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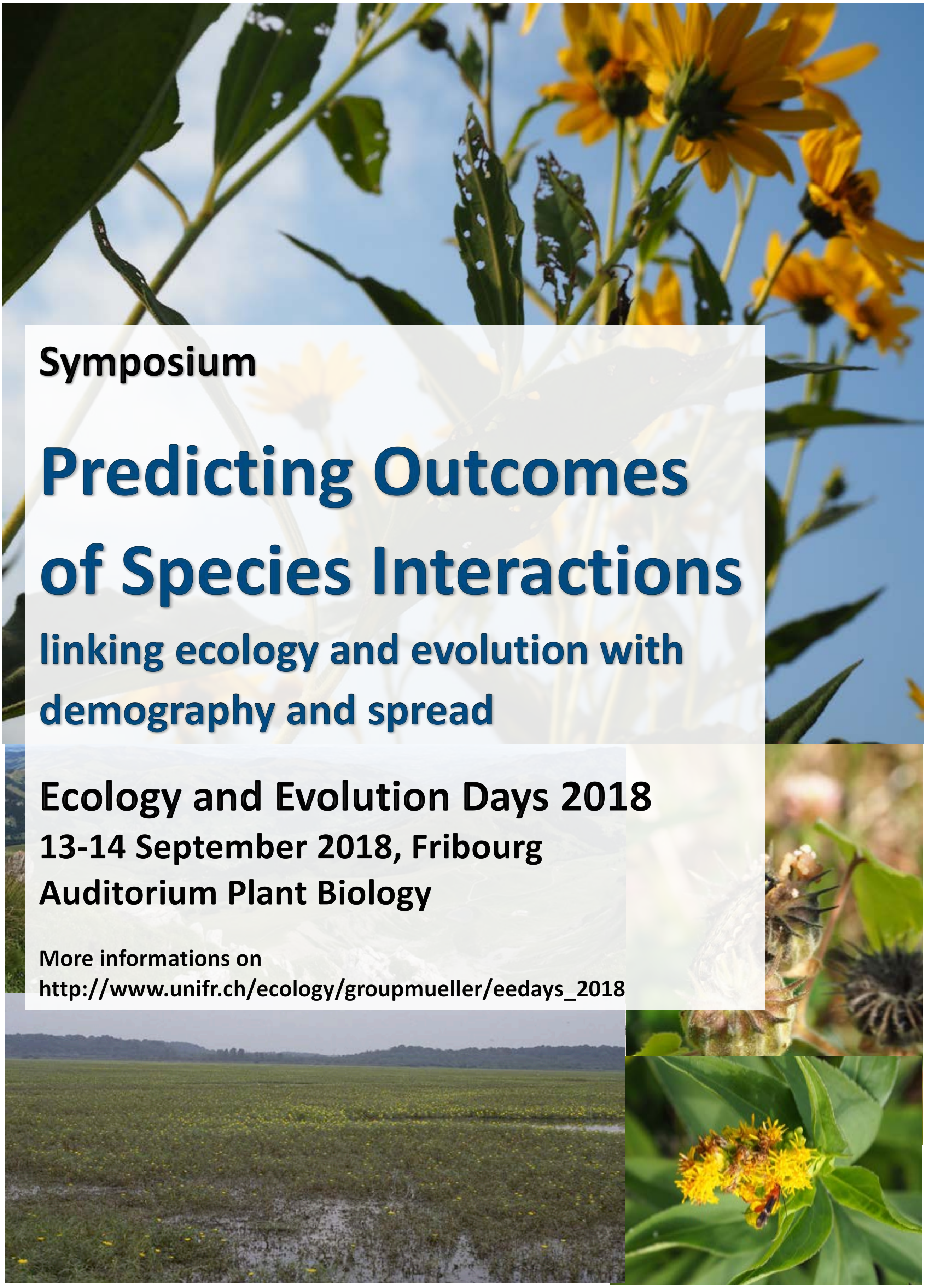
DOCTORAL PROGRAM IN ECOLOGY AND EVOLUTION
INTER-UNIVERSITY DOCTORAL PROGRAM IN ORGANISMAL BIOLOGY



