



Centre for Marine Evolutionary Biology

Virtual Conference 8–10 March 2021

Evolution of Species Ranges

Book of Abstracts

Organizing committee

Marina Rafajlovic, Department of Marine Sciences, University of Gothenburg

Roger Butlin, Department of Animal and Plant Sciences, University of Sheffield

Kerstin Johannesson, Department of Marine Sciences, University of Gothenburg

Key note speakers

Ary Hoffmann

Opening talk: Evolutionary studies on species ranges. Where were we and where are we heading?

Ary Hoffmann, University of Melbourne, Australia

In an overview of the evolutionary (and ecological) factors determining species ranges published in 1994 (Hoffmann and Blows, *Trends in Ecology and Evolution*), we examined some of the trends emerging from research on the topic. At that time when we commented that “species borders continue to be largely ignored in evolutionary biology” even though researchers had already identified a number of interesting questions that needed to be addressed empirically and theoretically to understand range limits. In this talk I revisit some key issues outlined in that paper and some of the classic studies that were involved. I then briefly consider the renewed relevance of the topic within the current context of managing species under climate change and I point to some ways in which the old issues are being linked new data and approaches. Such issues include the impact of gene flow on range limits, the links between range limits and adaptive variation including plastic responses, the challenges of identifying variation in relevant traits and their genetic basis, the impact of trade offs in limiting ranges, and the roles of small population size at margins in limiting adaptation.

Camille Parmesan

Potentials and limitations of evolution in shaping the impacts of climate change on wild species

Camille Parmesan, SETE - CNRS, France; University of Plymouth, UK; University of Texas at Austin, USA & Michael C. Singer, SETE-CNRS, France

As climate change continues to accelerate, there is an emerging literature on population-level ecological and evolutionary responses that complement the large numbers of studies documenting species' range shifts. Localized responses can take the form of changes in dispersal behavior, voltinism, dietary specialization, camouflage, phenology or microhabitat choice. While studies of underlying processes often reveal variation based on plasticity, rapid changes can also be the results of rapid local evolution. These local changes are expected to differ qualitatively between expanding range limits and range interiors. Better understanding of the interplay between events at range limits and in range centers, and the extent to which plastic vs evolutionary processes prevail are important for conservation planning in the face of continued climate change. We highlight the highly climate-sensitive group of butterflies in the *Euphydryas* (North America) and *Mellitae* (Europe) groups to illustrate the complexity of possible population-level responses to climate change.

Jake M. Alexander

Novel biotic interactions and species range dynamics

Jake M. Alexander, ETH Zürich Eidgenössische Technische Hochschule, Switzerland

Species' distributions are determined by a combination of limits to adaptation across environmental gradients, the outcome of biotic interactions with other species, and dispersal processes. Species' distributions are being reshuffled at unprecedented rates as a result of biological invasions and in response to rapidly changing climate, giving rise to novel communities of resident and range shifting species. I will present evidence from experiments conducted along elevation gradients that the ecological effects of novel competitors can be pivotal for the persistence of plant populations at their trailing range edge as climate warms. We can therefore expect that biotic interactions will also influence selection acting on plants adapting to changing climate, and conversely that the outcome of biotic interactions will be affected by adaption to climate. We can see these eco-evolutionary dynamics playing-out in biological invasions, as species adapt to new climates and also engage in new biotic interactions during range expansion. In sum, combining perspectives from community and evolutionary ecology could lead to a deeper understanding of how the interplay between ecological and evolutionary processes shapes species (re)distributions.

Jon Bridle

Closing talk: Summing up the Webinar

Jon Bridle, Department of Genetics Evolution and Environment, University College London, UK

Presentations

Abstracts are listed alphabetically according to the speakers surname. Authors and affiliations are given under the titles.

