# The effects of a major road on the population processes of the Yellow-footed Antechinus: evidence from genotypic analyses

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## Background

The original woodland habitat in northern Victoria has been largely cleared for agriculture, and less than 6% tree cover remains. Most remnant vegetation is arranged as narrow strips along streams and roadsides, with fewer, larger patches of habitat.

Where the current study took place, Yellow-footed Antechinus *Antechinus flavipes* occurs within remnant roadside vegetation and road reserves (remnant linear strips of vegetation fragmented by farmland and dissected by major roads).

Yellow-footed Antechinus. Females are philopatric. Dispersal is male-biased.

Genetic analyses are commonly used to quantify population processes for a variety of organisms and are informative at a range of spatial and temporal scales.

Using a genotypic approach with microsatellite loci, the study investigated dispersal, relatedness and genotypic structure of populations of Yellow-footed Antechinus between sampling locations on either side of the Hume Highway in southeastern Australia, to investigate the effects of the highway on the species at the population level.

**Aim: To investigate the effects of a major road on population processes of Yellow-footed Antechinus using genetic techniques.**

## Study Design

Yellow-footed Antechinus were sampled at ten sites along the Hume Highway in north eastern Victoria: nine road reserves and one larger patch, Reef Hills State Park.

All ten sample sites are bisected by the freeway, fragmenting the habitat of the road reserves to either side of the highway. Sites with and without culverts were chosen.

Road reserves contain many old-growth trees: habitat for Yellow-footed Antechinus.

Trapping for Yellow-footed Antechinus was conducted at all sites on both sides of the highway within the road reserves and adjacent to the road.

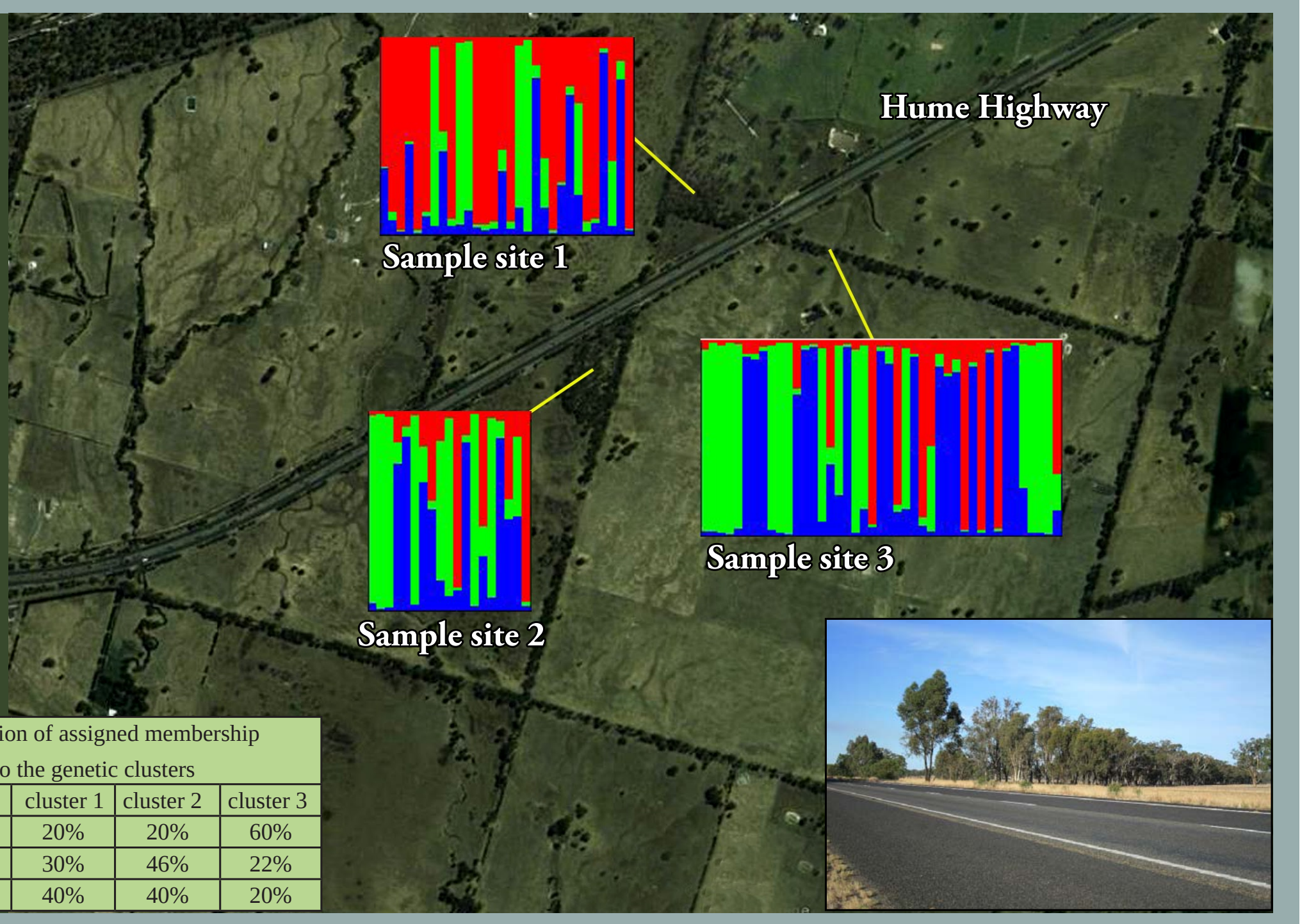
Tissue samples were taken from individuals and the DNA genotyped at ten microsatellite genetic markers. The genotypic data obtained were analysed for movement of individuals and genetic structuring of sample sites.