Symposium

Predicting Outcomes of Species Interactions

linking ecology and evolution with demography and spread

Ecology and Evolution Days 2018

13-14 September 2018, Fribourg
Auditorium Plant Biology

More informations on
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Predicting Outcomes of Species Interactions

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Ecology and Evolution Days 2018

13-14 September 2018, Fribourg

Program

Thursday 13th September

8.30 *Registration*

Heinz Müller-Schärer **Uni Fribourg (CH)**
9.00 *Welcome to the symposium*

Antoine Guisan **Uni Lausanne (CH)**
9.15 *Spatial modelling of biodiversity in alpine landscapes: from species to communities and ecosystem services*

Rudolf Rohr **Uni Fribourg (CH)**
10.15 *Structural Approach to Coexistence Theory*

10.45 **Coffee break / Poster session**

Marjo Saastamoinen **Uni Helsinki (FI)**
11.15 *Metapopulation dynamics of the* Glanville fritillary *butterfly in Finland - importance of ecology and evolution*

Heidi Mod **Uni Lausanne (CH)**
12.15 *Incorporating biotic interactions into species distribution modelling (SDM) frameworks for more realistic biodiversity forecasts*

12.45 **Lunch Time at the menza of Pérolles**

John Maron **Uni Montana (US)**
14.00 *Assessing the role of species interactions in setting range limits*

Yan Sun **Uni Fribourg (CH)**
15.00 *Herbivores as drivers of demographic and evolutionary change in a plant invader under climate change*

15.30 **Coffee break / Poster session**

Jake Alexander **Uni Lausanne (CH)**
16.00 *Reshuffling the ecological deck: novel species interactions and the dynamics of species' ranges*

Anne Kempel **Uni Bern (CH)**
17.00 *Response to biotic interactions of common and rare plant species in relation to their position along a resource gradient*

Maria Litto **Uni Fribourg (CH)**
17.30 *Adaptive potential to local conditions - a case of a potential biocontrol agent of the invasive weed* Ambrosia artemisiifolia *in China*

18.00 Bar at "La Fonderie"
19.00 Social Dinner at the restaurant "La Fonderie"

Friday 14th September

Stephen Keller **Uni Vermont (US)**
8.45 *Evolving on the edge: interactions between genomes and their environments in range edge populations*

Anìbal Pauchard **Uni Concepcion (CL)**
9.45 *Pine invasions in Patagonia: assessing impacts and legacies on the invaded communities and ecosystems*

10.15 **Coffee break / Poster session**

Elizabeth Crone **Tufts University (US)**
10.45 *Faster movement in habitat matrix promotes range shifts in heterogeneous landscapes*

Daniel Scherrer **Uni Lausanne (CH)**
11.45 *Disentangling the processes driving plant assemblages in mountain grasslands across spatial scales and environmental gradients*

Martin Kapun **Uni Fribourg (CH)**
12.15 *Genomic signals of clinal variation in European and North American* D. melanogaster

12.45 **Lunch Time at the menza of Pérolles**

Round tables
14.00 *Discussion between speakers and students (3 groups lead by invited speakers)*

15.00 *Feed-backs by one student of each group*

15.30 **Break**

Tobias Züst **Uni Bern (CH)**
16.00 *Summary of the symposium*

16.30 **Goodbye drinks and end of the symposium**

Sessions
- 🟩 *Towards predicting spread mechanistically*
- 🟨 *Interactions of a focal species with the biotic environment*
- 🟦 *Interaction of a focal species with the abiotic environment*

Organizers: Yan Sun, Sarah Bouchemousse, and Heinz Müller-Schärer

Where to go?

