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# Southern European common lizard populations are threatened by global warming

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## Abstract

Gene flow is one of the most important factors determining the evolution of a species, since it directly affects population structure, species' adaptation, and evolution. The European common lizard (*Zootoca vivipara*) is the terrestrial reptile with the widest and farthest north distribution of the world. For this reason, this species has been highly studied, but the lack of a large, reliable and highly variable panel of microsatellite loci has hindered the study of its population genetics. Here we produced highly variable microsatellites and investigated for the first time the population genetics of the Ibero-Pyrenean common lizard (*Zootoca vivipara louslantzi*). We analysed gene flow among populations of this sub-species by employing 34 newly developed polymorphic microsatellite markers. The analyses unravelled the presence of isolation by distance, inbreeding, bottlenecks, genetic differentiation, and low levels of gene flow among most populations, in line with physical barriers hindering longitudinal migration and climatic conditions being probably the reason for differences in gene flow on the Southern and Northern Pyrenean slope. The results point to isolation of *Zootoca vivipara* populations, especially those located on the Southern Pyrenean slope, which may be threatened by global warming, if temperatures continue increasing in the future.

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