## Results

The numbers of Antechinus trapped at the following three sites were sufficient for analyses of assignment tests and investigation of genotypic population structure of sample sites on opposite sides of the highway. Presented is genetic clustering of individuals from sample sites, derived from a Bayesian algorithm clustering method based on the individual's genotype. Each bar within a histogram represents an individual Antechinus.

### NO CULVERT. SPARSE VEGETATION IN MEDIAN STRIP:

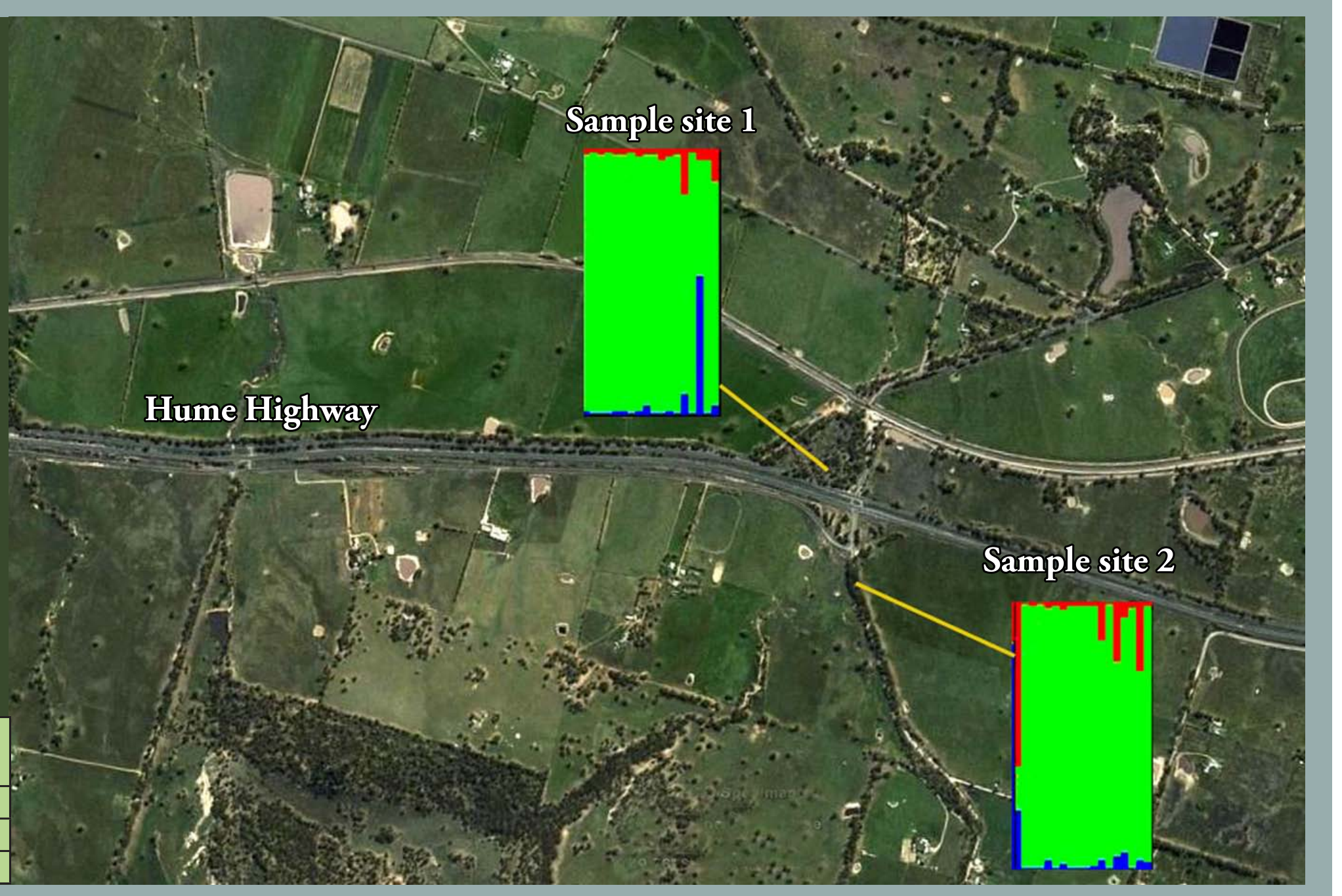
- **Three sample sites.**
- **Individuals from sample site 2 and 3 (same side of highway) more genetically similar to each other than to individuals from sample site 1 on opposite side of highway.**



| Proportion of assigned membership to the genetic clusters | | | |
|---|---|---|---|
| | cluster 1 | cluster 2 | cluster 3 |
| sample site 1 | 20% | 20% | 60% |
| sample site 2 | 30% | 46% | 22% |
| sample site 3 | 40% | 40% | 20% |