- Address of the Biology auditorium: room 0.110, PER04, Route Albert Gockel 3, 1700 Fribourg
- Address of the Restaurant “La Fonderie”: Route de la Fonderie 11, 1700 Fribourg
- Address of the meeting room for the Round Tables (Friday afternoon): room 001, PER17, Chemin du Musée 18, 1700 Fribourg

How to reach the University of Fribourg Pérolles?

- From the train station, take bus Nr 1 or Nr 3 (direction Marly-Gérine or Pérolles - Charmettes), get off at bus stop "Pérolles - Charmettes"
- From the train station, take bus Nr 7 (direction Cliniques), get off at bus stop "Jardin Botanique"

Predicting Outcomes of Species Interactions: linking ecology and evolution with demography and spread

Ecology and Evolution Days 2018, 13-14 September 2018, Fribourg

Background and objectives

The factors that determine the rates of population increase or decline and the differential contributions from individuals are central to the demography and evolution in natural populations. Besides abiotic factors, such changes are driven by species interactions. Scaling up to predicting species distributions is an especially challenging task, as abiotic tolerances, dispersal capacity and biotic interactions each vary in time and space.

The workshop will explore the most recent advances towards predicting the spread of species using a mechanistic approach. For this we will bring together knowledge on linking outcomes of ecological species interactions with demography and evolutionary dynamics and ranging from genomics to modelling tools to better understand and predict future spread of species. This becomes more complex when environments are changing, such as in the face of climate change or in novel environments in the case of biological invasions and biological control. Understanding such outcomes of species interactions is relevant both for basic science, but also for its application to pest species in agriculture, invasion biology and for conservation issues.

This 3rd cycle seminar will bring together renowned international researchers in the field of species interactions interested in synergizing knowledge towards better predicting future species spread. Each invited speaker will give a talk combining a general overview of a specific issue or concept related to the topic of our workshop with a case study involving species interactions.

The course is aimed at students with a general interest in ecological and evolutionary aspects of species interactions, demography and species distributions relevant both for basic science as well as for applied fields such as pest management and conservation ecology. The workshop will be structured into three different sessions and a final wrap-up composed of a discussion in small groups and a summary by an invited expert.

The settings we want to explore are rather novel ones for the focal species, ranging from colonization and invasion processes, assisted migration and biological control up to global change including altered land use and climate change.

Session: Towards predicting spread mechanistically

In this session, we want to explore ways to extend changes at the local population level over time across the space towards predicting future spread of a focal species.

Keynote: Spatial modelling of biodiversity in alpine landscapes: from species to communities and ecosystem services

Antoine Guisan
Department of Ecology and Evolution, University of Lausanne, Switzerland

Advancing our capacity to obtain and understand the spatial distributions of key biotic and abiotic environmental factors is a major challenge in predicting the response of alpine ecosystems and their services to climate change. Meeting this challenge requires integrating intensive biodiversity field surveys across large environmental gradients, high resolution numerical environmental data and advanced modelling methods, which is best achieved by focusing multidisciplinary research efforts in a same mountain area. Here, I present an overview of biodiversity modelling research performed during sixteen years in the Western Swiss Alps. Models were early developed there to predict the spatial distribution of species and communities of various groups of organisms (plants, insects, soil micro-organisms), and were later used to develop climate and landuse changes projections. Yet, their predictive power has remained so far limited by the recurrent absence of some key environmental data, such as soil or geomorphological maps, which can now be acquired by advanced remote sensing and modelling technologies. Meeting these challenges in order to improve forecast of alpine ecosystem services is the main aim of the new ongoing EcoGeoINTEGRALP project, from which I will present some preliminary results and future perspectives.

