



Why do we need to incorporate phenotypic variation into species distribution models?

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Human driven scenarios for evolutionary and ecological changes

Abstract book

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Sp.09: Local adaptation in the Mediterranean

Sp.09-1-Main talk

Why do we need to incorporate phenotypic variation into species distribution models?

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Here I will focus on trees and explore i) how considering phenotypic variation can change species distributions ii) the difficulties arising for accounting for phenotypic variation due to the experimental designs and iii) how species and populations models based on the phenotypic variation can be used in management decisions. Extensive experiments with translocations of several tree species across Europe do exist and can be used to estimate the amount of the variation due to plasticity and to local adaptation with statistical approaches that account for the origins of phenotypic variation. However, in some cases, these experiments do not cover the entire range of the species because they have not been designed to understand the ecophysiological limits of the species. Including phenotypic variation into species distribution models gives a more realistic output than classical species distribution models and allows us to visualize the phenotypic variation at species and population levels, a useful tool to design assisted migration programs for the future.

Sp.09-2-Oral

Ecological mechanisms underlying hybridization and its constraint in genus *Erysimum*

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Hybrid zones have the potential to shed light on evolutionary processes driving local adaptation and speciation. Secondary contact hybrid zones are particularly powerful natural systems where study the interaction between divergent genomes to understand the mode and rate at which reproductive isolation accumulates during speciation. Using 10 microsatellites markers we studied five populations from two *Erysimum* (Brassicaceae) species presenting a secondary contact zone in Sierra Nevada Mountains (SE Spain). We have estimated the genetic differentiation, the genetic structure, and the amount of recent gene flow between populations. We found a narrow unimodal hybrid zone where the hybrid genotypes were more frequent than the parental genotypes. Afterwards, we carried out two experiments to explore the pre-zygotic and post-zygotic reproductive barriers underlying the origin and maintenance of this narrow hybrid zone. Post-zygotic barriers were evaluated performing over 1000 hand crosses on 44 plants from both species till the second generation. While to evaluate the pre-zygotic barriers, a plot of parental and hybrid flowering plants were presented to the pollinators in the natural populations to evaluate their preferences. We did not identify any significant reproductive barrier at the generation of F1 hybrids nor the pre-zygotic barriers. However, we identify a strong and significant postzygotic reproductive barrier in the F2 hybrid production. Our results suggest that the pollinators are the main promoters of the hybrid zone, but a constant migration of plants from the parental population would be necessary for the long-term maintenance of that narrow hybrid zone.

Sp.09-3-Poster

Spatio-temporal flowering patterns in Mediterranean Poaceae. A community study in SW SpainCabrino Cruz, J.¹, García-Castaño, J.L.², Domínguez-Vilches, E.³, Galán, C.⁴

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Grasses are one of the largest plant families and they are worldwide distributed. Numerous studies have focused on the phenology of different plants. However, lower attention has been given to grass species and to the effects of different land covers. The goals of this work were (i) to study the grass community composition in different land covers; and (ii) to assess the importance of the species and the land cover in the grass flowering phenology start and duration in two study years. Twenty-nine sampling points were randomly selected in three different land covers. We found differences among plants covers in grass species composition, showing the scrub the highest number of species. In addition, we detected differences on the flowering start date for some species –i.e. *Hyparrhenia hirta* (L.) Stapf was the earliest species whereas *Melica magnolii* Gren. & Godr. was the latest one-. Moreover, we detected differences for the land cover type and the study year. Species in the scrub flowered the latest whereas they flowered the earliest in the pasture in 2014 and in the riverbank in 2015. In general, the flowering start occurred later in 2014 than in 2015. In relation to the phenological length, differences for some study species were detected, being the shortest season for *Aegilops triuncialis* L. and the longest one for *Hyparrhenia hirta*. This study provides information for species and, especially, a spatially dependent answer, which might be important in the scenario of the predicted climate change.

