# Assessing the genetic costs of recurring population crashes in the Woylie (*Bettongia penicillata ogilbyi*)

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The Woylie has gone through genetic bottlenecks. One took place during early European settlement, and the other is occurring at the moment. These provide an ideal theoretical paradigm to study the genetic effects of genetic population bottlenecks & conservation strategies


Photo: Dr Sabrina Trocini


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## Objectives

Characterise the historical genetic profile since European settlement by using ancient DNA approaches.

Characterise the genetic profiles (e.g. genetic variability) of remaining Woylies in Western Australia.

Investigate the genetic consequences of previous population declines.

Model and quantify the genetic responses within translocated populations.

Predict the genetic implications of recent woylie declines, and the likely consequences for the future recovery and conservation of the species.

Describe information on paternity, social structure, home range and individual's movements between adjacent populations.


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## Number of sample per sites

| | |
|---|---|
| Batalling State Forest, WA | 89 |
| Upper Warren, WA | 535 |
| Karakamia Sanctuary, WA | 256 |
| Dryandra Forest, WA | 60 |
| Tutanning Nature Reserve, WA | 44 |
| St Peter Island, SA | 119 |
| Wedge Island, SA | 80 |
| Venus Bay Island, SA | 31 |
| Venus Bay Conservation Park, SA | 50 |
| Total | **1264** |

**$P_{ID}$ (probability of identity) of 1 in 10,000,000**

**Twenty-eight primers that were originally developed for different macropodidae species were tested to assess their suitability and polymorphism in woylies.**

| Locus | Source Species | Locus | Source Species |
|---|---|---|---|
| Bt64 | *Bettongia tropica* | Pa597 | *Petrogale assimilis* |
| Bt76 | | Pa593 | |
| Bt80 | | Pa297 | |
| Pl2 | *Potorous longipes* | Pa385 | |
| Pl3 | | Pa595 | |
| Pl13 | | B90 | *Onychogalea fraenata* |
| Pl18 | | B123 | |
| Pl22 | | Me15 | *Macropus eugenii* |
| Pl26 | | Me16 | |
| Y175 | *Petrogale xanthopus* | Me17 | |
| Y170 | | T17-2 | |
| Y151 | | T31-1 | |
| Y76 | | MeY01 | |
| G31-1 | *M. giganteus* | MeY37 | |

## Preliminary results

| | Heterozygosity | | |
|---|---|---|---|
| **Locus** | Observed | Expected* | **Alleles** |
| **Mean** | 0.6640 | 0.7913 | 6.69 |
| **St.Dev** | 0.2911 | 0.0574 | 2.05 |

*Nei's (1973) expected heterozygosity

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