

An endangered flightless grasshopper with strong genetic structure maintains population genetic variation despite extensive habitat loss

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Abstract

Conservation research is dominated by vertebrate examples but the shorter generation times and high local population sizes of invertebrates may lead to different management strategies. Here we investigate the genetic structure of an endangered flightless grasshopper, *Keyacris scurra*, used in classical evolutionary studies in the 60s. It had a wide distribution across New South Wales (NSW) and Victoria in pre-European times but has now become threatened because of land clearing for agriculture. We revisited remnant sites of *K. scurra*, with populations now restricted to only one area in Victoria and a few small patches in NSW and the Australian Capital Territory (ACT). Using DArTseq to generate SNP markers as well as mtDNA sequence data, we show that the remaining Victorian populations in an isolated valley are genetically distinct from the NSW populations and that all populations are genetically unique, with large F_{ST} values up to 0.8. We also find that, with one exception, the NSW/ACT populations separate genetically into chromosomal races ($2n = 15$ vs. $2n = 17$). Isolation by distance was detected across both the SNP and mtDNA data sets, and there was substantial differentiation within chromosomal races. Genetic diversity as measured by heterozygosity was not correlated with the size of remaining habitat patches, with high variation present in some remnant cemetery sites. However, inbreeding correlated negatively with estimated habitat size at 25-500 m patch radius. These findings emphasize the importance of small fragments in conserving genetic variation across the species, and they highlight populations suitable for future translocations.

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