Additional presentation: Structural Approach to Coexistence Theory

Rudolf Rohr
Department of Biology, Ecology & Evolution, University of Fribourg, Switzerland

Modern coexistence theory introduces the concepts of niche difference and fitness ratio to understand coexistence among competitors. Yet, the mathematical derivation of those coexistence measures has been limited to species pairs and, therefore, do not incorporate the effects of indirect interactions emerging in rich communities. During this talk, I will present the concepts of niche difference and fitness ratio as introduced in modern coexistence theory. I will explain the fundamental limitation to move above species pairs. Then, I will present how the structural approach can define niche difference and fitness ratio beyond the scope of species pairs. Finally, I will show how those new structural measures can be used to quantify the extent to which the conditions for coexistence in multispecies systems differ from those that allow pairwise coexistence.

Keynote: Metapopulation dynamics of the Glanville fritillary butterfly in Finland - importance of ecology and evolution

Marjo Saastamoinen
Organismal and Evolutionary Biology Research Programme, University of Helsinki, Finland

The long-term viability of metapopulations is dependent on independent dynamics of local populations, mitigating fluctuations in the metapopulation size as a whole. I will talk about our recent study in which we assessed if a recently reported increase in metapopulation synchrony of the Glanville fritillary butterfly in Finland could be explained by climate change induced change in synchrony of weather conditions. We used 23 years of survey data together with monthly weather records for the same period. We first examined the associations between population growth rates within different regions of the metapopulation and weather conditions during different life-history stages of the butterfly. We then examined the association between the spatiotemporal trends in the synchrony of these weather conditions and the synchrony of the metapopulation dynamics as well as the potential role of dispersal and trophic interactions in driving the observed patterns. I will also discuss our work where we examined how landscape characteristics and individual variation in dispersal combine to predict genetic structure within the butterfly metapopulation using genomic and spatial data. I will finish by discussing our recent attempts to include GxE interactions in models to determine their influence on the future spatial population dynamics of the butterfly.

Additional presentation: Incorporating biotic interactions into species distribution modelling (SDM) frameworks for more realistic biodiversity forecasts

Heidi Mod
Department of Ecology & Evolution, University of Lausanne, Switzerland

Species distribution models (SDMs) aim to predict species' whereabouts in space and time by quantifying species-environment relationships. One of the main critiques of traditional SDMs is that the predictions rely only on abiotic drivers, omitting for example the influence of biotic interactions on species assemblages. Many attempts have (successfully) incorporated biotic interactions to the SDMs, yet we still lack a comprehensive understanding and methodology to realistically and effectively account for biotic interactions.

One of the earliest and simplest methods to incorporate biotic interactions in SDMs is to include dominant species as independent variable(s). While such approach has provided improved predictions of distribution of focal species, it only accounts for one or few pairwise species associations of the whole species community. To disentangle the possibly interacting species pairs within the community, co-occurrence analyses, after partialling out the influence of abiotic environment using SDMs, have been applied, i.e. environmentally constrained null model approach. Alternatively, Joint-SDMs rely on ordination techniques and hierarchical modelling to identify the associated species pairs, and the meaningful interactions can be included in the predictions. Variants of Joint-SDMs also allow to account for trophic and asymmetric interactions. There are also attempts in incorporating indirect interactions, for example by combining SDMs and Bayesian networks. Finally, species traits provide additional information of species competitive (or facilitative) abilities under varying environmental conditions to be utilized in SDM frameworks.

These different approaches have provided great progresses in accounting for biotic interactions in SDMs, and thus contributed to more realistic species distribution predictions. However, even the most complex methods are simple in relation to complexity of nature. Further, the evaluation of SDMs and predictions incorporating biotic interactions is hindered by missing knowledge of the actual biotic interactions in nature and the influence of environmental conditions and observation scale on the outcome of interactions hinder. While the modelling methods still require further development to account for the complexity and the interrelatedness of different drivers, simultaneous experimental studies of biotic interactions are also required to allow realistic forecasts of biodiversity.