Nick Barton

Response of a metapopulation to a changing environment

Nick Barton (IST, Austria), Himani Sachdeva (University of Vienna), Oluwafunmilola Olusanya (IST Austria)

A species that is distributed across heterogeneous environments may adapt to local conditions, and such local adaptation may be necessary for it to exploit a broad range of resources. There is a positive feedback between adaptation and deme size: poorly adapted demes become smaller, making selection less effective in the face of drift and gene flow. Szep et al. (2020, bioRxiv) modelled this process in the island model, by following the joint distribution of deme size and allele frequencies. We extend this approach to ask how metapopulation respond to changes in carrying capacity, or the proportions of different habitats. Our approach is based on the diffusion approximation, which may be approximated by considering the loss and near-fixation of the alleles that underly a polygenic trait.

Jon Bridle

Evolution at ecological margins: how do biotic and abiotic interactions interact?

Jon Bridle (Department of Genetics Evolution and Environment, University College London, UK), Eleanor O'Brien (School of Biological Sciences, University of Bristol, UK), Maaïke de Jong (Netherlands Science Center, Amsterdam), Alex van Rensburg (Department of Genetics Evolution and Environment, University College London, UK)

We will summarise our recent work on two insect systems that tests how ecological limits are determined by interactions between species, the relationship of these interactions with climate, and genetic variation in these parameters. We will put this work into the context of recent population genetic theories of ecological margins. Ecological and genomic data will be included from transplant experiments in rainforest *Drosophila*, and from the evolution of biotic interactions during range shifts in the UK Brown Argus butterfly. Lessons from these data for predicting the evolution and persistence of ecological communities in response to global change will be discussed.

Emma Dawson-Glass

Does pollen limitation limit plant ranges? Evidence and implications

Emma Dawson-Glass (Department of Biology, McGill University, Montreal, Canada), Anna L Hargreaves (Department of Biology, McGill University, Montreal, Canada)

Geneflow plays a central role in the evolutionary flexibility of species range edges, but small or isolated range-edge populations may suffer reduced geneflow due to lack of mates. Outcrossing plants may face an additional challenge –lack of pollinators– if small populations or infrequent flowering fail to attract sufficient visitors. Despite decades of pollen

supplementation experiments, few have tested whether seed set is increasingly limited toward plant range edges. We test this via a quantitative meta-analysis, using a new global data base (GloPol) of pollen supplementation experiments combined with plant occurrence data. We find little evidence that pollen limitation generally increases toward the edges of plant ranges. We also note several challenges that hamper a synthetic understanding of pollinations role in limiting plant distributions, and promising avenues for future research.

Martin Eriksson

The role of phenotypic plasticity during range expansions

Martin Eriksson (University of Gothenburg), Marina Rafajlovic (University of Gothenburg)

Because adaptive phenotypic plasticity may improve the tolerance of a population to variable environmental conditions, it has been suggested that plasticity may be a prominent factor facilitating range expansions. However, during range expansions, populations at the expansion front are typically small, and hence subject to strong genetic drift. This may allow for the establishment of locally disadvantageous alleles. As a consequence, an expanding population may evolve either locally adaptive or maladaptive plasticity. In the latter case, expansion may be halted. Furthermore, even if locally adaptive plasticity evolves, it may involve large fitness costs. In this case, successful range expansions will rely also on sufficient amount of local genetic adaptation, that populations at the expansion front may be lacking. To our knowledge, these intricate feedback dynamics of evolving plasticity and genetic adaptation during range expansions have not been studied to date. Here, we employ computer simulations to assess 1) the role of evolving phenotypic plasticity during range expansions over steepening environmental gradients, and 2) how the process of range expansion itself impacts on the evolution of plasticity. Our results will also allow us to assess the conditions under which West-Eberhard's "plasticity-first" verbal model applies.

Luc De Meester

An eco-evolutionary perspective on species ranges

Luc De Meester (Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Germany & KU Leuven, Belgium)

In this contribution I want to ask the question when ecological and when evolutionary processes dominate in shaping species ranges. In our models and approaches to the study of species ranges and the role of evolution therein, we need to explicitly incorporate the role of the presence of other species. The concepts underlying the evolving metacommunity framework might provide some guidance. For example, guiding principles for assessing the relative importance of ecological and evolutionary processes in setting range limits or fostering range expansion might be the race between species sorting and intraspecific trait change as well as the race between local and regional processes (local sorting versus immigration) in achieving a match of community trait distributions to the local environment.

