

Genetic approaches: essential tools for best-practice assessment, monitoring and mitigation of organismal responses to human transportation networks

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Dispersal and geneflow: importance and measurement

Dispersal and geneflow are critical to population persistence and (re)colonization. The spatial and temporal scales at which these operate are generally poorly understood and have been difficult to measure.

Molecular genetic analyses have become extremely well-developed and highly informative in population biology. Nonetheless, their uptake has been slow in some countries and for some applications.

Major roads have the potential to act as filters to the movement of wildlife. We are conducting a collaborative study to quantify the barrier effect of roads in a highly fragmented landscape in central Victoria, Australia and to evaluate the effectiveness of mitigation structures.

The Hume Freeway is the major highway connecting Melbourne and Sydney, and was progressively widened to dual-carriageway in the 1970s and 1980s (Vicroads unpublished data).

Aims of the collaborative project

- To combine field and genetic data to understand how diverse animal species use habitat and landscape features for dispersal, and to quantify the filtering effect of roads on the movement and dispersal of mammals and reptiles (Fig. 1)
- To assess the effectiveness of structures and road designs intended to mitigate reduced mobility and geneflow.
- To contribute data about mobility and geneflow for modelling of population persistence under different scenarios.

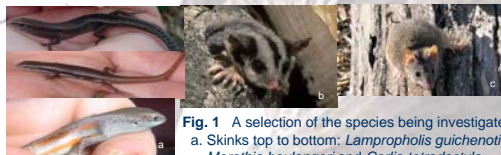


Fig. 1 A selection of the species being investigated:
a. Skinks top to bottom: *Lampropholis guichenoti*,
Morethia boulengeri and *Carlia tetradactyla*
b. Squirrel Glider *Peteurus norfolcensis*
c. Yellow-footed Antechinus *Antechinus flavipes*

Methods

Fauna were live-trapped on both sides of the Hume Freeway and tissue/DNA samples taken at a range of spatial scales to investigate habitat structures associated with mobility. Field techniques including capture-mark-recapture and radio-tracking were conducted on several species to investigate key aspects of habitat use (reported on elsewhere).

Individuals were genotyped with a suite of highly-resolving DNA genetic markers, microsatellites. Spatial genetic analyses were conducted to estimate individual and population genetic measures that are informative about individual mobility and gene flow.

Results

1. Squirrel Gliders and Antechinus showed reduced mobility and geneflow across the Hume Freeway (Figs. 2 & 3). For Squirrel Gliders, this was associated with presence of large trees (Fig. 3), and presence of vegetation and culverts are indicated as important for Antechinus. These results are consistent with our capture-mark-recapture and radio-tracking, which help to confirm detailed use of habitat features (presented elsewhere).

2. Both species also showed larger-scale genetic differentiation among samples taken a few kilometers apart. These patterns are not obviously correlated with each other geographically, nor with major landforms or habitat variables, and may be driven by idiosyncratic differences in biology/ecology.

3. While the extent of habitat is greatly reduced in this landscape (Fig. 2), both species appear to operate as meta-populations that achieve some mobility through the highly connected network of roadside and riparian strips.

Conclusions

1. Genetic approaches combined with field ecology yield important information about mobility and geneflow and habitat/landscape structures that promote or reduce these.
2. The techniques are suitable for monitoring success of mitigation efforts and environmental change.
3. Major roads can reduce mobility and geneflow in Squirrel Gliders and Yellow-footed Antechinus to produce genetically-detectable effects in 30 years or less.
4. Even highly reduced woody vegetation cover can be important in sustaining populations of woodland marsupials, at least where it is highly connected and contains large individual trees that provide key habitat resources.

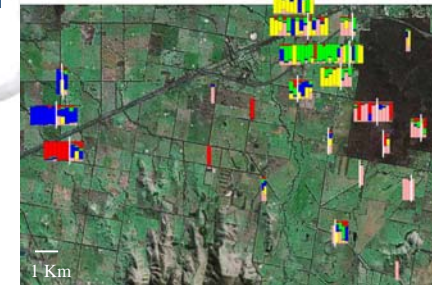


Fig. 2 Genotypic structure of Yellow-footed Antechinus. Each vertical bar represents the colour-coded genetic signature of an individual. There are some genetic differences at fine scales, across the freeway, as well as larger-scale population genetic structure. Dispersal is male-biased (females are to the left and males to the right of the white lines - where there is no line, all are female). Note the extremely low percentage cover of woody vegetation that is almost entirely at the side of roads or streams, but is very highly connected into a network.

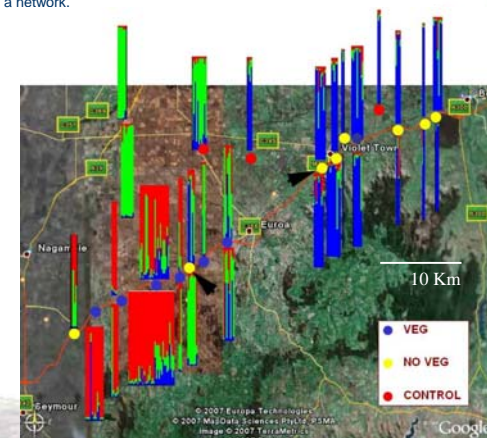


Fig. 3 Genotypic structure of Squirrel Gliders. The two sites marked with black arrows showed significant genetic difference across the freeway, and had no mature vegetation in the centre median. There is larger-scale population patterning.