Predicting Outcomes of Species Interactions: linking ecology and evolution with demography and spread

Ecology and Evolution Days 2018, 13-14 September 2018, Fribourg

Here, we want to better understand how the numbers and the genetic make-up of a focal population influence each other and how and why they change over time (interaction between the population dynamic and evolutionary change). In the two sessions, we focus on different types of predominant species interaction studied, thus of a focal species with its biotic and abiotic environment.

Session: Interactions of a focal species with the biotic environment

In this session, we will consider both horizontal (competitive) interactions, thus within a trophic level, as well as vertical (food chain) interactions, thus between trophic levels.

Keynote: Assessing the role of species interactions in setting range limits

John Maron
Division of Biological Sciences, University of Montana, USA

Species interactions are notoriously context-dependent. The underlying drivers of this variability, however, are often unknown. As a result, we have yet to create a framework for predicting when any given interaction should be weak or strong. One approach to this challenge is quantifying whether interactions predictably change in strength across steep environmental gradients. Understanding biotic controls on geographic range limits offers the opportunity to take this approach, since abiotic conditions often vary predictably with latitude. In my talk, I will discuss a case study that examines how the impacts of predispersal seed predation by insects and pollen limitation vary from the range center to the northern range edge of the perennial forb, *Astragalus utahensis*. Combining experiments with demographic monitoring enabled us to determine how abiotic suitability interacts with the demographic effects of seed loss to influence stochastic population growth of *A. utahensis*. We also tested the extent to which dispersal limitation influences the northern range boundary of *A. utahensis* by transplanting individuals beyond the range edge. Our results support some of the predictions of more comprehensive ‘metapopulation-like’ models for the establishment of stable range boundaries.

Additional presentation: Herbivores as drivers of demographic and evolutionary change in a plant *invader under climate change*

Yan Sun
Department of Biology, Ecology & Evolution, University of Fribourg, Switzerland

Invasive alien plants together with their natural enemies from the native range used as biocontrol agents are ideal study system to address questions of whether and how fast organisms adapt to changing environments. Our study aims to get insights into the demography and evolvability of the European plant invader *Ambrosia artemisiifolia* to a recently introduced and potential biocontrol insect, *Ophraella communa*. Combining a species distribution model with underlaying mechanistic processes, we are able to predict the abundance of the *O. communa*, and thus its impact on *A. artemisiifolia* across the area suitable in Europe for both the plant and its insect herbivore. Besides these ecological interaction studies, we presently also explore potential evolutionary changes in this plant-herbivore interaction. In an ongoing field selection experiment in N-Italy, using artificial populations of *A. artemisiifolia* exposed to *O. communa,* we assess the evolutionary changes of *A. artemisiifolia* populations. Pooled samples from each of the experimental populations will be analysed over four years (a) for their genetic composition using next-generation sequencing (pool-seq) and (b) in various bio-assays. By now, we collected seeds from the second (F2) generation from all four field treatments (warming by *Ophraella* herbivory) and grew them alongside their parents in growth chambers, in the quarantine and greenhouse to assess the beetle preference and plant performance. Our results showed a significant reduction by *O. communa* on population growth rate, seed size and seed germination of *A. artemisiifolia.* I will present preliminary results of the quarantine preference and performance studies with *O. communa* on F2 plants from the field selection populations, and of the competition ability of F2 plants from greenhouse studies. I then will present the top differentiated SNPs (0.1%) among two generations from pool-seq analyses. These studies will improve forecasting of the biocontrol efficiency, and of the spread of invasive alien plants in a changing world.

Keynote: Reshuffling the ecological deck: novel species interactions and the dynamics of species’ ranges

Jake Alexander
Department of Ecology and Evolution, University of Lausanne, Switzerland

Species' distributions are being reshuffled across the globe at an unprecedented rate, occurring through the spread of non-native species and range shifts of native species responding to climate and land use changes. This redistribution of species’ ranges is giving rise to novel assemblages, in which species interact that were not previously in contact. Biological invasions show us that the impacts of these novel interactions can sometimes be dramatic. However, the impacts of novel interactions following climate change are poorly understood. In this presentation I will draw on research conducted in our lab in alpine plant communities and with non-native plants to ask how novel interactions could affect the responses of species and communities to climate change. I also ask how evolution could affect the outcome of novel interactions. This work suggests that novel interactions could play a central role in mediating the ecological impacts of climate change, and I highlight several key challenges and opportunities to better understand and predict these impacts.

