



Genetic relationships of *Isoodon* bandicoot species in southern and western Australia

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Background

Short-nosed bandicoots, genus *Isoodon* (family Peramelidae), are small to medium-sized Australian marsupials that can be found across Australia. Bandicoots are terrestrial omnivores, with a bounding gait and forelimbs adapted for digging for food. As digging mammals, they play an important role as ecosystem engineers, contributing to altered soil nutrient and moisture dynamics that enhance plant germination and growth. Facing pressure from introduced predators and human disturbances, many *Isoodon* species now persist in only small remnants of their former ranges.

The taxonomy of *Isoodon* bandicoots has changed multiple times over the last 70 years. Confusion over taxonomic boundaries has made decisions over management of *Isoodon* species and subspecies difficult. Currently, five species are recognised including *I. macrourus*, *I. peninsulae*, *I. obesulus*, *I. auratus* and *I. fusciventer*. A recent study (Cooper et al. 2020) has indicated further complexity in the relationships of southern and western *Isoodon* sp. They found that *I. o. obesulus* specimens from South Australia (SA) are more closely related to *I. fusciventer* from Western Australia (WA) than *I. o. obesulus* from south-eastern Australia, and that despite morphological differences in size, skull, teeth characters and fur colour, there was a lack of clear genetic distinctiveness between WA taxa *I. fusciventer* and *I. auratus* in their samples.

To aid clarification, we focused on identifying genetic conservation units within the southern (*I. obesulus* in Victoria (Vic) and SA) and western (*I. auratus*, *I. a. barrowensis* and *I. fusciventer*) *Isoodon* bandicoots based on nuclear and mitochondrial DNA data from published studies with expanded sampling from northern and southern WA.

Methods

We collated 497bp of mitochondrial D-loop sequences and 10 microsatellite loci from previously published sources with new sampling for a total of 731 and 218 additional samples, respectively. These samples were collected across multiple locations in WA, SA, and Vic and across multiple years from 2002 to 2018.

Findings

- *I. auratus* (northern WA), *I. fusciventer* (southern WA) and *I. obesulus* (Vic) are largely resolved as three major lineages in phylogenetic analysis of mitochondrial DNA. The relationship of *I. obesulus* in SA to western lineages remains unclear, with SA haplotypes nested in both WA clades (Figure 1 middle). This may be due to incomplete lineage sorting at this marker.
- Data from nuclear microsatellite markers (which are more rapidly evolving) indicated a geographic cline stretching from northern WA (*I. auratus*) to South Australia with *I. fusciventer* in southern WA as a connecting population in PCoA analysis (Figure 1 bottom right). However, in hierarchical Bayesian clustering analysis *I. obesulus* (SA) was resolved as a distinct cluster from the two WA bandicoots.
- Within WA, three sub-clusters separating *I. a. auratus* in the Kimberley, *I. a. barrowensis* on Barrow Island and *I. fusciventer* in southern WA were evident, consistent with current taxonomy.

- All populations sampled had high genetic distinction at nuclear microsatellite markers, and the presence of locally unique mitochondrial haplotypes, indicated limited gene flow.
- Vic and SA populations appear to be in genetic decline with reduced genetic diversity, but southern and northern WA populations retain high diversity with Kimberley mainland having the highest microsatellite diversity and number of unique haplotypes.

