



Congress of The European Society for Evolutionary Biology

19 to 24 August 2013
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ABSTRACT BOOK

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**FROM AFRICA AND BACK AGAIN: BIOGEOGRAPHY AND
DIFFERENTIATION OF A SPECIALIST WEST-MEDITERRANEAN
BUTTERFLY IN A FRAGMENTED GLACIAL REFUGE**

Eduardo Marabuto¹, Maria Teresa Rebelo², Octávio S Paulo¹

¹ *Faculty of Sciences, University of Lisbon, Department of Animal Biology, Portugal*

² *Faculty of Sciences, University of Lisbon, Department of Animal Biology, Portugal*

eduardo.marabuto@gmail.com

The Mediterranean area is well known for retaining and generating biodiversity during climate and habitat shifts taking place since the end of the Miocene. This important biodiversity hotspot is both the source and the result of a complex process of differentiation and interaction between evolving lineages and their changing environment. However, regarding stationary Mediterranean specialists, which are expected to benefit and expand northwards with climate amelioration, little is still known. Using the butterfly *Euchloe tagis*, an Atlanto-Mediterranean ecological specialist with a fragmented and restricted distribution, this study attempts at answering pertinent biogeographic aspects on the species and its interaction with the changing ecosystem. We sequenced a 599bp barcode region fragment of the COI gene from all major populations to better understand current its genetic patterns and evolutionary history. Main results suggest an origin in North Africa, from where the sister species *Euchloe pechi* is endemic. While one of the Moroccan populations diverged earlier from the remaining stock, all remaining are more closely related despite the existence of differentiated major mitochondrial lineages. It seems that Iberia has played a pivotal role in the generation of diversity in this species: two consistent genetic clusters are partly sympatric whereas French and Italian populations are considerably different. The second Moroccan population from the Rif Mountains shows little segregation from French samples and this issue is discussed on a phylogeographic framework supported by molecular-clock analysis. This pattern suggests this species experienced polycentric refugia during climate cycles, leading to such genetic structure and a putative re-colonization of Africa. Moreover, the neutral genetic pattern reported in this study challenges current taxonomy based on morphological differentiation and suggests a more complex evolution of this species.