Additional presentation: Response to biotic interactions of common and rare plant species in relation to their position along a resource gradient

Anne Kempel, Hugo Vincent & Markus Fischer
Institute of Plant Sciences, University of Bern, Switzerland

Understanding why some plant species are rare while others are common is of central interest in ecology. While traditionally theories attempting to explain rarity mainly focused on abiotic factors affecting species niche breadth or width, it is more and more recognized that also the way how species cope with biotic pressures can determine the abundance and distribution of species. A long-standing hypothesis is that common species are competitively superior than rarer species, and recently, interactions with plant enemies have been suggested to be potential drivers of large-scale plant rarity if rare species are more susceptible to e.g. predation or disease. However, evidence that rare and common species respond differently to biotic stresses is still scarce and often controversial, potentially because the importance of certain plant traits for plant success is context dependent. In a large multi-species experiment, we compared the competitive ability, the tolerance to herbivory and ambient herbivore damage of 19 rare and endangered and 21 common congeneric plant species from Switzerland. The species originate from many different habitats, which vary greatly in resource availability. We could show that context dependency is important - common species were better competitors than rare species but only when species originated from resource rich and moist habitats. Tolerance and herbivore damage on the other hand, did not differ between common and rare species. However, as one would suggest from the resource availability hypothesis, common species from resource rich habitats where more damaged by herbivores (less defended) than common species from resource poor habitats – interestingly, such a growth-defense tradeoff was lacking in rare species. Our results show, that at least for species originating from habitats where aboveground competition for light is usually strong our results support the long-standing hypothesis that common species are competitively superior compared to rare species. Thus – taking the position of species along a resource gradient into account is important if we are to identify traits that predispose species to be common or rare, invasive or non-invasive. Further, our results hint to the fact that important evolutionary tradeoffs might have gotten lost in rare species, potentially due to low levels of genetic diversity.

Additional presentation: Adaptive potential to local conditions: a case of a potential biocontrol agent of the invasive weed *Ambrosia artemisiifolia* in China

Maria Litto, Sarah Bouchemousse, Heinz Müller-Schärer
Department of Biology, Ecology & Evolution, University of Fribourg, Switzerland

Accidental introductions offer unprecedented bio-geographical experiments to study ecological and evolutionary processes such as phenotypic plasticity and rapid adaptation to local conditions. As a potential biocontrol agent of the invasive weed *Ambrosia artemisiifolia*, the leaf beetle *Ophraella communa* is an interesting case to study such processes. Native to North America, the beetle is currently considered as an effective biocontrol agent in China, where it was accidentally introduced in 2001 in Nanjing. Besides its natural spread, mass rearing and releases of the beetle have been performed from 2007 to 2010 in several provinces in China. Given the climatic variability and the presence of non-target plants, which have been previously described as potential host like *Ambrosia trifida*, China represent an excellent arena to test the adaptive potential of this beetle to biotic and abiotic conditions. To explore phenotype-environment correlations, we perform a controlled experiment, investigating the response of Southern and Central beetle populations from China to three plant species (*A. artemisiifolia, A. trifida* and *Helianthus annuus*) and three temperature regimes (20°C, 27°C and 31°C). Larval performance has been evaluated in our quarantine facilities at the University of Fribourg, Switzerland of four populations from China. We found different survival and feeding among populations and families. Populations from Central China feed more than the population from Southern China even if the adult dry mass does not differ between the two. We observe that populations from Central China feed less on *A. trifida* and there is the same tendency in the population from Southern China. The developmental time does not differ between ranges. Finally, the survival probability is lower in populations from Central China, especially for second instar larvae at 31°C, compared to the population in Southern China. In conclusion, larval performance is mainly affected by the temperature regimes. This could indicate a local differentiation of the Southern population, which experience warmer conditions in nature. These results could imply fast local adaptation to abiotic factors and could have an impact on future biocontrol management strategies.