### CULVERT PRESENT. SPARSE VEGETATION IN MEDIAN STRIP:

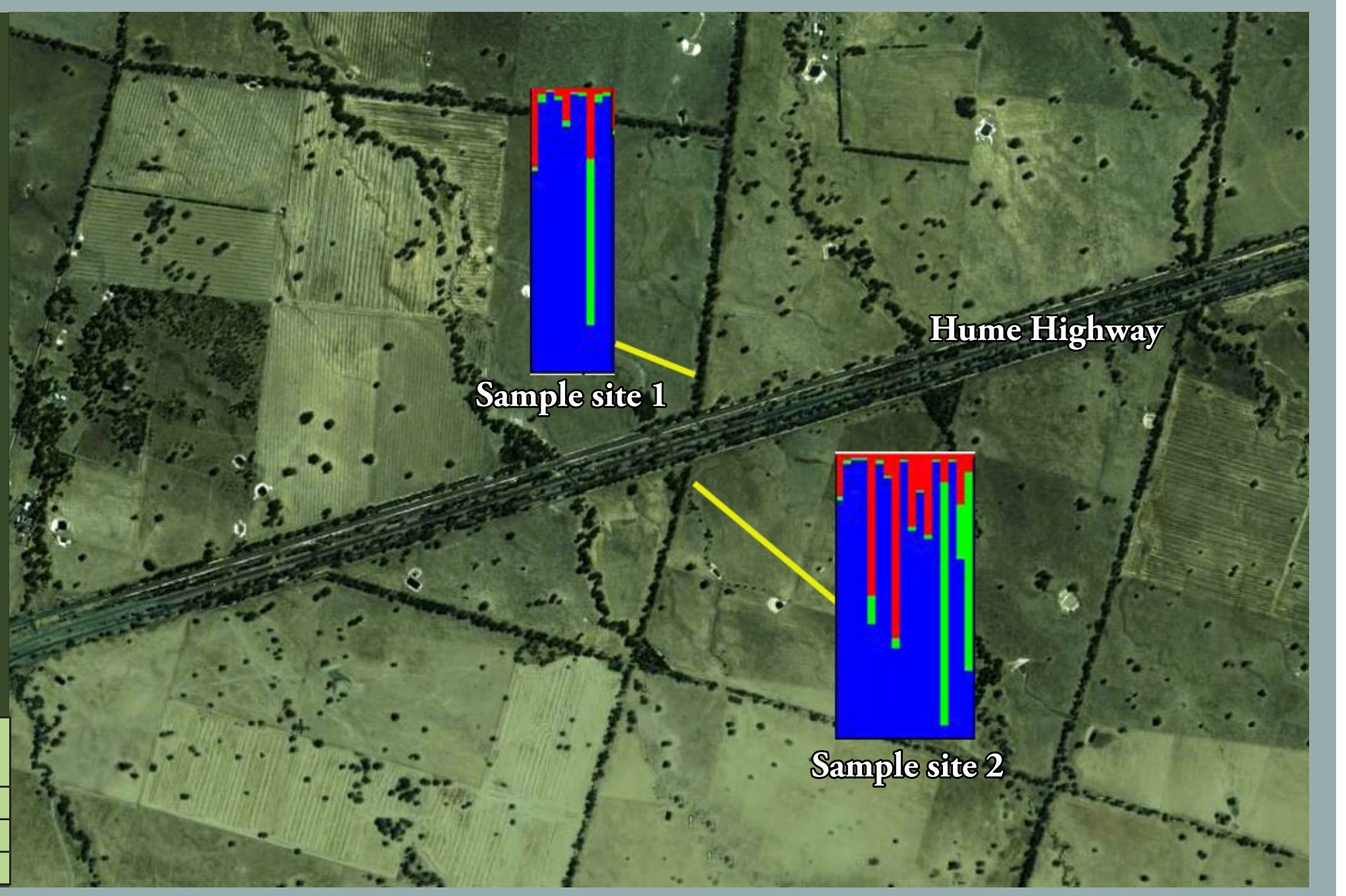
- **Two sample sites.**
- **Individuals from both sample sites are genetically similar.**



| Proportion of assigned membership to the genetic clusters | | | |
|---|---|---|---|
| | cluster 1 | cluster 2 | cluster 3 |
| sample site 1 | 4% | 91% | 5% |
| sample site 2 | 8% | 88% | 4% |

### CULVERT PRESENT. OLD-GROWTH VEGETATION IN MEDIAN STRIP:

- **Two sample sites.**
- **Individuals from both sample sites are genetically similar.**



| Proportion of assigned membership to the genetic clusters | | | |
|---|---|---|---|
| | cluster 1 | cluster 2 | cluster 3 |
| sample site 1 | 7% | 7% | 86% |
| sample site 2 | 14% | 12% | 74% |

Populations on opposite sides of the highway at two sites with culverts, showed less genotypic differentiation than those at the site without a culvert. This suggests that at the site without a culvert, Antechinus road crossings were reduced to a level that maintained genetic differences between the populations on either sides of the highway. The study was limited by lack of replicate site treatments due to poor trapping results at remaining road reserves.

## Conclusions

The combination of genetic and traditional field ecology approaches was necessary in determining the nature and extent of restriction to movement of Yellow-footed Antechinus caused by the presence of the highway. The genotypic approach yielded information on population processes where a capture-mark-recapture method did not or could not.

The results will contribute to demographic modelling that can be informative about persistence and recolonization probabilities for Yellow-footed Antechinus in a landscape of networked, linear strips of habitat featuring a major road.

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