Sp.09-4-Oral

Clinal variation in phenological behavior, size at flowering and biomass allocation reveals adaptation to climatic divergence in annual *Thrinchia hispida* across its rangePedro, M. de¹, Mayol, M.², González-Martínez, S.C.³, Regalado, I.⁴, Riba, M.⁵

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Understanding and predicting the consequences of global change on species persistence and distribution requires considering the extent and potential for local adaptations. It is generally accepted that local adaptation in plants is a widespread phenomenon. However, recent theoretical and empirical work suggests that adaptation could be constrained in short-lived plants during range expansions due to demographic processes and phenotypic and genetic correlations among traits. Our aim is to produce new experimental evidence of evolutionary mechanisms during plant range expansions. Here we present preliminary data on population differentiation in several life history traits: time to germination and flowering, size at flowering and biomass allocation in 42 populations covering the whole range of the short-lived colonizing plant *Thrinchia hispida*. We found significant phenotypic variation among population in all measured traits in a common garden experiment. The timing of germination and flowering followed environmental clines with temperature and inter-annual variation of precipitation, indicating potential drivers of selection. Size at flowering was strongly correlated with phenology. Compared with plants from northern populations, plants from southern populations germinated later and flowered earlier, were smaller and allocated more biomass to reproduction. We conclude that southern populations have evolved to face short growing periods by evolving traits favoring short life cycles. This study provides clear evidence for local adaptation in phenological traits in response to environmental varying selection, and highlights the role of selection on phenological traits in explaining the variability in other correlated traits (e.g. size) closely linked to fitness.

Sp.09-5-Oral

Reproductive isolation of colour morphs in *Lysimachia arvensis* through a combination of incomplete pre- and postzygotic barriersJiménez-López, F.J.¹, Pannell, J.R.², Ortiz, P.L.³, Arista, M.⁴

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The boundaries that define plant species have been much debated. Although absolute reproductive isolation is accepted as an unequivocal sign of speciation, partial isolation between divergent populations can also lead to speciation. Evolution of reproductive isolation depends on a considerable number of barriers. To understand the speciation process, it is necessary to identify all reproductive barriers that limit hybridization. In this study, we estimated the strength of prezygotic and postzygotic barriers between the two flower colour phenotypes, red and blue, of the herb *Lysimachia arvensis*. Our study points to a temporal separation between morphs at two stages: the blue morph begins to flower 10-20 days earlier than the red morph; and blue flowers open about 1 hour earlier in the morning and close about 1 hour later in the evening than red flowers. Pollen flow between morphs carried out by pollinators was always less frequent than expected, based on morph frequencies. Pollen of each morph showed the same fertilization capacity on the ovules of the other morph. F1 and F2 hybrids had lower seed production than parental plants. Our results indicate that none of these barriers to hybridization are complete, but it seems that a sum of incomplete barriers may cause effective isolation of each morph, reducing the chance of F1 hybridisation and contributing to the speciation process.

Sp.09-6-Poster

Adaptive divergence despite small population sizes and strong genetic drift in English yew (*Taxus baccata* L.)Mayol, M.¹, Riba, M.², Grivet, D.³, Vendramin, G.G.⁴, Vincenot, L.⁵, González-Martínez, S.C.⁶

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English yew (*Taxus baccata* L.) is a dioecious long-lived gymnosperm occurring in a great diversity of habitats in most of the European continent. However, populations are often small and isolated, show irregular size/age structures and biased sex ratios, and neutral genetic diversity is highly structured, so that the ability of this species to cope with local changing conditions in the face of impending climate change may be severely reduced. Here we provide an overview of our research on adaptive patterns of variation in this conifer, both at the phenotypic and molecular levels. Results from a clonal common garden experiment revealed the existence of two basic adaptive phenological patterns according to the regional origin ("mild-type" and "continental-type") associated to temperature and precipitation clines. At the molecular level, new-generation outlier detection and environmental association analysis of 25,726 SNPs (1,210 candidate genes) in 120 individuals distributed along an environmental gradient in Europe identified several outliers associated with temperature and precipitation. In particular, 4 SNPs located on an early-responsive to dehydration stress protein (ERD4) were identified as a target of selection by all the different approaches used. Our results suggest that, despite small population sizes and strong genetic drift, divergent selection have contributed to population divergence in this conifer. However, we found that both current and past climatic data could explain the environmental associations detected, so adaptive patterns might be likely reflecting processes occurred in the distant past.