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Ecology and Evolution Days 2018, 13-14 September 2018, Fribourg

Session: Interactions of a focal species with the abiotic environment

Keynote: Evolving on the edge: interactions between genomes and their environments in range edge populations

Stephen Keller
Department of Plant Biology, University of Vermont, USA

It is a classic tenant of population ecology and genetics that small, isolated populations are subject to stochastic demographic and genetic processes. Therefore, towards the edges of a species' range where abundance and connectivity decline and environmental suitability becomes marginal, low standing genetic diversity and heightened genetic drift should pose serious constraints on local adaptation. In this talk, I will explore how studies of range edges help us understand adaptation to environmental change, and how landscape genomic studies that incorporate range edges offer a unique perspective on the evolutionary processes shaping interactions between genomes and their environments across a species' range. An important realization is that the adaptive potential of current populations not only reflects their current position in the selective landscape, but also the influence of biogeographic and evolutionary history that underlies the distribution of adaptive diversity in different parts of the range. I will illustrate these themes with recent work from my lab investigating interactions between range context and response to selection in the genomes of forest trees – important ecological model systems for studying the genomic basis of local adaptation. Our approaches integrate measurement of functional phenotypic traits in common gardens, genome-wide sequencing of single nucleotide polymorphisms (SNPs), and spatial modeling of SNP-environment associations to estimate how history, range context, and environment interact to affect adaptation in range edges. After exploring the processes that have shaped the current landscape of adaptive diversity, I take a look towards the future by suggesting ways in which genomic data can be combined with predictive models to estimate where populations may be most vulnerable to loss of fitness under global change.

Additional presentation: Pine invasions in Patagonia: assessing impacts and legacies on the invaded communities and ecosystems

Anìbal Pauchard and Rafael García
Facultad de Ciencias Forestales, Universidad de Concepción, Chile
Institute of Ecology and Biodiversity (IEB), Chile

Pine invasions have been for long of major interest for invasion biology both for their conservation implications and for their use as a model group. However, little has been done to measure and monitor the impacts of pine invasions into biodiversity and ecosystem processes. Here we discuss observational and experimental evidence on the multiple impacts of *Pinus contorta* in forests and open environments of Patagonia, Chile. We have studied two sites in southern Chile, the subalpine *Araucaria araucana* open forest and the Patagonian steppe. We are measuring specific impacts of pines in microsite environmental variables (i.e. light, soil temperature and humidity, nutrients), vegetation and mycorrhizal community. We use a set of observation and experiments in permanent plots along the invasion gradient, including the removal of pines to study the persistence or legacy of pine invasion impacts. Our method is framed in the larger context of the Global Invader Impacts Network (GIIN) and has the potential to quantify impacts using multiple approaches and networking with researchers in other regions of the world. We have found a strong pine biomass gradient reaching up to 200 ton/ha in the forest and 50 ton/ha in the steppe, which has affected the microsite climate. Plant diversity decreases with pine invasion, in association with increased tree cover and reduced light. Pines also act as filters for community traits differentially affecting plant composition. After, pine removal areas with low invasion have been able to recover their pre-invasion composition, while areas under heavy invasion maintain an invasion legacy. Study funded by CONICYT PFB-23 and Fondecyt 1140485.