Louise Fouqueau

The benefit of asexuality at the range margins

Louise Fouqueau (Biological Station of Roscoff, Sorbonne University, France), Denis Roze (Biological Station of Roscoff, Sorbonne University, France)

While temporally changing environments generally favour sex and recombination, the effects of spatial environmental heterogeneity have been less explored. Interestingly, asexual lineages often present different geographical distributions than their closest sexual relatives, a phenomenon described as “geographic parthenogenesis”. In a number of cases, asexuals are found at the limit of the species’ range, such as at higher altitudes or latitudes, which could further impact the adaptation and/or the expansion of the metapopulation. During my presentation I would like to present the theoretical models that I have developed to examine the validity of different hypotheses maintained to explain the benefit of asexuality at the range limits.

Kimberly Gilbert

The transition from background selection to associative overdominance promotes diversity in regions of low recombination

Kimberly J. Gilbert (University of Bern, Bern, Switzerland), Fanny Pouyet (Université Paris-Saclay, Paris, France), Laurent Excoffier (University of Bern, Bern, Switzerland), Stephan Peischl (University of Bern, Bern, Switzerland)

Linked selection is a major driver of genetic diversity. Selection against deleterious mutations removes linked neutral diversity (background selection [BGS]), creating positive correlations between recombination rates and genetic diversity. Purifying selection against recessive variants, however, can also lead to associative overdominance (AOD), due to apparent heterozygote advantage at linked neutral loci that opposes the loss of neutral diversity by BGS. We present a model describing how and under which conditions multi-locus dynamics can amplify the effects of AOD. We derive the conditions for a transition from BGS to AOD due to pseudo-overdominance (a form of balancing selection that maintains complementary deleterious haplotypes that mask the effect of recessive deleterious mutations). Simulations confirm these findings, showing that multi-locus AOD can increase diversity in low-recombination regions much more strongly than previously appreciated. While BGS is known to drive genome-wide diversity in humans, the observation of a resurgence of genetic diversity in regions of very low recombination is indicative of AOD. We identify 22 regions in the human genome consistent with multi-locus AOD. Our results demonstrate that AOD may play an important role in the evolution of low-recombination regions of many species and could have implications for the spread of deleterious load during species range expansions.

Jane K. Hill

Climate change and species range shifts

Jane K Hill (Department of Biology & Leverhulme Centre for Anthropocene Biodiversity, University of York, UK)

Species ranges are not static, and my research group has been documenting rates of range shifting uphill and/or to higher latitudes by species tracking climate change, which have resulted in expansions at cool leading-edge boundaries and local extinctions at warm trailing-edge boundaries. Such range shifts are evident over the past few thousand years of post-glacial warming, as well as over the past few decades of anthropogenic warming. Our research has shown that these range shifts have impacts for community composition and their size-structure, as well as the distribution of genetic diversity, which may impact future range shifts and adaptation in situ. I will discuss our recent research which is revealing genetic consequences of post-glacial range expansion, and how habitat availability affects anthropogenic range shifting rates. There is considerable variation in rates of range shifting among species within all taxa we have studied, and difficulties in improving habitat connectivity imply that translocations of genes and species may be necessary for some species and populations, if breeding habitats are too isolated to be reached by colonists or for gene flow.

Robert D. Holt

How does temporal variation influence the eco-evolutionary dynamics of range limits? Messages from source-sink models

Robert D. Holt (University of Florida, USA), James H. Peniston (University of Florida, USA), Michael Barfield (The University of Florida, USA)

Temporal variation is ubiquitous in nature and can lead to variation in birth, death, or dispersal rates. A well-established result in conservation biology is that temporal variation can enhance extinction risk, particularly in populations low in abundance. One might thus expect that along environmental gradients, temporal variation might lead to shrinkage in species ranges. In this talk, we will present models suggesting the opposite might at times be true. Models for adaptive evolution in source-sink systems (with either clonal variation, or quantitative genetic variation, using both analytical models and individual-based simulations) reveal that moderate fluctuations in birth, death, or dispersal rates can at times facilitate adaptation to a sink habitat. Interactions with other species (e.g., competitors, natural enemies, mutualists) can provide a particularly potent source of temporal variation in demographic parameters, with implications for the interplay of community interactions and evolution in determining species' range limits along environmental gradients.

