

2016 EVENET Symposium

Abstracts

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Keynotes

Resilience and evolution: oxymoron or partnership?

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Understanding how species are adapted to, cope with and rebound from disturbances is crucial in times when planet Earth undergoes fast change of social-ecological baselines. Big strides have been made in our understanding of evolution of species and communities to the ever-unfolding change of our environment. However, few attempts have been made to use evolutionary concepts and theories to inform evolution at hierarchically higher levels of biological organization; that is, evolution at the ecosystem level. Ecosystems, which subsume population and community processes, undergo complex dynamics to adapt environmental change. The concept of ecological resilience has taken center stage in academic and practitioners circles for scrutinizing adaptation. A hallmark of ecological resilience is the ability of complex (eco)systems to exist in alternative, often stable equilibria. This definition differs fundamentally from other resilience concepts that are often used in population and community ecology, which focus only on recovery (engineering resilience) after disturbances and which have a single equilibrium focus. A large body of theory and empirical evidence has accumulated about the factors that mediate resilience (e.g., structural and functional attributes of species within and across objectively identified scales of ecosystems). Some of these attributes have been explored as early warning indicators to predict when ecosystem resilience is exhausted and a regime shift becomes imminent. Much of this research is correlative and lacks a mechanistic basis. Evolutionary theory and concepts are deemed important to address current knowledge gaps.

The main aim of this lecture is to seek common ground between eco-evolutionary research and resilience theory and strives for identifying points of interaction where both disciplines can cross-pollinate each other. The lecture will give an overview of ecological resilience theory and its quantifiable components. The quantifiable components of resilience might provide the starting points for seeking synergies between eco-evolution and resilience as a systemic feature.

Eco-evolutionary dynamics and patterns of parallel evolution of host and virus populations

L. Becks ⁽¹⁾

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Different lineages of the same species that independently evolve similar adaptations in identical environments (parallel evolution) denote a certain level of repeatability of evolution. Parallel evolution is most frequently found on the phenotypic level, but is less frequently observed looking at the underlying genetic level. Both evolutionary and ecological dynamics, and their feedbacks will affect the evolutionary trajectories at the individuals phenotype and genotype, e.g. through changes in population size and bottlenecks, as well as selective sweeps. Using experimental evolution with replicate populations provides a powerful way to replay evolution and test for parallelism of evolution on the phenotypic and genotypic level. Here, we show high levels of phenotypic parallelism (host resistance) between replicate experimental coevolving populations of an asexual eukaryotic host (alga) and a large dsDNA virus. Yet, when examining variants at the genotypic level (point mutations and small indels) we did not find such parallelism in the host populations across replicates. However, all host populations evolved by duplication of a large genomic region, reflecting the parallelism found at the phenotypic level (host resistance). We explain this pattern by rapid changes in demographic and selective sweeps, which can be an inherent part of eco-evolutionary dynamics.

Adaptation from standing genetic variation the future of marine animals in a rapidly changing world?

P. De Wit ⁽¹⁾

⁽¹⁾ University of Gothenburg, Sweden

In this presentation, I will briefly discuss the theoretical importance of standing genetic variation (presumably neutral variants present in a population which could become adaptive in a changing environment), and how it might be critical to organisms facing global environmental changes. I will then discuss the peculiarities of the marine system and why adaptation from standing genetic variation could be particularly important here. Finally, I will give some examples from my recent research on gastropods and crustaceans, where I show that standing genetic variation has had an important role in allowing populations to persist in face of changing water carbonate chemistry, salinity and toxic algal blooms.

Host-parasite coevolution in variable temperature environments

A. Duncan ⁽¹⁾

⁽¹⁾ CNRS, Montpellier, France

I will talk about a study investigating coevolution between bacteria and phage (*Pseudomonas fluorescens* and the lytic phage SBW2) under variable temperature environments. In this study we show that the frequency of environmental change between temperatures, permissive (28C) and stressful (32C) for the phage, matters for the induction of temporary coevolutionary coldspots. For this study we devised a coevolution score, which enabled us to show how the precise effects of our different temperature environments impacts coevolution through time. We demonstrated that coevolution is arrested only after spending a threshold amount of time, 4 days, at 32C, thus creating transient, infection-free, refuges for the host. Nevertheless, coevolution resumed immediately upon return to 28C, and overall linear increases in bacterial resistance, characteristic of arms-race-dynamic coevolution, were observed under all fluctuation regimes. The coevolution score also allowed us to disentangle the effects of host and parasite demography on coevolution. Temperature variation affected population density, providing evidence that eco-evolutionary feedbacks acted through variable bacteria-phage encounter rates. This permits more precise estimates of eco-evolutionary feedbacks occurring in our populations and the mechanisms inducing the emergent phenomena of coevolutionary hot and cold spots.

The eco-evolutionary dynamics of range expansions

E. Fronhofer ⁽¹⁾

⁽¹⁾ EAWAG, Zurich, Switzerland

Understanding and predicting the (macro)ecological and evolutionary dynamics of range expansions and biological invasions is of great ecological and economical interest. While theoretical and comparative work has advanced significantly over the last years, some of the most basic predictions concerning evolutionary changes during range expansions and their feedbacks on ecological dynamics and patterns remain to be tested experimentally. Central predictions that have yet to be tested include that range expansions select for increased dispersiveness at range margins and that population density decreases from range core to range margin due to trade-offs between dispersal and competitive ability. Furthermore, the impacts of environmental gradients and species interactions on the eco-evolutionary dynamics of species ranges remain untested, to name but a few examples.

In order to provide causal evidence in favour or against these predictions we combined theory with range expansion experiments using microcosm landscapes and protists as model organisms. While we find that range expansions indeed select for increased dispersal at range margins we do not find that population densities

decrease from range cores to ranges margins. We also find that invasion dynamics are disturbingly insensitive to gradients in local mortality. Biotic interactions differentially impact both ecological and evolutionary dynamics.

Reconstructing the evolutionary history underlying the genomic landscape of species divergence using haplotype-resolved genomes

P.-A. Gagnaire ⁽¹⁾

⁽¹⁾ CNRS, Institut des Sciences de l'Evolution, University of Montpellier

Understanding how genetic variants are arranged into chromosomal haplotypes within individual genomes represents an important source of information for reconstructing the history of species divergence. In particular, haplotype data are useful for detecting signals of historical admixture between divergent lineages, thus allowing a more precise assessment of genome-wide variation in the intensity and the timing of gene flow. Here, we use haplotype-resolved whole-genome sequences to investigate genome-wide differentiation patterns between naturally hybridizing Atlantic and Mediterranean sea bass lineages (*Dicentrarchus labrax*). We show that genomic islands of increased differentiation tend to map disproportionately to low-recombining regions. In order to reconstruct the sequence of events associated with the formation of genomic islands, we infer sea bass divergence history from the spectrum of shared haplotype lengths. Our results support that divergence has been shaped by several cycles of allopatric isolation and secondary contact between Atlantic and Mediterranean populations during the Pleistocene. The direct identification of introgressed migrant tracts shows that asymmetrical introgression during secondary contact episodes has resulted in a highly heterogeneous distribution of haplotypes of Atlantic origin within Mediterranean genomes. Finally, reconstructing the ancestral diversity of Mediterranean genomes shows that linked selection has also increased the rate of lineage sorting in low-recombining regions during allopatric episodes. Altogether, these results support that the formation of genomic islands in sea bass results from repeated phases of linked selection and reduced introgression in low-recombining regions.

