COLONIZATION, GENETIC DIVERSITY AND FITNESS-RELATED CONSEQUENCES IN NON-NATIVE POPULATIONS OF *Podarcis muralis* IN ENGLAND

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Human activities are increasingly modifying the abundance and distribution of organisms and this is evident by the occurrence of numerous species beyond their native range. The common wall lizard, *Podarcis muralis*, has a wide distribution in Southern Europe. The species has also been repeatedly introduced in England with currently more than 25 extant populations. We used mtDNA sequences, microsatellite markers and a combination of Bayesian analytical techniques to unravel the colonisation history of *P. muralis* in England. There were at least nine independent introduction events from native populations in France and Italy. We found evidence of admixture and support for secondary introductions within the non-native range. We further tested how introduction history influences genetic structure. Genetic diversity was significantly lower in England and for older non-native populations. The loss of genetic variation was greater for populations originating from sources with high levels of genetic diversity. There was no further loss in secondary introductions and admixture did not have significant positive effects. Finally, we collected data on hatching success from both native and introduced populations to assess the consequences of colonisation at the individual and population level. We found increased embryonic mortality in the non-native range indicative of inbreeding depression. Hatching failure was particularly high for populations with greater loss of genetic diversity. However, there was no evidence that heterozygosity is correlated with fitness at the population or individual levels. Combined, our study represents a comprehensive example linking introduction history, genetic diversity, individual fitness and population viability in a non-native species.