Keynote: Faster movement in habitat matrix promotes range shifts in heterogeneous landscapes

Elizabeth Crone
Department of Biology, Tufts University, USA

Ecologists often assume that range expansion will be fastest in landscapes composed entirely of the highest quality habitat. Theoretical models, however, show that range expansion depends on both habitat quality and habitat-specific movement rates. Using data from 78 species in 70 studies, we find that animals typically have faster movement through lower-quality environments (73% of published cases). Therefore, if we want to manage landscapes for range expansion, there is a tradeoff between promoting movement with non-hostile matrix, and promoting population growth rates with high-quality habitat. We illustrate how this tradeoff plays out using an exemplar species, the Baltimore checkerspot butterfly. For this species, we calculate that range expansion is fastest in landscapes with ~15% high-quality habitat. Behavioral responses to non-habitat matrix have often been documented in animal populations, but rarely included in empirical predictions of range expansion. Considering movement behavior could change land planning priorities from focus on high-quality habitat only to integrating high- and low-quality land cover types, and evaluating the costs and benefits of different matrix land covers for range expansion.

Additional presentation: Disentangling the processes driving plant assemblages in mountain grasslands across spatial scales and environmental gradients

Daniel Scherrer
Department of Ecology & Evolution, University of Lausanne, Switzerland

Habitat filtering and limiting similarity are well-documented ecological assembly processes that hierarchically filter species across spatial scales, from a regional pool to local assemblages. However, information on the effects of fine-scale spatial partitioning of species, working as an additional mechanism of coexistence, on community patterns is much scarcer.

In this study, we quantified the importance of fine-scale spatial partitioning, relative to habitat filtering and limiting similarity in structuring grassland communities in the western Swiss Alps. To do so, 298 vegetation plots (2 m × 2 m) each with five nested subplots (20 cm × 20 cm) were used for trait-based assembly tests (i.e., comparisons with several alternative null expectations), examining the observed plot and subplot level α-diversity (indicating habitat filtering and limiting similarity) and the among-subplot β-diversity of traits (indicating fine-scale spatial partitioning). We further assessed variations in the detected signatures of these assembly processes along a set of environmental gradients.

We found habitat filtering was the dominating assembly process at the plot level with diminished effect at the subplot level, whereas limiting similarity prevailed at the subplot level with weaker average effect at the plot level. Plot-level limiting similarity was positively correlated with fine-scale partitioning, suggesting that the trait divergence resulted from a combination of competitive exclusion between functionally similar species and environmental micro-heterogeneities. Overall, signatures of assembly processes only marginally changed along environmental gradients, but the observed trends were more prominent at the plot than at the subplot scale.

Synthesis. Our study emphasises the importance of considering multiple assembly processes and traits simultaneously across spatial scales and environmental gradients to understand the complex drivers of plant community composition.

Additional presentation: Disentangling the processes driving plant assemblages in mountain grasslands across spatial scales and environmental gradients

Martin Kapun
Department of Biology, Ecology & Evolution, University of Fribourg, Switzerland

Clines, which are gradual changes of genotypes or phenotypes along environmental transects, are often taken as prima facie evidence for the action of spatially varying selection. However, only due to recent advances in sequencing technology it now becomes possible to compare genome-wide clinal patterns and test for alternative models. With the help of a newly founded population genetics consortium (DrosEU), we, for the first time, conduct genome-wide analyses of clinal genomic variation in *D. melanogaster* on the yet largely unexplored European continent. These analyses reveal complex demographic patterns and pronounced clinal genetic variation along different geographical transects. Multiple clinal variants, including chromosomal inversions are shared across continents and are also found along a latitudinal temperature gradient at the North American east coast. In particular, we find evidence for steep and temporally stable clinal variation strongly associated with *In(3R)Payne*, a common cosmopolitan inversion, that cannot be explained by demography alone. To learn more about the potential adaptive effect of this inversion, we compare karyotype-specific genomic variation on multiple different continents. We find genomic regions in the center of the inversion that are in strong linkage disequilibrium with the inversion breakpoints possibly as a result of selection for inversion-specific genetic variation.

List of participants

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