Adaptation or acclimation to urban anthropogenic stressors: A case study of the great tit

C. Isaksson ⁽¹⁾

⁽¹⁾ University Lund, Sweden

To estimate the past and future impact of urbanisation on birds, it is important to understand the mechanistic underpinnings of a physiological response to anthropogenic stress. It is well known that air pollution such as nitrogen oxides and particulate matter, directly associated with urban habitats, increases oxidative stress - a state when the detoxifying antioxidant system is overwhelmed by reactive oxidants, which may cause tissue damage linked to disease and pre-mature senescence. Urban great tits (*Parus major*) have, repeatedly, shown to have a higher antioxidant activity than rural conspecifics, sometimes sufficient enough to prevent tissue damage and sometimes not. Regardless, an increased antioxidant defence is probably not cost free for the urban birds, which is why we need to understand the mechanistic cause(s) for generating this habitat difference in physiology. Is it a result of: i) the evolutionary history (i.e. a strong selection pressure for greater antioxidant capacities in urban habitats); ii) the present environment (i.e. direct physiological up-regulation in response to current urban stressors); or iii) the individual history combined with the present environment (i.e. developmental programming of gene regulation and the potential for match/mis-match between environment and optimal physiological response). By using the European great tit as our model system, we address these three mechanistic pathways for generating variation in antioxidant capacities between populations and individuals.

How is diversity maintained in pathogen populations?

A.-L. Laine ⁽¹⁾

⁽¹⁾ University of Helsinki, Finland

Understanding what maintains diversity in host and pathogen populations is the key to predicting short-term risks of infection and risks of pathogen evolution. Natural host and pathogen populations have been shown to support considerable diversity yet the mechanisms maintaining this diversity are unclear. Generally trade-offs in life-history traits has been proposed to the maintenance of diversity in natural populations. The fungal pathogen, *Podosphaera plantaginis*, occurs as a highly dynamic metapopulation with considerable genetic diversity that is unevenly distributed. We find a strong link between ecological and evolutionary dynamics as metapopulation dynamics are the key to understanding both numerical and genetic dynamics of this pathogen. Moreover, we find that strains that represent the most common multi-locus genotypes in the natural pathogen metapopulation exhibit contrasting life-history strategies, suggesting that there are different, but equally successful, ways to persist across space and time. These different life-history strategies are

likely to promote the maintenance of variation in wild pathogen populations that are subject to spatial and temporal variation in their environments.

Rapid evolution of dispersal modifies the ecological dynamics of biological invasion

T. Miller ⁽¹⁾

⁽¹⁾ Rice University, Houston, US

Ecologists are increasingly aware that genetic and evolutionary mechanisms can have important effects on the ecological dynamics of biological invasions. Yet, because most invasions in nature are unreplicated and play out over heterogeneous landscapes, quantifying the contributions of these mechanisms can be difficult. I will discuss experimental studies of the eco-evolutionary dynamics of invasive range expansion, using insect populations that spread through replicated mesocosms. First, I will address the role of multiple introductions. Because multiple introductions affect the genetic diversity of incipient invasions, they may influence the dynamics of spread through both short-term (heterosis) and long-term (evolutionary) effects. Our work shows that multiple introductions can accelerate spread, likely through a short-term fitness advantage of outcrossing. Second, I will address the ecological consequences of spatial allele sorting that occurs when variation in dispersal ability has a genetic basis, as it often does. Our experiments show that spatial allele sorting leads to the evolution of increased dispersal ability at expanding invasion fronts, and this increases both the mean invasion speed and its variance. Collectively, this work identifies the ecological importance of genetic and evolutionary processes that are intrinsic features of biological invasions, and highlights the value of studying spread dynamics in simple, controlled, and replicated settings.

Intraspecific variation, environmental heterogeneity, and their influence on metapopulation dynamics in the freshwater snails of Guadeloupe

J.H. Pantel ⁽¹⁾, T. Lamy ⁽²⁾, J.P. Pointier ⁽³⁾, P. Jarne ⁽¹⁾, and P. David ⁽¹⁾

⁽¹⁾ Centre d'Ecologie fonctionnelle et Evolutive, CNRS ⁽²⁾ Santa Barbara Channel Marine Biodiversity Observation Network, University of California, Santa Barbara, UCSB, Marine Science Institute, ⁽³⁾ Centre de Recherches Insulaires et Observatoire de l'Environnement

Metapopulation models are often used to understand whether a single species can persist in a landscape with multiple patches of potentially connected habitat. However, these models do not take into account the coexistence of multiple species inhabiting the same landscape. It is currently unclear whether the assembly of metacommunities can be understood by modeling the metapopulation dynamics of multiple species independently of one another or whether a community context, where species influence one another's extinction and colonization, is needed.

We analyzed metapopulation dynamics for 27 species of freshwater snails inhabiting 278 sites on the island of Guadeloupe, sampled annually from 2001 to 2015. For each species, we used occurrence data to estimate colonization and extinction rates as well as the effects of environmental covariates, such as habitat connectivity and rainfall, using a multistate occupancy model. The Bayesian model estimates the probability of transitioning between occupied and unoccupied states and considers the influence of imperfect species detection and persistence of aestivating snails in dry sites.

For most species in the system, average extinction rates exceeded average colonization rates, but the influence of environmental covariates led to prolonged persistence in some species compared to models where no environmental covariates were considered. Remarkably, the colonization and extinction parameters, inferred only from annual transitions between occupied and unoccupied states of sites and therefore in the absence of any species-specific trait or composition information, represented known dimensions of niche partitioning among the various species. We also successfully modeled intraspecific variation in metapopulation dynamics for one of the species. However, the models do not yet take into account species interactions, and do not consider that the extinction and colonization rates of some species may differ after the extinction of other species. An important next step for metapopulation models is to determine the influence not only of environmental heterogeneity among sites, but also intra- and interspecific biodiversity in the system.

