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Candidate genes, population genomics and climate

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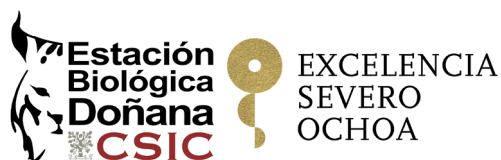


XIV MEDECOS & XIII AEET meeting

Human driven scenarios for evolutionary and ecological changes

Abstract book

31st January - 4th February 2017
Seville, Spain



Abstract book of the XIV MEDECOS & XIII AEET meeting,
Seville, Spain, 31st January - 4th February 2017

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Sp.11: Evolutionary responses to climate change. Evidence from Mediterranean plant populations**Sp.11-1-Main talk****Candidate genes, population genomics and climate**González-Martínez, S.C.¹

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Population and ecological genomics hold promise to identify relevant drivers of genetic adaptation to climate, as well as the relevant genes and gene networks associated with this process. Most important variation for adaptation is expected to be polygenic. However, most research to date has been based on single loci. Moreover, there is an urgent need to establish field experiments that help connecting molecular variation with fitness surrogates in a wide variety of natural environments. In this talk, I first provide a conceptual framework for population genomic studies to better understand the genetic bases of adaptation to climate. Second, I will briefly present case studies in European conifers and white oaks, reporting evidence on molecular adaptation to climate, in particular based on own collaborative research in two widespread conifers with highly contrasted population structure, the maritime pine (*Pinus pinaster* Aiton) and the English yew (*Taxus baccata* L.). For these two conifers, common gardens and quantitative genetic analyses of fitness-related traits were fundamental to either identify selection drivers (e.g. continentality in yew) or to validate genotype-environment associations (in maritime pine) by associating allelic make-up with fitness under extreme environmental conditions. For maritime pine, we also present preliminary results on the relevance of polygenic adaptation to climate, and on how studies that consider gene interactions may overcome previous limitations to identify relevant adaptive variation in this species. Finally, I will provide insights on risks of maladaptation of current forest tree populations in the face of climate change.

Sp.11-2-Poster**Genomic markers of plant adaptation to climate: Responses from one of the widest screening of natural intraspecific genetic diversity across Europe**Blanco Pastor, J.L.¹, Barre, P.², Manel, S.³, Hegarty, M.⁴, Dehmer, K.⁵, Willner, E.⁶, Roldán-Ruiz, I.⁷, Ruttink, T.⁸, Muylle, H.⁹, Roschanski, A.M.¹⁰, Sampoux, J.P.¹¹

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Grassland species are indeed adapted to their local environment, but there is a risk that local populations will often lack sufficient variation to adapt rapid climatic shifts. Our study focus on perennial ryegrass (*Lolium perenne* L.), which is a major grass species naturally distributed over Europe and surroundings. We perform Landscape Genomics analyses to discover genetic variability involved in climatic adaptation. This study is among the firsts to address a large number (>500) of populations in a pool-sequencing approach (300 individuals per pool) across the whole distribution area of a plant species with several tens thousands of genomic markers obtained by Genotyping-By-Sequencing (GBS). Using genotype-environment correlation-based methods and outlier-detection methods we detected genes that have been presumably subject to natural selection and are associated with environmental factors linked to climate change. Our results aim to contribute to a more comprehensive understanding of the distribution of climatic adaptive diversity in vast landscapes.