

Long-term biogeographic processes dominate patterns of genetic diversity in a wingless grasshopper despite substantial recent habitat fragmentation

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December 16, 2022

Abstract

Low vagility species may hold strong genetic signatures of past biogeographic processes but are also vulnerable to habitat loss. Flightless grasshoppers of the morabine group were once widespread in south-eastern Australia including Tasmania but are becoming restricted to remnant patches of vegetation, with local ranges impacted by agriculture and development as well as management. Habitat fragmentation can generate genetically differentiated “island” populations with low genetic variation. However, following revegetation, populations could be re-established and gene flow increased. Here we characterise SNP based genetic variation in a widespread chromosomal race of the morabine *Vandiemena viatica* (race 19) to investigate the genetic health of remnant populations and to provide guidelines for restoration efforts. We update the distribution of this race to new sites in Victoria and Tasmania, and show that *V. viatica* populations from northern Tasmania and eastern Victoria have reduced genetic variation compared to other mainland populations. In contrast there was no effect of habitat fragment size on genetic variation. Tasmanian *V. viatica* populations fell into two groups, one connected genetically to eastern Victoria and the other connected to south-western Victoria. Mainland populations showed isolation by distance. These patterns are consistent with expectations from past biogeographic processes rather than local recent population fragmentation and emphasize the importance of small local reserves in preserving genetic variation. The study highlights how genomic analyses can combine information on genetic variability and population structure to identify biogeographic patterns within a species, which in turn can inform decisions on potential source populations for translocations.

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