A conceptual and empirical framework for unifying trait ecology and community phylogenetics

P. Perez Neto ⁽¹⁾

⁽¹⁾ Concordia, Montreal, Canada

Understanding the mechanisms by which species assemble into local communities has a long history in ecology, yet it is one of the most active fields of ecological research today. The study of mechanisms underlying complex spatial patterns of biodiversity has a long and challenging history because of the idea that ecological communities have intractable multidimensional spatial patterns that are hard to describe and explain. Two emerging fields, metacommunity ecology, and trait-based and phylogenetic community ecology have been providing important insights into the complex nature of regional and local processes structuring biodiversity patterns at different spatial scales, though rather independently. Because metacommunity studies are often based on patterns of species distributions and co-occurrence, they tell us little about how community assembly actually results from the interactions between local and regional processes, e.g., Does low connectivity in warmer patches versus high connectivity in colder patches facilitate or hinder species co-existence? Alternatively, trait and phylogenetic community ecology explore how species that share similar traits (morphology, behaviour, physiology) and evolutionary histories (phylogenetic relationships) coexist, though they do not sufficiently examine trait and phylogenetic patterns in relation to local and regional mechanisms, particularly ignoring spatial and multi-scale environmental effects. In this presentation, I will try to summarize the different approaches in trait and community phylogenetics into a single framework compatible with metacommunity ecology that explores local and regional processes underlying species distributions and their patterns of co-occurrence.

Seasonality, acclimation and biotic interactions under climate change

V. Nilsson-rtman ⁽¹⁾

⁽¹⁾ University Lund, Sweden

Many organisms can respond beneficially to prolonged temperature exposures, a phenomenon known as acclimation. Although it is widely believed that acclimation should be beneficial in seasonal environments, it remains poorly understood how latitudinal differences in acclimation will affect biotic interactions under climate change. We present a conceptual model showing how both the magnitude and the rate of seasonal changes in temperature determine the adaptive benefit of acclimation at different latitudes. To test predictions from the model, we performed a microcosm experiment using competing species of damselflies that differ in latitudinal distribution. We find that weakly acclimating high-latitude species can become

outcompeted by strongly acclimating mid-latitude species under the seasonality imposed by climate change. These findings highlight the need to incorporate the rate of acclimation in predictive climate change frameworks.

Coping with life in soil: comparative analysis of springtail genomes

D. Roelofs ⁽¹⁾

⁽¹⁾ University of Amsterdam, Netherlands

Collembola (springtails) represent a soil-living lineage of hexapods in between insects and crustaceans. Consequently, their genomes may hold key information on the early processes leading to evolution of Hexapoda on land. Recently, we generated transcriptomes and very high quality reference genomes for two collembolan species, *Folsomia candida* and *Orchesella cincta*, using Illumina and Pacific Bioscience sequencing platforms.

Total size of *O. cincta* genome is 280 Mbp, while *Folsomia* genome is about 60 Mbp smaller in size. In contrast, *F. candida* contains 28.734 genes, while *O. cincta* contains about 20.459 genes. Analysis of synonymous mutation rates among orthologous gene pairs shows that the extended gene repertoire in *Folsomia* was caused by whole genome duplication. Also, extensive gene family expansions and contractions seem to have driven the divergence between the two springtail species. Several expanded gene families could be linked to evolution of stress tolerance in the soil. Still, about 30% of gene clusters did not show any homology to organisms in genome databases, suggesting that they evolved *de novo* in springtails.

About 1.5-1.8% of the genes have evolved after horizontal gene transfer (HGT) events. Remarkably, a gene cluster resembling a complete functional antibiotic biosynthesis pathway could be identified among HGT genes in *Folsomia*, and active β -lactam compounds could be detected *in vivo*. This is in line with previous observations that *Folsomia* is very resistant to microbial pathogens, which are abundant among soil microbial communities. Finally, an unusual high number of HGT genes in both springtail genomes seem to originate from fungi. They mostly code for enzymes involved in cell wall degradation, suggesting that they were instrumental in adaptation to specific food resources in the soil ecosystem. I will discuss these findings in the context of arthropod evolution.

Eco-evolutionary resilience in the Anthropocene

M. Urban ⁽¹⁾

⁽¹⁾ University Connecticut, US

Understanding the resilience of natural systems to anthropogenic disturbances is necessary to predict and ameliorate future impacts on biodiversity and ecosystem dynamics. Yet, most research fails to address one or more of these fundamental forms of resilience, and these gaps currently limit our ability to predict ecological responses with accuracy. Here I evaluate evidence for both ecological and evolutionary resilience in response to the climate-fueled expansion of an apex predator in temporary ponds. Results demonstrate that the apex predator is substantially affecting community and ecosystem properties in whole-pond manipulations. Experiments show that two prey species have adapted to the predator at fine scales at one field site. We show how these adaptations could increase the resilience of some, but not all, ecological properties of ponds. However, populations located outside of the current marbled salamander range are adapted to other selection regimes that could interfere with these dynamics as the predator spreads north. Understanding the full complexity of both ecological and evolutionary responses will often be necessary to predict the future of biodiversity and ecosystems in the Anthropocene.

Regular and flash talks: spatial ecology and evolution

Intra- and interspecific genetic composition of a meta-community: The *Phengaris alcon* system

H. De Kort ⁽¹⁾, M. Baguette ⁽¹⁾ and V. Stevens ⁽¹⁾

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Environmental changes affect species beyond their individual ability to respond directly to these changes. Abiotic disturbances may genetically and/or plastically alter the dispersal, phenology and morphology within a species, thereby posing new challenges to species directly or indirectly depending on them. More specifically, environment-driven changes in the fitness of a species population may strongly compromise the local survival of interacting species depending on their ability to co-evolve. Understanding such eco-evolutionary dynamics is key to the preservation of community functions and ecosystem services in the context of global change. In an attempt to gain insights into the effects of habitat fragmentation and temperature on the genetic diversity of the various players in a meta-community, we collected DNA samples from the *Phengaris alcon* butterfly, its plant host *Gentiana pneumonanthe*, and its ant host *Myrmica scabrinodis* at ca. 30 Pyrenean locations differing in altitude and degree of connectivity. Pooled RADseq was used to obtain approximate genetic marker (SNP) allele frequency estimates for each population. The resulting SNP datasets are being examined for intra- and interspecific patterns of genetic diversity in relation to habitat connectivity and altitude using population and multivariate landscape genetic analyses. Population genetic diversity (expected heterozygosity) was strongly positively correlated between *P. alcon* and its plant host *G. pneumonanthe* ($R=0.74^{***}$), as opposed to its ant host *M. scabrinodis* ($R=0.15$), which may suggest that dispersal among, and drift within, *P. alcon* populations are governed by factors affecting the diversity within its least widespread host species. The relative contributions of landscape connectivity and altitude to this pattern are currently being assessed.

Local adaptation despite gene flow through habitat choice

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Local adaptation is a central eco-evolutionary process driving response to environmental changes, population differentiation and speciation. Limited gene flow or strong local selection have been considered as pre-requisites for local adaptation to occur, but accumulating evidence for local adaptation with high gene flow and weak selection challenges classical theory. One explanation would be if gene flow is due to a non-random subset of genotypes from source populations, as should occur with habitat choice, but experimental evidence for this effect is lacking. Here, we experimentally demonstrate a temperature-based adaptive habitat choice in spatially explicit microcosms of the actively dispersing ciliate *Tetrahymena thermophila*. Furthermore, we demonstrate that this adaptive habitat choice favours local adaptation at the upper margin of the species thermal niche. Our study challenges the idea that high gene flow generally counteracts local adaptation and instead shows that adaptation to novel environmental conditions can in fact be facilitated by high gene flow in the presence of habitat choice.