Jamie Hudson

The history of anthropogenic transport of species shape colonisation histories of biological invasions

Jamie Hudson (School of Ocean and Earth Science, University of Southampton, National Oceanography Centre, UK), Hanno Seebens (Senckenberg Biodiversity and Climate Research Centre, Frankfurt, Germany), Mark A Chapman (Biological Sciences, University of Southampton, UK), Marc Rius (School of Ocean and Earth Science, University of Southampton, National Oceanography Centre, UK; Centre for Ecological Genomics and Wildlife Conservation, Department of Zoology, University of Johannesburg, Auckland Park, South Africa)

An undesirable consequence of the Anthropocene is the global transport of non-indigenous species (NIS). Unravelling introduction pathways of NIS is key for understanding the current distribution of species. However, little is known on how the history of anthropogenic transport affects our ability to reconstruct introduction routes. Here, we first investigated shipping networks (which act as NIS vectors) from 1750 onwards to infer the history of anthropogenic transport among world's regions. We then genotyped 550 individuals of two widespread marine NIS to obtain population genomic data from across their ranges and to reconstruct their introduction routes using Bayesian methods. The preliminary results highlight the importance of considering the history of anthropogenic transport for the study of NIS dynamics and for understanding present-day species distributions.

Kamal M. Ibrahim

Genetic Consequences of Anthropochorous Range Expansion of Gazelles on Islands around the Arabian Peninsula

Kamal M. Ibrahim (School of Biological Sciences, Southern Illinois University Carbondale, USA), Phillip C Williams (School of Biological Sciences, Southern Illinois University Carbondale, USA), Rufayda Adam (School of Biological Sciences, Southern Illinois University Carbondale, USA)

Several insular populations of gazelles on islands in the Red Sea, the Gulf of Aden, the Arabian Sea, the Gulf of Oman, and the Persian Sea show dwarfism compared to their mainland counterparts. We discuss their genetic and morphometric divergence with special emphasis on their colonization histories and possible evolutionary causes and trajectories of the size dimorphisms. As a case study, we present simulation-based analyses of genetic data obtained from island (Dahlak Kebir on the Red Sea) and mainland (coastal Eritrea) populations of Soemmerring's gazelles, *Nanger soemmerringii*. Isolation with migration (IM) analyses reveal split time and estimates of demographic parameters that are consistent with recent colonization.

Kerstin Johannesson

The genomics of a recent expansion of a facultative asexual seaweed

Ricardo T. Pereyra (Tjärnö Marine Laboratory, Department of Marine Sciences, University of Gothenburg), Marina Rafajlović (Department of Marine Sciences, University of Gothenburg), Kerstin Johannesson (Tjärnö Marine Laboratory, Department of Marine Sciences, University of Gothenburg)

The genetic mechanisms underlying the expansion of organisms into new territories is a central question to understand biological invasions. In facultative asexual species, cloning will interfere with sex and recombination but how this affects the genetic structure during range expansion remains unclear. Genomic analysis of a postglacial expansion of a seaweed (*Fucus vesiculosus*) into a marginal marine ecosystem (the Baltic Sea) revealed that clonal

lineages formed multiple times from sexual lineages and remained dominant at the margins of the expansion. Modelling the expansion shows that clones will spread ahead of sexual lineages, with genetic variation being gained from the accumulation of new mutations in clones but lost through recombination and drift when a local population becomes sexual. This results in strong temporal and spatial fluctuations in genetic variation and a complex population genetic structure shaped by the different phases of clonal and sexual expansion; a pattern that is supported by our empirical data.

