polyrhiza* populations that represent the majority of genetic diversity in this species for more than 80 generations (two years) under natural conditions. We will quantify the extent to what herbivory drives changes in the plant phenotype, allele frequency, and microbiota. We will further assess the herbivory-dependent fitness consequences of the observed changes in plant traits and allele frequencies, and investigate whether and how changes in the plant microbiota alter the herbivory-imposed selection on plant defenses.

Using a combination of experimental evolution and cutting-edge genetic and genomic tools, this research will push the research boundaries in the field of plant–herbivore interaction by elucidating the mechanisms and processes of plant defense evolution in a multitrophic community. The resources generated in this project will not only open new research avenues of plant experimental evolution, but will also accelerate the use of duckweeds for industrial applications.

P76 Phytochemical Networks of Invasive Species provide evidence for Novel Weapons Hypothesis

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Biological invasions involve long-distance dispersal of species to regions where they have not previously occurred, followed by rapid multiplication and range expansion. Decades of ecological research have identified many shared ecological features amongst invasive species following invasion but little is known about the genomic or genetic traits that may facilitate invasive success, even though the most accepted hypotheses like ‘enemy escape’ and ‘novel weapons’ need triggers within the genome as a pre-requisite.

The existing methods used for evaluation of the mechanisms and impacts of biological invasions primarily involve broad-scale observational studies or small-scale removal/addition experiments in invaded communities/gardens, with varying levels of reliability. In particular, alteration in the rich suite of species specific phytochemical responses between native and invaded habitats, despite being documented, has not been quantitatively assessed, nor linked to the ecological sophistication of invasive species.

In this work, we superimpose the species interaction networks of *Ageratum Conyzoides* L, one of the world’s worst invasive species, with records of phytochemical emissions across diverse geo locations on the globe, to construct an invasion network. Perturbation of network hub nodes revealed distinct classes of toxic phytochemicals to play a role in network robustness in the invaded habitat, as compared to native habitats. The distinct quality and quantity of phytochemicals in native and invaded habitats provides insights into the evolution of plant emission traits, apart from reinforcing the role of these compounds as key players in invasivity of *A. conyzoides*.

Integration of ecological, analytical and computational approaches in this manner enabled a thorough investigation of the invasion phenomenon, in terms of chemical ecology, biogeography and phytochemistry, followed by association of these factors to rapid adaptive changes in DNA/RNA/amino acids, in order to understand whether, and to what extent, changes in the terpenome may regulate invasion success. The strength of this approach lies in the use of modern data science techniques for assessing cross-continental studies spanning several decades in real invasion scenarios.

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Chemical communication explains plant–herbivore interaction networks: an information theory approach

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Through millions of years of arms-race between plants and insect herbivores, plants have developed diverse chemical weapons against herbivores, which insects have evolved to cope with. However, the semantic pattern of this chemical language spoken by plants and heard by insects is still unknown. In this study, we employ information theory to show that a stable plant–herbivore chemical lexicon can emerge from a conflicting information process between plants and herbivores. We validate this theory with a unique combination of field data recording hundreds of plant–herbivore interactions and plant–VOC (volatile organic compound) associations. Specifically, we find that the observed mutual information between VOCs and plants can be reproduced by an optimization process where plants aim to maximize the uncertainty of information (many targeted herbivore species per VOC); whereas herbivores aim to minimize the uncertainty (few VOCs per herbivore). Deciphering the coding strategy between plants and herbivores has the potential to unveil central biological mechanisms driving the maintenance of entire ecosystems.