Movement variation matters for predicting dispersal of *Tetrahymena* ciliates

N. Schtickzelle ⁽¹⁾, J. Clobert ⁽²⁾ and F. Pennekamp ⁽¹⁾

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Understanding how and when individual movements translate into dispersal between populations is a long-term goal in ecology. Whereas movement is defined as any change in the spatial location of an individual, dispersal is more narrowly defined as a movement that may lead to gene flow. Being a three phase process, dispersal also comprises behavioural decisions that may be detectable in the underlying movement behaviour. Dispersing individuals have been shown to have specific sets of traits that help them to cope with the costs of dispersal, and movement behaviours that mitigate costs should be under selection. Individual movement behaviour has been shown to have a genetic component, an environmental component and some interactions between the two. Few studies have linked genotype, movement behaviour and dispersal, due to the difficulty of measuring all these parameters simultaneously. Using the actively dispersing unicellular, aquatic model organism *Tetrahymena thermophila* in two-patch microcosms, we quantified individual cell

movement and dispersal rate experimentally for 44 genotypes. We then used individual based simulations to predict dispersal from movement data and assessed the match with observed dispersal rates. Genotypes were shown to express different movements in terms of speed and path linearity. We also detected marked movement differences between individuals that dispersed and those that remained resident, further mediated by the genotype. Movement simulations showed that genetic differences in small scale movement were a good predictor of the variations of dispersal rate among genotypes (38% explained variation). However, accounting for within genotype differences that indicate different movement strategies for dispersers and residents improved model predictions and resulted in more than 50% of explained variation in observed dispersal rate, acknowledging that other factors than just the movement are important. A detailed understanding of movement variation has hence the potential to improve dispersal predictions on broad spatio-temporal scales.

Genetic connectivity of the Skunk Clown Fish in the Indian Ocean using different types of markers

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Knowledge of connectivity, the exchange of individuals among populations on coral reefs, is vital for a correct spacing of Marine Protected Areas. For almost all coral reef associated fishes, dispersal between reefs in this patchy environment is limited to a weeks to months-long pelagic larval stage. This study uses the Skunk Clown Fish (*Amphiprion akallopisos*) as a model species to assess connectivity. It has a disjunct distribution, occurring in the Western Indian Ocean (WIO) and the Eastern Indian Ocean (EIO), separated by more than 4.500 km of open sea. We use a combination of mitochondrial (MtDNA, Control Region) and 15 highly polymorphic microsatellite markers. Fin tissue of 394 individuals from 21 different sites in the WIO (Kenya, Tanzania, Madagascar, and Mozambique) and the EIO (Indonesia) was analysed. Mitochondrial and nuclear markers concurred in detecting strong population structure between the EIO and the WIO populations (AMOVA: $ct = 0.63$; $F_{ct} = 0.10$ respectively, $P < 0.001$ both), and panmixia within the EIO. Within the WIO, however, results were different depending on the marker. With MtDNA, a genetic break was detected between the East-Madagascar population of St-Marie and the rest. Microsatellite markers also identified genetic differentiation between Madagascar and the East African coast, but the break was located more to the West of Madagascar. Microsatellite also revealed differentiation between Northern Kenyan populations and the rest, not detected by MtDNA. Both genetic breaks can be explained by dominant sea surface currents that promote larval detention in the Mozambique Channel, creating a barrier to dispersal across the channel, and the influence of the Somali Current which may hamper dispersal towards North-Kenya

from populations further south. Alternatively, as demonstrated using DAPC, the differentiation of the North-Kenyan populations may be driven by hybridization with sister species *Amphiprion nigripes*, occurring in the Central Indian Ocean.

Conditional dispersal in response to food shortage and predator cues in an arachnid

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It is renowned that animals move away from their home range in response to different external stimuli, like mate searching, climate changes, food shortage and presence of predators. Such conditional responses are, however, not fixed and expected to be strongly dependent on the environmental cue. Moreover, we expect changes to happen not only in dispersal rates, but also in the phenotypic profile of the dispersing individuals. Both numbers and identity may have strong consequences on both short- and long-term population dynamics. In order to answer this question, we prepared a two-by-two experimental design in which we crossed the effect of food shortage and the presence/absence of predators cues on the dispersal propensity of the two-spotted spider mite *T.urticae*. Synchronized individuals from a stock population were moved to different leaf cutouts, each of which contained one of the four treatments, and left free to disperse towards identical, non-colonized patches; after 48 hours, they were collected and their movement patterns analyzed. We also monitored their ecological performances for one generation after the dispersal event in a food-rich, stress-free environment and recorded traits like mortality, fecundity and offspring development rate to highlight any difference between the treatments. From preliminary analysis, we inferred that the number of dispersing mites in low-food treatments is, as expected, higher than in the control patches; however, when exposed to predator cues, mites tend to move less than when the cues are absent, a behavior completely opposite to what expected a priori. More analysis are actually in progress to determine if there are also differences in the quality (dimension, behavior, ecological performances) of the dispersing individuals between treatments.

Costs and consequences of dispersal evolution in a ciliate model system

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In spatially structured populations, dispersal carries around individuals and genes. Dispersal may therefore act as an evolutionary engine, driving evolutionary processes and local adaptation. However, we still know relatively little about how dispersal itself evolves. What are the ecological factors driving dispersal evolution, and does its evolution feed back on other life-history traits? Here we revisit a recently explored idea that evolution of increased dispersal may help accelerate range expansions. Using experimental microcosm populations of the freshwater protozoan *Paramecium caudatum*, we demonstrate a rapid and strong response to directional selection for increased dispersal, and a weak and slow response to selection for decreased dispersal. Divergent selection on dispersal was accompanied by the evolution of trade-offs with population growth parameters and biomass production (cell size). Surprisingly, *Paramecium* from high-dispersal selection lines also swim less fast than their counterparts from low-dispersal lines, indicating that the mechanistic link between swimming activity and dispersal is less straightforward than anticipated from similar experiments with the ciliate *Tetrahymena*. Combined phenotypic and molecular analysis further suggests that a large part of the observed evolutionary changes is explained by selection from standing genotypic variation in the founder population. Taken together, our experiment illustrates how relatively simple experimental setups can produce complex and biologically relevant results. One general implication of our results is that dispersal evolution may be limited by trade-offs with other life-history traits, thereby setting a speed limit to range expansions.

