

Testing phylogeographic hypotheses in Iberian and north African *Podarcis*: the influence of latitude in shaping historical demography and substructure

C. PINHO¹; D.J. HARRIS^{1,2} & N. FERRAND^{1,2}

¹ CIBIO, Campus Agrário de Vairão, Rua Padre Armando Quintas, 4485-661 Vairão, Portugal; catarina@mail.icav.ip.pt

² Faculdade de Ciências da Universidade do Porto, Praça Gomes Teixeira, 4099-002 Porto, Portugal

The aim of this study was to test simple biogeographic predictions related to the differential influence of the Ice Ages according to the latitude: (i) northerly distributed species should have experienced a greater loss of suitable habitat, resulting in higher lineage extinction, than species distributed in southern latitudes. This would be reflected in lower diversity and number of differentiated lineages in northern areas. (ii) a signature of demographic expansion following the climate amelioration should be obvious in northern species, contrasting to evidence of long-term effective population size stability in the south. We used as models for this study three species of wall lizards (*Podarcis bocagei*, *P. carbonelli* and *P. vaucheri*) which replace each other along a latitudinal gradient. Our results based on mitochondrial DNA variation show that *P. bocagei* presents remarkably low levels of diversity and subdivision, a shallow coalescent history and a strong signature of demographic growth. *P. vaucheri*, on the other hand, presents large levels of genetic diversity, strong geographic subdivision, no evidence of demographic growth and an ancient coalescence time, probably dating back to the initial stages of the Pleistocene. The intermediately distributed *P. carbonelli* presents average values of all studied variables. Taken together, these results entirely fit to our main predictions and demonstrate that the effects of the Ice Ages were indeed different according to the latitude.

Additionally we analysed a battery of nuclear markers in *P. bocagei* and *P. carbonelli* in order to study in more detail these species' evolutionary history and validate phylogeographic hypotheses suggested by the study of mtDNA.