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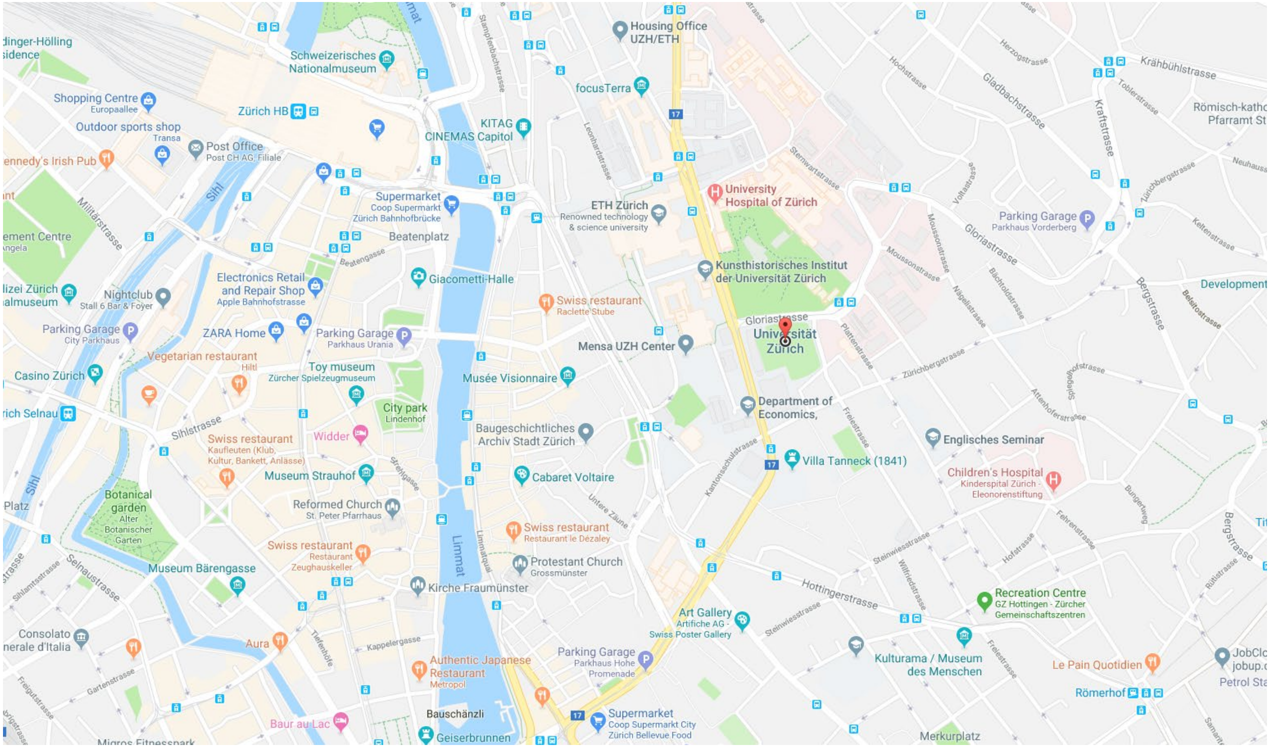
City map


Shopping Centre
Europaallee
Outdoor sports shop
Transa
Post Office
Post CH AG, Filiale
Zürich HB
Schweizerisches Nationalmuseum
KITAG CINEMAS Capitol
Housing Office UZH/ETH
focusTerra
Supermarket
Coop Supermarkt Zürich Bahnhofbrücke
Beatenplatz
Electronics Retail and Repair Shop
Apple Bahnhofstrasse
Nightclub
Stall 6 Bar & Foyer
Parking Garage
City Parkhaus
ZARA Home
Parking Garage
Parkhaus Urania
Vegetarian restaurant
Hiltl
Toy museum
Zürcher Spielzeugmuseum
Casino Zürich
City park
Lindenhof
Sihlstrasse
Swiss restaurant
Kaufleuten (Klub, Kultur, Bankett, Anlässe)
Widder
Museum Strauhof
Reformed Church
St. Peter Pfarrhaus
Swiss restaurant
Restaurant Zeughauskeller
Botanical garden
Alter Botanischer Garten
Museum Bärengasse
Consolato Generale d'Italia
Aura
Baur au Lac
Authentic Japanese Restaurant
Metropol
Bauschänzli
Geiserbrunnen
Kirche Fraumünster
Limmat
Sihl
Giacometti-Halle
Swiss restaurant
Raclette Stube
ETH Zürich
Renowned technology & science university
University Hospital of Zürich
Kunsthistorisches Institut der Universität Zürich
Gloriastrasse
Universität Zürich
Mensa UZH Center
Musée Visionnaire
Baugeschichtliches Archiv Stadt Zürich
Department of Economics,
Cabaret Voltaire
Swiss restaurant
Restaurant le Dézaley
Protestant Church
Grossmünster
Parking Garage
Parkhaus Hohe Promenade
Supermarket
Coop Supermarkt City Zürich Bellevue Food
Art Gallery
Artifiche AG - Swiss Poster Gallery
Villa Tanneck (1841)
Englisches Seminar
Children's Hospital
Kinderspital Zürich - Eleonorenstiftung
Hottingerstrasse
Recreation Centre
GZ Hottingen - Zürcher Gemeinschaftszentren
Kulturama / Museum des Menschen
Le Pain Quotidien
Römerhof
Merkurplatz
Parking Garage
Parkhaus Vorderberg
Gloriastrasse
Bergstrasse
Gladbachstrasse
Krähbühlstrasse
Kraftstrasse
Development
Zürichbergstrasse
Moussonstrasse
Militärstrasse
Selnaustrasse
Kappelergasse
Platz
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University map

See https://www.uzh.ch/cmsssl/en/about/info/sites/city.html for more maps and campus information.