Seascape genetics of a top predator, European sea bass

F. Volckaert ⁽¹⁾

Local adaptation is often found to be in a delicate balance with gene flow in marine species with high dispersal potential. Genotyping with mapped genome-derived markers and advanced statistical analyses taking into account the environment are proven tools to uncover the drivers of adaptation. Using a panel of 2459 single nucleotide polymorphisms (SNPs) sourced from a double digest RAD sequencing exercise with a custom made bioinformatics pipeline, we genotyped 32 geographic samples ($n = 1039$) of European sea bass (*Dicentrarchus labrax* L.) caught in the Northeast Atlantic Ocean and Mediterranean Sea. In total 2349 neutral SNP loci identified three units in the Atlantic Ocean: northern North Sea, from the southern North Sea to off the coast of Galicia, and off the Portugese coast and the Strait of Gibraltar. The latter group showed evidence of a historical secondary contact zone with introgression of the genome of the Mediterranean clade in the genome of the

Atlantic clade. SNP loci identified in the Mediterranean basin four units: western Mediterranean, Adriatic and Ionian Sea, Levantine Sea and Aegean Sea. The 110 outlier SNP loci were used for a node-based seascape analysis, which pointed to the importance of distance and temperature (showing a latitudinal gradient) in explaining the genetic structure. Our results are consistent with published evidence and point to the importance of historical factors, contemporaneous dispersal and local adaptation.

A planktonic diatom displays genetic structure over small spatial scales

J. Sefbom ⁽¹⁾

Marine planktonic microalgae have a potentially global dispersal, yet reduced gene flow has been confirmed repeatedly for several species. Over larger distances (>200 km) geographic isolation and lack of oceanographic connectivity have been recognized as instrumental in driving population divergence. Here we investigated whether similar patterns can be observed at smaller (6-152 km) geographic scales. Specifically we tested whether microalgae are panmictic or structured, and whether geographic isolation and/or oceanographic connectivity are equally significant barriers to gene flow at geographic distances of only <152 km. To test this we established 425 clonal cultures of the planktonic diatom *Skeletonema marinoi* collected from 11 locations in the Archipelago Sea (northern Baltic Sea). The region is characterized by a complex topography, entailing several mixing regions of which the sampling area included four. Using eight microsatellite markers and conventional F-statistics significant genetic differentiation was observed between several sites. Patterns of genetic differentiation could not be explained by geographic isolation or oceanographic connectivity. Our data reveal that, despite their high dispersal potential, significantly diverged populations can also develop over small spatial scales. In addition, our results suggest that biological characteristics and historical events may be more important barriers to gene flow at small spatial scales.

Gene flow and effective population sizes of the Alcon blue butterfly *Maculinea alcon* in a highly fragmented, anthropogenic landscape

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Understanding connectivity among populations in fragmented landscapes is of paramount importance in species conservation because it determines their long-term viability and helps to identify and prioritize populations to conserve. Rare and sedentary species are particularly vulnerable to habitat fragmentation as they occupy narrow niches or restricted habitat ranges. Here, we assess contemporary inter-population connectedness of the threatened, myrmecophilous butterfly, *Maculinea alcon*, in a highly fragmented landscape. We inferred dispersal, effective population sizes, genetic diversity and structure based on 14 locations of *M. alcon* in Belgium and the Netherlands using data from 12 microsatellite loci. Despite the reported sedentary behaviour of *M. alcon*, we observed moderate levels of contemporary dispersal between patches, but only in landscapes where populations were located within a distance of 3 km from neighbouring populations. Estimates for effective population sizes (N_e) were very low (ranging from 1.6 to 17.6) and bottleneck events occurred in most of the studied populations. We revise the functional conservation units delineated based on a former mark-release-recapture study, and formulate appropriate conservation strategies to maintain viable (meta)populations in highly fragmented, anthropogenic landscapes.

Regular and flash talks: Evolution of/in metacommunities

Effect of island size and dispersal on adaptation in a mainland-island system

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In a mainland-island system, island size and distance from the mainland are key factors for population success in colonizing new habitats. On one hand, small islands sustain smaller populations than large ones. Small populations are therefore more vulnerable to extinction and to experience a reduced genetic variation, inbreeding depression and genetic drift. On the other hand, distant islands receive less immigrants from the mainland than near ones. Immigrants can boost genetic variation, providing genetic and demographic rescue, necessary for adaptation. Here, we conducted an evolutionary experiment simulating a mainland-island system to test the effect of island size and immigration on adaptation to a novel habitat. From a mainland population of the two-spotted spider mite (*Tetranychus urticae*) on bean plants, we started island populations on tomato plants. Each island varied in size and the level of immigration from the mainland. Both island size and immigration have a positive effect on adaptation after controlling from juvenile and maternal effects. Populations from small islands never adapt to the tomato islands, regardless dispersal. These populations additionally are smaller and experience more extinction events than their larger counterparts. although Immigration from the mainland does not affects population sizes, it helps reducing extinction, especially important for populations in small islands. Adaptation is also a function of time and we show the time that a local population have been on a tomato island can influences its level of adaptation. Our results experimentally show how island size and dispersal can jointly affect adaptation to novel habitats.

Evolution-mediated priority effects: implications for the distribution of genetic variants and species

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The importance of rapid evolution and eco-evolutionary interactions in determining ecological processes is rapidly gaining acceptance. Here we argue that eco-evolutionary interactions may especially be important during colonization and have longstanding effects on population and community composition and features. Adaptation following colonization can produce a strong positive feedback loop that promotes priority effects and context-dependent trajectories of population or species assembly. Monopolization, and more generally evolution-mediated priority effects, can influence ecological patterns at multiple scales of space, time, and biological organization. We highlight some underappreciated implications for our understanding of population and landscape genetics, adaptive evolution, community diversity, biogeography, and conservation biology.

A dynamic model for phylogenetic community ecology

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The classical approach in phylogenetic community ecology involves static randomization test to detect non-random community structure. Here we show with a dynamic model of community assembly that ignoring speciation history and spatial structure may lead to incorrect conclusions, and hence previous inference on the role of habitat filtering or competition may be incorrect.

The evolution of the G-matrix: an example of *Daphnia magna*

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Central questions at the interface between ecology and evolution are how selection changes genetic variance in natural populations and whether and which genetic correlations limit the ability of populations to respond to selection. Selection works on different traits at the same time and the multivariate genetic relationships among a set of traits can be summarized by the additive genetic variance-covariance matrix (G). The additive genetic variance-covariance matrix describes patterns of genetic variation for multiple traits in terms of their variance and covariance and may therefore provide information on evolutionary potential in multivariate space and genetic constraints. A key question is, however, whether the G-matrix itself can evolve. We estimate additive genetic variance-covariance matrices for a *Daphnia magna* population sampled at three different time points corresponding to different fish predation pressures (i.e. from no fish to high fish to reduced fish predation pressure). Using recently developed methods involving Bayesian statistics, Monte-Carlo Markov-chain and tensor methods, we investigate how the variance-covariance matrix changes through time, quantify genetic constraints, and evaluate the genetic basis of multivariate plasticity in the studied *D. magna* population.

The evolution of an optimal size distribution in food webs

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Size is a crucial factor in explaining variation in metabolic rate between individuals. On its turn, metabolic rate interacts with crucial aspects of organisms such as their developmental strategies and dispersal, thereby shaping an individual's life history.

