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Hybridization between native and introduced populations of the Common wall lizard (*Podarcis muralis*) at the northern range margin

The Common Wall Lizard (*Podarcis muralis*) represents one of the few reptile species that have successfully colonized regions in north-western Europe far outside their Mediterranean native range. DNA barcoding revealed that 85 introduced populations stem from eight geographically distinct invasive evolutionary lineages. Although the high phenotypic variability in colour pattern of wall lizards at both the intra-specific and intra-population level might lead to a delayed recognition of introductions and little awareness of the problem of introgression in conservation management, there is increasing evidence of introductions at the native range margin of the species in south-western Germany. In order to infer the level of potential hybridizations in contact zones of alien and native lineages, we analysed a combination of maternally (mtDNA; cytochrome *b*) and bi-parentally inherited molecular markers (13 microsatellite loci). A total of 316 wall lizards from five mixed populations as well as one native and one pure introduced reference population were analysed. Based upon model-based clustering methods our results suggest a rapid genetic assimilation of native populations through strong introgression of introduced Italian lineages. We also found a positive relationship between genetic diversity and the number of source populations. This high genetic diversity might be caused by the introduction of founders from different native populations from the Apennine Peninsula, which is a hotspot of the species' genetic diversity. High levels of intraspecific admixture may have promoted the invasion success of mixed populations. Nevertheless, introduced pure-bred populations with a low number of founders also retained rather high levels of genetic diversity like native populations and no evidence for a genetic bottleneck was found. The extent of introgression within artificial hybrid populations suggests that introductions of non-native lineages are threatening the genetic integrity of native populations at the northern range margin through a rapid creation of hybrid swarms.

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Past, present, and future biogeographical patterns of Iberian herpetofauna

The biogeographical patterns in species density of herpetofauna have been analysed in the Iberian Peninsula recently, but only for the present time. Therefore, we want to analyse how biogeographical patterns change from the past to the future, in order to determine if biogeographical regions have changed along time, as well as the species chorotypes. Also, we measured expansions and retractions in species distributions and identified possible areas of refugia in the past and in the future. The study area was the Iberian Peninsula only, that is, excluding the Balearic Islands, and other islands outside the continental platform. The study included all the species of amphibians (28) and reptiles (45) considered in the Atlas of Portugal and of Spain. We calculated the realized niche model of each species using Maxent