

Metapopulation management of the critically endangered Woylie



Common name/s: Woylie, Brushtail bettong

Scientific name: *Bettongia penicillata*

CONSERVATION BACKGROUND

Woylies were listed as Critically Endangered by the IUCN in 2008 ([IUCN, 2020](#)) following a significant population decline of more than 90% between 1999 and 2006. To mitigate the extinction risk for woylies a series of management strategies exist, these include the use of conservation translocations and reintroduction into fenced or island havens.

PROJECT AIMS

1. Provide conservation recommendations for woylies using contemporary genomic molecular techniques for all currently managed woylie populations
2. Provide guidance to conservation managers on how these recommendations align with those previously made using traditional microsatellite data

KEY FINDINGS

- Reference genome produced and published
- 13,194 SNPs were generated from woylie's across 13 populations (indigenous, reintroduced and haven populations).
- Observed heterozygosity was significantly less than expected heterozygosity reflecting the historical bottleneck for the species.
- Only 4 of the 13 populations showed evidence of inbreeding, and effective population sizes ranged from 9.9 to 268.9.
- Trends in observed heterozygosity were broadly similar between microsatellite and SNP marker sets providing confidence to previous management recommendations for the species.

IMPLICATIONS FOR SPECIES CONSERVATION

The genetic data informs the current situation, prioritisation of populations and actions to protect and recover the species, and how best to do this. These findings were provided to the Woylie recovery team in real time, playing an important role in managing both the fenced and wild Woylie populations. The genetic data has since played a key role in informing the selection of source populations for translocations.

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