Because of the size dependency of both life history and dispersal, we expect habitat fragmentation to induce a strong selection pressure on the mean size and its variance on species associated in food webs. The inclusion of size evolution among- and within species within food webs is thus essential to understand the trait-distribution of species belonging to different trophic levels in spatially structured populations and communities. Such evolutionary responses are then again expected to feedback on food web properties and functioning.

Starting from a simple individual-based resource-consumer model we demonstrate how variation in habitat fragmentation affects the optimal size distribution within food webs.

Regime shifts in eco-evolutionary systems

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Regime shifts and hysteresis are well studied phenomena in ecology. However, the study of these phenomena in an eco-evolutionary context has been limited. By means of relatively simple mathematical models on eco-evolutionary dynamics I investigated the presence of regime shifts and hysteresis in systems with eco-evolutionary dynamics and found that regime shifts should indeed be a general phenomena in these systems. More specifically, I find that populations can be in either an optimally or suboptimally adapted regime and that, once a population becomes optimally adapted, effective immigration rate is reduced. Furthermore, newly founded populations normally evolve towards the adapted regime, which can lead to an eco-evolutionary priority effect called monopolization, in which the first few colonizing lineages locally adapt, thereby obtain a competitive advantage over later arriving lineages and outcompete them. The low effective immigration rates of populations in a monopolized regime could restrict their ability to adapt to global change. One noteworthy implication of my findings is that a temporary boost in the immigration rate could mitigate this by causing a regime shift resulting in a persistent higher effective immigration rate.

Modelling the eco-evolutionary dynamics of meta-communities

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Recent advances in meta-community theory have demonstrated the importance of spatial processes such as dispersal for the assembly dynamics of natural communities. The structure of the network of species interactions, as well as that of the spatial network of local communities creates a complex picture of ecological dynamics that ultimately determine persistence and stability of communities at the regional level. In parallel to this research, evolutionary models of food webs have shown that adaptive evolution has the potential to further enhance community persistence and biodiversity. In this talk I will present preliminary results of eco-evolutionary model of meta-communities in which ecological community dynamics of complex interaction networks are coupled with evolutionary dynamics of species traits in a spatially explicit framework. This theoretical framework can be employed to explore the role of the interplay between ecological and evolutionary processes in the emergence of complex ecological networks of interactions that we encounter in nature.

Uncoupling habitat selection from species sorting in aquatic insect communities

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Many studies suggest that colonization patterns of animals involve active habitat selection (HS). However, upon closer inspection, the design of most HS studies does not allow to separate effects of HS from the strict definition of species sorting (SS), i.e. non-selective, unrestricted dispersal followed by differential survival. We propose an improved design to distinguish both processes by contrasting species assemblages that colonize spontaneously in the presence or absence of cues with assemblages that result from differential survival after a regional species pool was inoculated under the same set of conditions. For this, a regional species pool of aquatic insects was inoculated in tanks containing either a free -, a caged - or no fish. The resulting assemblages in covered tanks, only allowing differential survival (SS) and communities in open tanks, also allowing dispersal (HS) were then compared to assemblages that emerged after spontaneous colonization. Patterns emerging in spontaneously colonized communities could not be explained by SS alone, yet were highly similar to patterns that emerged under HS. Manipulating access and emigration in tanks also revealed that some species avoided predator cues but did survive when they were inoculated artificially. We conclude that HS studies would benefit from improved designs that are not limited to colonization of virgin empty patches, followed by quantifying the composition of emerging assemblages in the presence or absence of a cue. Identifying the regional species pool of potential colonists and inoculating these can help to ascertain that emerging patterns are indeed the result of HS.

Regular and flash talks: Evolutionary ecology of stress responses

Urban Heat Islands: The evolution of thermal tolerance, life history, and physiological traits in response to urbanization in the water flea *Daphnia magna*

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Growing urban population densities and the increase of urbanization rates have caused tremendous anthropogenic environmental alterations. Amongst others, urbanization causes microgeographical climate modifications, such as the urban heat island effect. This well-known phenomenon can serve as a proxy to study biological responses to future climate change. Literature is abundant with thermal response studies on a broad range of organisms. However, most field-based studies report phenotypic observations lacking a clear view on the evolutionary background of the observed trait divergence, whereas only a few quantitative genetic studies focus on urbanization and future climate change. In addition, as most studies focus on terrestrial ecosystems, little evidence of adaptive thermal evolution in aquatic organisms inhabiting urban areas is present. We exposed 13 populations of *Daphnia magna*, a key stone grazer in freshwater ecosystems, occurring along a well-defined urbanization gradient to 20 C and 24 C in a common garden experiment. We scored their thermal tolerance (CTMAX) and assessed body condition and haemoglobin content to identify possible adaptive and plastic responses along the urbanization gradient and unravel potential underlying physiological drivers of thermal evolution. We found an increase in CTMAX with higher levels of urbanization and exposure temperature, as well as substantial clonal genetic differentiation in thermal tolerance. Moreover, individuals of urban populations contained higher concentrations of total and haem-containing proteins per unit of dry weight. Our results provide the evidence of adaptive evolution to urbanization and probe for the evolutionary potential and adaptive phenotypic plasticity of rural and urban populations to respond to increasing warming, either as a consequence of urbanization, global warming, or a combination of both. Given the importance of large zooplankton species, these adaptive responses might impact food web dynamics, top-down control of algae and water quality related ecosystem functions as well as the socio-economical value of urban ponds.

Rapid evolution of increased vulnerability to an insecticide at the expansion front in a poleward-moving damselfly

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The increase in mean temperature under global warming is causing widespread poleward range expansions. However, many species are too slow to track their moving climate niche and knowledge about factors influencing the speed of range expansion is crucial from a conservation perspective. One explanatory factor may be pesticide exposure, since it reduces population growth and impairs the flight ability. Moreover, edge populations at the moving range front may have a higher vulnerability to pesticides due to the rapid evolution of traits to increase their rate of spread that shunt energy away from detoxification and repair. We exposed replicated edge and core populations of the poleward moving damselfly *Coenagrion scitulum* to the pesticide esfenvalerate at low and high densities. The pesticide reduced survival and growth rate, and increased development time in the larval stage and negatively affected flight-related adult traits (mass at emergence, flight muscle mass and fat content). At the high concentration the pesticide-induced mortality was 17 % stronger in edge populations. These results indicate that pesticide exposure may slow down range expansion by lowering population growth rates, especially because edge populations evolved a higher sensitivity to pesticides, and by negatively affecting dispersal ability by impairing flight-related traits. Our study highlights the need for direct conservation efforts toward edge populations for facilitating future range shifts under global warming.

