



## ORAL COMMUNICATIONS

### EVIDENCE OF LONG TERM FRAGMENTATION AND GLACIAL PERSISTENCE IN THE ITALIAN WALL LIZARD *Podarcis siculus*

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The current genetic distribution of species inhabiting the Mediterranean basin is the result of a vast array of microevolutionary processes, including short-term demographic and ecological mechanisms and long-term allopatric isolation in response to Quaternary climatic fluctuation. The Italian peninsula is considered an important hotspot of intraspecific diversity, having played as refugial area during Pleistocene glacial phases. Here, we investigated past processes that drove the population differentiation and spatial genetic distribution of the Italian wall lizard *Podarcis siculus* by means of sequences of mitochondrial (cytb, n = 277) and nuclear (mc1r, n = 262) genes from all its distribution range. The pattern emerging from the genetic data was corroborated by current and past (last glacial maximum) species distribution modeling (SDM). The observed mtDNA genetic diversity is, to the best of our knowledge, among the highest ever observed in any vertebrate species from the area. We identified seven parapatric clades which presumably remained isolated in different refugia scattered mainly throughout the Tyrrhenian coast. Conversely, the Adriatic coast showed only two haplogroups with low genetic variability. These results appear to agree with the SDM prediction indicating a narrow area of habitat suitability along the Tyrrhenian coast and much lower suitability along the Adriatic one. However, the considerable land exposure of the Adriatic coastline favored a glacial colonization of the Balkan Peninsula. Our population-level historical demography showed a common trend consistent with glacial expansions and regional persistence during the last glacial maximum (LGM). This complex genetic signature appears to be distant from the expectation of the expansion-contraction model and post-LGM (re)colonizations from southern refugia. Hence it is one of an increasing number of cases in which these assumptions are not met, indicating that long-term fragmentation and pre-LGM events such as glacial persistence were more prominent in shaping genetic variation in this temperate species.