Stephen R. Keller

The evolution of genotypic variation and plasticity in climate-adaptive traits after range expansion and fragmentation of the forest tree, red spruce (*Picea rubens* Sarg)

Anoob Prakash (University of Vermont), John Butnor (USDA Forest Service), Stephen Keller (University of Vermont)

Species with fragmented ranges are acutely vulnerable to environmental change. Fragmentation constrains populations from tracking a shifting climate through dispersal, and limits opportunities for gene flow and genetic rescue from maladaptation. Many populations within a fragmented range must depend upon existing plasticity and genetic variation for responding to novel climate pressures. However, we expect the availability of adaptive plastic and genetic responses to vary as a result of historical processes of past range shifts and selection, resulting in heterogeneity in which parts of the range are likely to be resilient versus vulnerable to changing selection pressures. Here, we report on a large-scale common garden study of adaptive phenological traits in red spruce -- a climate-sensitive forest tree with a highly fragmented distribution. We studied the performance of 340 maternal families sampled from 65 populations, from the connected range core in the north to its highly fragmented southern range edge. We estimated phenotypic plasticity, heritability, genetic variation for plasticity (GxE) in phenological traits across three latitudinally arrayed garden sites. The results reveal red spruce's potential for adaptive responses necessary to maintain climate adaptation, and how this variation is distributed across regions that vary in connectedness and hence opportunity for natural migration.

Lesley Lancaster

The range shift – niche breadth hypothesis

Lesley Lancaster (University of Aberdeen, UK)

I will summarize results from some recently published papers in which I reanalyzed classical, macroecological patterns of latitude-niche breadth relationships to understand how a (shared) history of range shifting may have resulted in these famous, global patterns. During warming periods, parallel range shift evolutionary processes of poleward gene flow, release from selection, spatial sorting, and drift are replicated across multiple, range shifting lineages. These parallel spatial evolutionary processes can misleadingly appear to reflect replicated adaptation to (more polar) conditions. Therefore, the methodological and ecological implications of range shift evolution on a global scale are discussed, as well as ways forward.

Alexandre Mestre Perez

Host-symbiont dynamics during colonisation of new habitats: an individual-based modelling approach

Alexandre Mestre Perez (Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia, Spain), Joaquín Hortal (Museo Nacional de Ciencias Naturales, Consejo Superior de Investigaciones Científicas, Spain), Roger Butlin (Department of Marine Sciences, University of Gothenburg), Marina Rafajlovic (Department of Marine Sciences, University of Gothenburg)

We will present an individual-based modeling framework to investigate eco-evolutionary processes underlying range dynamics of symbiont-host associations inhabiting fragmented habitats. The framework will be particularly useful to analyse interactions among processes across scales. We will use object-oriented programming techniques based on C++ language. The framework will include three classes of interacting objects structured in a nested fashion: 1. Land patches with spatial, environmental, and biotic properties; 2. Free-living individuals (i.e. hosts) nested within the land patches; 3. Individual symbionts nested within hosts. Both host and symbiont individuals will have their own phenotype, genotype, and niche properties. Niche properties will define the ways individuals interact with other objects (either land patches, hosts or symbionts) across scales (either within a host, within a land patch or in the off-patch environment during dispersal among land patches). We will propose a variety of specialised versions of this framework that can be used to improve our current understanding of the responses of species ranges to environmental changes, involving dispersal evolution, adaptation and/or phenotypic plasticity, through a multiscale theoretical perspective.

Torsten Nygård Kristensen

A field study on the evolutionary and ecological importance of thermal plasticity in ectotherms across temperate and tropical regions

*Natasja Krog Noer (Aalborg University, Denmark), Michael Ørsted (Aalborg University, Denmark), Simon Bahrndorff (Aalborg University, Denmark), Michele Schiffer (James Cook University, Australia), Ary A. Hoffmann (University of Melbourne, Australia), **Torsten N. Kristensen** (Aalborg University, Denmark)*