A learnt behavioural response to climate change may produce maladaptation

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The role of learning in mate choice has not yet been assessed in ecologically-relevant environments such as those induced by climate change. Here we test whether learning of mate preference leads to (un)suitable mate choice and hence, risk of population extinction. In nature, the tropical butterfly *Bicyclus anynana* alternates wet, intermediate and dry morphologies adapted to corresponding seasons in Africa. Female fitness depends on mating with either forms. Here we showed that: 1) increasing unpredictability of climate during seasonal transitions alters the emergence of seasonal forms; 2) females show an innate mate preference for dry seasonal males, but

females learn new mate preference by exposure to male phenotypes during sexual maturation. Our results suggest that, if learning of female mate preference is based on the most abundant male phenotype present in the environment during sexual maturation, learning mate preference could become maladaptive for the species as a response to global warming.

Thermal adaptation and lowered pesticide accumulation counteract the negative effects of multiple pesticide applications under global warming

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While an increasingly negative impact of pesticides is expected under global warming, this may be counteracted by gradual thermal evolution and the faster degradation rates of pesticides at higher temperatures. Therefore, we investigated in larvae of the damselfly *Ischnura elegans* effects on mortality of multiple pulse exposure to the pesticide chlorpyrifos (CPF) combined with a simulated global warming scenario (ambient + 4C). By studying both low- and high-latitude populations we applied a space-for-time substitution to assess the role of gradual thermal evolution in shaping the vulnerability to CPF under global warming. CPF exposure resulted in a higher mortality, however, under simulated warming (+4C) CPF caused lower mortality than at the ambient temperature (20C). This could be explained by the lower degradation of CPF at 20C leading to a higher accumulation after four pulses compared to the treatment at 24C. This indicates that testing effects of global warming on the impact of pesticides may be misleading in experiments that keep pesticide concentrations artificially constant. Furthermore, this temperature effect on mortality was fine-tuned by local thermal adaptation with at a given temperature the CPF-induced mortality being lowest in larvae tested at their local mean summer water temperature. This pattern suggests that the lower impact of CPF under a temperature increase of 4C because of faster degradation can be further strengthened in case of gradual thermal evolution in the high-latitude larvae.

Aridity promotes bet hedging via delayed hatching in two temporary pond crustaceans along a latitudinal gradient

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Climate change does not only affect average rainfall and temperature but also their variation, which can reduce the predictability of suitable conditions for growth and reproduction. This situation is problematic for inhabitants of temporary waters, whose reproductive success strongly depends on rainfall and evaporation that determine the length of the aquatic phase. For organisms with long lived dormant life stages, bet hedging models suggest that, in variable environments, a fraction of these should stay dormant during each growing season to buffer against the probability of total reproductive failure. Thus far, however, little empirical evidence supports this prediction in aquatic organisms. Here, we study geographic variation in delayed hatching of dormant eggs in natural populations of two crustaceans that occur in temporary rock pools along a 725 km latitudinal aridity gradient in Western Australia. Consistent with bet hedging theory, populations of both species were characterised by delayed hatching under common garden conditions and hatching fractions decreased towards the drier end of the gradient where the probability of reproductive success was shown to be lower. This decrease was most pronounced in the species with the longer maturation time, presumably because it is more sensitive to the higher prevalence of short inundations. Overall, these findings illustrate that regional variation in climate can be reflected in differential investment in bet hedging and hints at a potential higher importance of delayed hatching to persist when the climate becomes harsher. Such strategies could become exceedingly relevant as determinants of vulnerability under climate change.

Evolution determines how warming and pesticides modulate predator-prey interactions with vector mosquitoes

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Both warming and pesticides may strongly alter interactions between predators and prey. Using a space-for-time substitution with damselfly predators from low- and high-latitude populations, we assessed how thermal evolution of the predators may shape the effect of warming (ambient + 4C) and exposure to endosulfan on the predation of damselflies on *Culex pipiens* mosquitoes, and its potential implications

for vector control. Warming was only lethal for the mosquitoes but it reduced predation rates on this prey. Possibly, under warming escape speeds of the mosquitoes increased more than the attack efficiency of the predators. Although endosulfan exposure only caused mortality in mosquitoes, it reduced predation rates by the low-latitude damselflies. This can be explained by the combination of the evolution of a faster life history and associated higher vulnerabilities to the pesticide (in terms of growth rate and lowered foraging activity) in the low-latitude predators and pesticide-induced survival selection in the mosquitoes. Our results suggest that mosquito control efficiency at the high latitude by damselfly predators will be reduced under warming unless high-latitude predators evolve toward the current low-latitude phenotype or low-latitude predators move poleward.

Pathways to mating success differ between urban and rural damselflies

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Urban and rural habitats differ in many aspects with, for example, higher temperatures and a more fragmented landscape in urban areas. These differences may impose constraints on the energy metabolism and morphology of animals, which in turn may affect flight performance and consequently patterns of sexual selection. We tested flight speed and flight endurance of 338 unmated and mated males of the damselfly *Coenagrion puella* from three urban and three rural populations. In addition, we quantified flight-related wing characteristics using geometric morphometrics, and measured two flight-related physiological traits (fat content and flight muscle mass). To investigate effects of the measured traits on mating success, whether these effects were direct or indirectly mediated via flight performance, and differed between urban and rural males, we used structural equation modelling (SEM). Urban males had shorter and slender wings, and a higher flight endurance compared to rural males. This may indicate spatial sorting with only the males with the best flight performance reaching the more isolated urban populations. Importantly, SEM revealed different covariation patterns between traits, flight performance and mating success between urban and rural males. A key finding was that flight endurance had a positive effect on mating success, but only in urban males. This indicates that sexual selection reinforces the effect of spatial sorting on flight endurance in urban populations. Our results highlight that urbanisation does not only affect mean trait values, but also the covariation patterns between traits. Moreover, we stress the importance and benefits of applying SEM to reveal complex networks of relationships, and how these path diagrams may differ between populations exposed to different levels of urbanisation.

Thermal evolution shapes the ability of damselfly larvae to deal with increases in both mean temperature and daily temperature fluctuations

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Global warming studies mainly focus on increases in mean temperature, while climate scenarios also predict stronger daily temperature fluctuations (DTF). Furthermore, several studies indicate that increases in DTF will have greater fitness effects than increases in mean temperature. While gradual thermal evolution may help populations deal with increased temperatures, this has not been explored for increases in DTF. We studied larval growth rates of *Ischnura elegans* damselflies in all combinations of two mean temperatures (20C and 24C) and three DTF scenarios (0C, 5C, 10C). We applied a space-for-time substitution approach by using replicated low- and high-latitude populations to assess the role of thermal evolution in shaping the sensitivity to global warming in the high-latitude populations. Growth rate was higher at 24C, indicating that this temperature is situated in the rising part of the thermal performance curve. However, when combined with the 10C DTF, animals performed worse at 24C. This indicates they exceeded their thermal optimum and experienced increased metabolic demands for body maintenance. The absence of a positive DTF effect on growth at 20C suggests that in this temperature region the increase of the thermal performance curve is quasi linear. The response to the temperature increase and DTFs was latitude-dependent with a stronger growth decrease with increasing DTF at the high latitude. These results underscore a key role for thermal evolution with low-latitude animals being better adapted to higher mean temperatures and higher DTF. Our study illustrates the importance of including DTF when assessing the sensitivity of ectotherms to global warming.