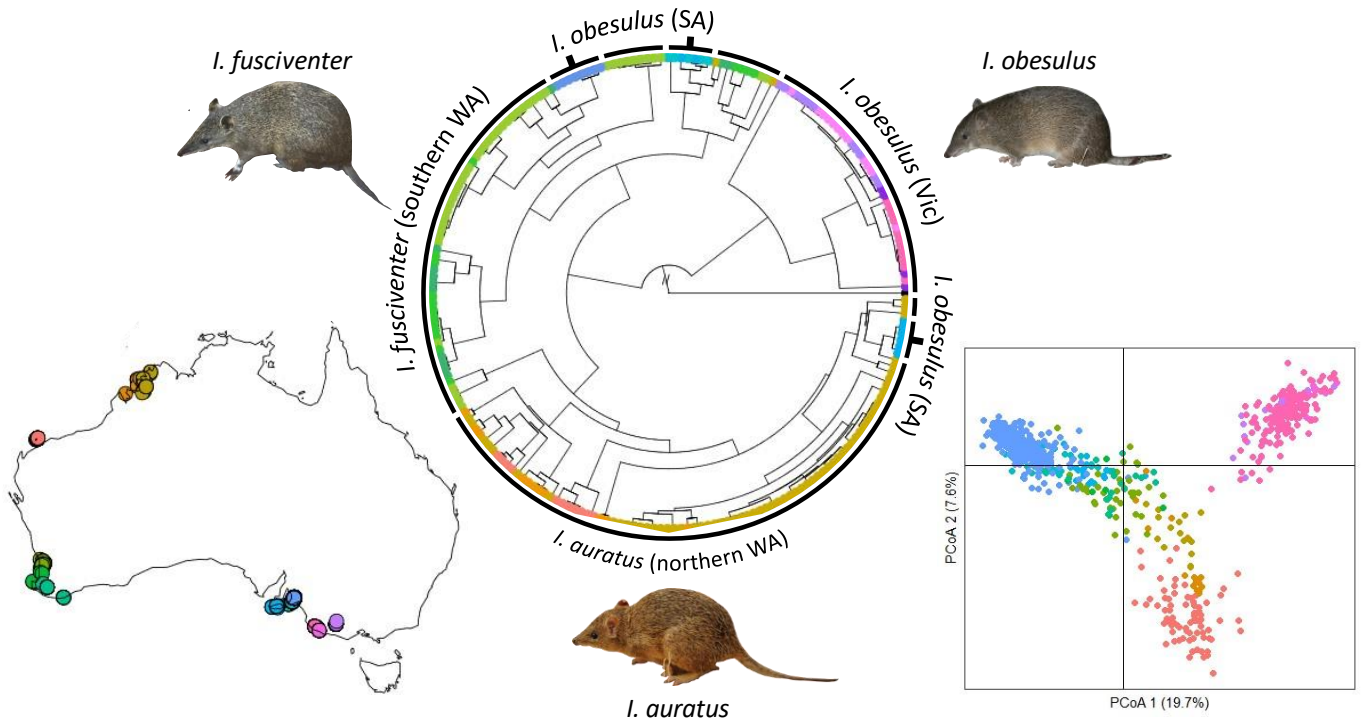


Figure 1: Bayesian phylogenetic tree derived from BEAST analysis of southern and western *Isoodon* taxa. Bottom left: Colour-coded geographic sampling locations. Bottom right: Principal coordinates analysis of nuclear DNA. Bandicoot photos: Australian Wildlife Conservancy (*I.a.*), Kenny J. Travouillon (*I.f.*), Museum Victoria (*I.o.*).

Management implications

- Mitochondrial DNA analysis, haplotype uniqueness, and significant divergence among populations in different regions suggested that *I. auratus*, *I. fusciventer* and *I. obesulus* in South Australia should be managed as separate units, and that SA *I. obesulus* requires further consideration to assess its taxonomy and conservation status.
- Populations suffering most heavily from habitat fragmentation and degradation show evidence of genetic decline. Western Australian populations retain high diversity, but conservation efforts should focus on improvement of habitat (e.g. management of introduced predators, fire regime) and landscape-scale connectivity to maintain gene flow into the future.
- As one of Australia’s important digging mammals, bandicoots are often targeted for translocation to restore ecological function in ecological restoration projects. There is evidence that bandicoots show morphological adaptation to local conditions, which has been demonstrated to have both genetic and environmental components, suggesting that translocation to similar habitat is important.

Further information

Cooper S, Ottewell K, Macdonald AJ, Adams M, Byrne M, Carthew SM, Eldridge MDB, Li Y, Pope LC, Saint KM and Westerman M (2020) Phylogeography of southern brown and golden bandicoots: Implications for the taxonomy and distribution of endangered subspecies and species. *Australian Journal of Zoology*, 66, 379-393.

Thavornkanlapachai R, Levy E, Li Y, Cooper SJB, Byrne M and Ottewell K (2021) Disentangling the genetic relationships of the three closely related bandicoot species across southern and western Australia. *Diversity*. 13, 2.