Understanding how environmental factors affect thermal tolerance and plasticity of species is crucial for predicting the impact of thermal stress on species abundance and distribution. To date, such data are typically assessed using coarse, low resolution, climate data that may not reflect microhabitat dynamics. Here, we examine the daily temporal variation in heat tolerance in six insects collected in temperate Victoria and four species from tropical Queensland, Australia. Individuals were collected in their habitats throughout the day and immediately tested for heat tolerance. Data on local microclimate were recorded at the collection sites prior to testing. These data were used to pinpoint microclimatic parameters important for determining temporal differences in thermal tolerance and plasticity for individual species. The results have important implications: First, we expand our knowledge of how climate conditions influence physiological performance in the field in non-model species. Second, we reveal that climatic variables of importance for predicting thermal plasticity are species-specific and must reflect the microenvironment that species are adapted to. In conclusion results suggest that coarse scale climate variables that are commonly used for modeling impacts of temperature on species do not necessarily reflect microclimatic events that is critical for thermal adaptation and distribution of species.

John R. Pannell

The effect of range expansions on genetic diversity and mating systems

John R. Pannell (University of Lausanne, Switzerland), Francisco Encinas-Viso (CSIRO, Canberra, Australia), Andrew G. Young (CSIRO, Canberra, Australia), Santiago González-Martínez (INRA, Bordeaux, France), Kate Ridout (University of Oxford, UK)

Range expansions typically coincide with the loss of genetic diversity in range-edge versus core populations as a result of repeated colonisation bottlenecks. The expected loss of diversity applies to not only neutral loci, but also to loci under positive or purifying selection. Because range-edge populations are thus expected to carry both an ‘expansion load’ of deleterious mutations and be subject to fewer selective sweeps, mean population fitness should be lower than in the species core (local adaptation notwithstanding). Nevertheless, colonisation bottlenecks cause range-edge populations to be more inbred, so that within-population inbreeding depression is, perhaps paradoxically, also reduced. This reduction in inbreeding depression can tip the balance in favour of mutations that increase a population’s selfing rate, and thus could be partly responsible for the well-known enrichment in self-fertilizing populations at the edge of species ranges. Here, I summarise theory leading to the above expectations, and present the results of simulations exploring the effect exploring the joint evolution of the mating system and inbreeding depression during a range expansion. I also illustrate the predicted effects of range expansion on genetic diversity in terms analyses of SNP variation in 17,500 genes across the range of the pan-European annual weed *Mercurialis annua*.

Stefan Peischl

Gene surfing of underdominant alleles promotes formation of hybrid zones

*Kimberly J. Gilbert (Institute of Plant Sciences, University of Bern, Switzerland), Antoine Moinet (Interfaculty Bioinformatics Unit, University of Bern, Swiss Institute of Bioinformatics, Institute of Ecology and Evolution, University of Bern, Switzerland), **Stephan Peischl** (Interfaculty Bioinformatics Unit, University of Bern, Swiss Institute of Bioinformatics, Institute of Ecology and Evolution, University of Bern, Switzerland)*

We develop a model for the establishment of clines in non-neutral genetic diversity which occur via heterozygote disadvantage due to the surfing of underdominant alleles during range expansions. We provide analytical approximations for the fixation probability of underdominant alleles, and demonstrate that such alleles can readily establish via gene surfing in 1D range expansions. We extend these results to multiple loci via a mixture of analytical theory and individual-based simulations. We study the interaction between the strength of selection against heterozygotes, migration rates, and local recombination rates on the formation of stable hybrid zones. A key result of our study is that clines created by surfing at different loci can attract each other and align after expansion, if they are sufficiently close in space and in terms of recombination distance. Our findings shed new light on how range expansions interact with selection and recombination, and suggest that range expansions can set the stage for parapatric speciation due to the alignment of multiple selective clines, even in the absence of ecologically divergent selection.