Regular and flash talks: Host-microbiota (inclusive parasite) eco-evolutionary dynamics

Ecological and evolutionary factors drive the specialization of two microsporidian parasites of *Artemia*

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Both ecological and evolutionary factors may shape parasite specialization. Here, we studied the horizontally transmitted microsporidians *Anostracospora rigaudi* and *Enterocytozpora artemiae* in their brine shrimp hosts, *Artemia franciscana* and *Artemia parthenogenetica*, in the salterns of Aigues-Mortes, France. In the field, both parasites infect both hosts, with prevalences ranging up to 90% or more in all host-parasite combinations. First, we studied the disease dynamics of the two microsporidians. Statistical models revealed that *A. rigaudi* is strongly seasonal, a pattern driven by the seasonality of *A. parthenogenetica*, which acts as a reservoir host. Despite this evidence of specialization, *A. rigaudi* is equally infective to both *Artemia* species when tested experimentally. In contrast, *E. artemiae* occurs throughout the year, and is more infective to, and more prevalent in, *A. franciscana*. Second, we used an experimental evolution approach to study the evolution of this specialization, and its underlying trade-offs. Our results suggest that infectivity in the two hosts is linked by a weak trade-off, allowing evolution towards generalism. However, this is counteracted by a strong trade-off in spore production across hosts, which dominates the final pattern of specialization. Together, these results indicate that *A. rigaudi*, which usually infects *Artemia* populations containing both hosts, has become as generalist as possible given the underlying trade-offs—specifically, it is generally infective to both, while *E. artemiae*, which often encounters *A. franciscana* only, remains specialized across the board.

Life history and eco-evolutionary dynamics in light of the gut microbiota

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In recent years, evidence has accumulated that the gut microbiota is not just a random set of micro-organisms, but rather a complex ecosystem that plays a crucial role in host physiology. In addition to provide their host with metabolic functions that are not encoded in its own genome, gut symbionts affect host traits previously thought to be solely under host genetic control, such as development and behavior. Metagenomics and metatranscriptomics studies further reveals that gut microbial communities can rapidly respond to changes in host diet or environmental conditions through changes in their structural and functional profiles, thus representing an important source of metabolic flexibility and phenotypic plasticity for the host. Hence, gut microbes appear to be an important factor affecting host ecology and evolution which is, however, not accounted for in life-history theory, or in classic population genetics, ecological and eco-evolutionary models. Here, we shed new light on life history and eco-evolutionary dynamics by viewing these processes through the lens of host-microbiota interactions. Especially, we demonstrate that the gut microbiota may be a crucial factor driving adaptation to changing environment, building on the example of adaptation to cyanobacterial harmful algal bloom (cyanoHABs) in the freshwater crustacean *Daphnia*. CyanoHABS in lakes, ponds and reservoirs worldwide have strongly increased in both frequency and intensity, as a result of eutrophication and climate change. Cyanobacteria produce powerful toxins, such as microcystins, which pose severe threats on livestock and human health, and disrupt the whole freshwater community through their strong impacts on zooplankton grazers. Through gut microbiota transplants in *Daphnia*, we showed that the gut microbiota likely mediates both genetic adaptation and acclimatization of zooplankton to cyanoHABs.

Diatom-bacteria interactions: from the field to the lab

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Diatoms are a successful group of eukaryotic microalgae. Since their origin, diatoms share their habitats with bacteria. This has led to strong interdependencies between the bacteria and algae. The interactions are, at least to a certain extent, specific as mostly Proteobacteria and Bacteroidetes are found in association with diatoms. The nature of the interactions are largely unknown, but can range from antagonistic to symbiotic. We found that both diatom species identity and environmental conditions were important in structuring the diatom associated bacterial community. Even closely related diatoms harboured distinct bacterial communities, and that the effect of bacteria on diatom growth could differ between closely related diatom strains. More positive effects of the bacteria on diatoms were observed under nutrient-limited conditions. Apart from effects of the bacteria on diatom fitness, the bacteria also caused remarkable behavioural changes in growth form and aggregation patterns in the diatoms. A competition experiment with different diatoms proved that bacteria can alter the resulting composition of the algal community. Together, our results show that bacteria-diatom interactions are highly specific and condition-dependent, and that they can have important ecological implications for the composition and functioning of the microbial community.

Phenotypic convergence and conservation of immune processes involved in the establishment of detoxifying symbiosis between coastal and hydrothermal annelids

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In chemosynthetic environments such as hydrothermal sources and sulfides-rich coastal sediments, certain marine organisms are regularly colonized by ectosymbiotic bacteria. Here, we describe for the first time, the association of the coastal annelid *Capitella* with a giant bacterium belonging to the *Thiomargarita* genus so far only described as a free-living species or attached to the byssus of hydrothermal mussels. The facultative insertion of this sulfur-oxidizing bacteria in the tegument of the annelid is observed when the concentration in sulfides in the habitat of the worm increases. Our data showed that this ectosymbiosis is controlled by an antimicrobial peptide, namely capitellacin, synthesized and secreted by the epidermis of associated *Capitella* only. While presenting no sequence identities, capitellacin harbors a conserved structure as well as a convergent function with alvinellacin, an AMP described to control the obligatory and detoxifying ectosymbiotic microflora of the hydrothermal annelid, *Alvinella pompejana*. Even if the fluctuating chemosynthetic environment appears as a key point in the establishment and the evolution of the symbiotic association, we highlight that the conservation and/or the convergence

of immune effectors such as AMPs also appear as an interesting factor to understand the functional modalities that govern long-lasting and facultative interactions in extreme environments.

Regular and flash talks: On genomes

Exploring the genetic underpinnings of diapause termination timing in *Daphnia magna* an approach combining QTL mapping and candidate gene association studies in natural populations

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The water flea *Daphnia* is a crustacean zooplankter which escapes unfavourable conditions through the production of diapausing eggs. Populations are adaptively differentiated in their timing of diapause termination, implying that this trait can evolve. However, field monitoring studies indicate that certain *Daphnia* populations were not able to advance their release from diapause sufficiently to adjust to climate driven phenology changes. Here, we present a research strategy to uncover the genetic architecture in control of this trait. Our overall objective is to understand by which evolutionary mechanisms timing of diapause release can evolve and how its evolution is constrained by genetic architecture. In a first step, quantitative trait loci affecting the timing of hatching will be identified, by assessing the hatch timing distribution of diapausing eggs derived from individual clones of the ‘Basel *D. magna* QTL mapping panel’, which was established by the research team of Dieter Ebert (University of Basel). In *Daphnia*, timing of hatching is largely determined by the genotype of the mother. Therefore, we are mapping timing of hatching against the maternal genotype. In a second step, candidate QTLs will be further resolved through candidate gene association studies with natural populations in order to identify causative allelic differentiation.