Jitka Polechová

On species' range fragmentation

Jitka Polechová (University of Vienna, Austria)

Himani Sachdeva

Effect of migration, drift and demography on genetic load and extinction in a peripheral population

Himani Sachdeva (University of Vienna), Olusanya Oluwafunmilola (IST Austria), Nick Barton (IST Austria)

We analyse how genetic load (due to deleterious recessive mutations) influences the survival of a peripheral island population subject to unidirectional migration from a large mainland population. Genetic drift inflates load in small populations; increased load causes population numbers to decline, which further exacerbates drift, resulting in a positive feedback which may ultimately extinguish peripheral populations in the absence of migration. We analyse the joint stochastic dynamics of population size and allele frequencies to clarify how extinction (or survival) of peripheral populations is influenced by the interplay between migration, mutation, hard selection, drift and demographic fluctuations. We also explore how changes in migration and/or carrying capacities affect the persistence of peripheral populations.

Justin Travis

The evolution of dormancy during range expansion

Justin Travis (University of Aberdeen, UK), Greta Bocedi (University of Aberdeen, UK), Elizabeth Clark (University of Aberdeen, UK)

We use an individual-based, spatially explicit model to investigate the evolution of seed dormancy during invasion. The landscape is represented as a two-dimensional lattice and dispersal between populations follows a stepping-stone pattern. When a population is at equilibrium on the landscape our model produces results that are consistent with previous theoretical studies: increased seed dormancy evolves due to sib competition and increases as temporal environmental variation increases. We simulate introductions by moving small numbers of individuals from stationary populations to empty landscapes and allow invasions to take place. Almost always, we observe evolution towards reduced rates of dormancy, and this leads to more rapid population range expansion. Behind the invading front there is selection for higher rates of dormancy and the resulting variation in dormancy rates from the core to the periphery can lead to considerable spatial variation in population abundances, particularly in temporally variable environments. Most notably, we observe that decreased dormancy towards the expanding margin reduces the regional resilience of populations to a series of poor quality years.

Yvonne Willi

Ubiquitous trade-offs in the evolution of climate niches and species ranges

Yvonne Willi (University of Basel, Switzerland)

Species range limits, when not caused by dispersal limitation, are a reflection of limits to the ecological niche. Therefore, while the main challenge of understanding distribution limits for ecologists is to define the parameter space that encompasses the niche, evolutionary ecologists face a much larger problem. They need to explain why niche evolution is constrained in general, and at range margins in particular. Both aspects are unresolved, and count among the major gaps of knowledge in evolutionary ecology. Ecological studies

document that most range limits are associated with a change in climatic conditions. In contrast, several evolutionary factors may be involved in constraining the expansion of the climate niche, one of which may be trade-offs on the level of species and on the level of populations. The talk will summarize hypotheses about the involvement of trade-offs in niche evolution and empirical evidence found so far.

Robert J. Wilson

Climate-driven variation in the quality and phenology of novel hosts presents a variable window of opportunity for a range-expanding herbivore

Robert J. Wilson (Museo Nacional de Ciencias Naturales, Madrid, Spain), *James E. Stewart* (College of Life & Environmental Sciences, University of Exeter, UK), *Ilya M.D. Maclean* (Environment & Sustainability Institute, University of Exeter, UK), *Jon Bridle* (Department of Genetics, Evolution & Environment, University College London, UK)

The ability of host specialists to exploit novel resources over expanding ranges depends on the degree of phenological synchrony between trophic levels, influenced by environmental conditions, and the cues, drivers and sensitivity of interacting partners. As geographic ranges shift and environmental conditions change, variation in stimuli over time and space can favour new interactions or generate mismatches. We conducted fieldwork to assess temporal variation in host plant availability for an oligophagous butterfly in the UK. Since the 1990s *Aricia agestis* has increasingly exploited annual host plants *Erodium cicutarium* and *Geranium dissectum*, permitting it to expand its range beyond the more geographically restricted perennial host *Helianthemum nummularium*. Warmer summers have favoured population growth on the annual plants, and in many colonized regions the species has evolved specialism for these novel host associations. Our assessments of host condition and phenology suggest that the ancestral (perennial) host is a more reliable resource, whereas the novel hosts show marked inter-annual and geographic variation in quality and phenology as a function of the climate. The ecological and evolutionary outcomes of range shifts may therefore be sensitive to geographically local and partner-specific effects of climate on phenological synchrony, adding complexity to biotic responses to global change.