

Context Summary

Genetic analysis of threatened species can provide important information to support and guide conservation management. In particular, genetic tools can be used to aid resolution of the taxonomic identity of species to determine whether they have appropriate conservation listing. At a population level, analysis of the genetic diversity present in extant populations provides information on genetic 'health' of threatened species and how this may be maintained or improved through management actions, leading to long-term positive conservation outcomes.

Aims Summary

- Resolve taxonomic boundaries of Western Australian bandicoots (*Isoodon* sp.), particularly *I. auratus* and *I. obesulus* and their subspecies, to determine appropriate conservation rankings.
- In collaboration with Brian Chambers (UWA) investigate the role of fauna underpasses in providing connectivity between quenda (*I. obesulus* ssp. *fusciventer*) populations impacted by main road construction.
- In collaboration with Mark Eldridge (Australian Museum), assess the genetic diversity and genetic structure of extant populations of black-flanked rock wallaby (*Petrogale lateralis* ssp. *lateralis*) to inform future conservation management, including translocations.
- Use of DNA barcoding to confirm species identifications.

Progress

- DNA sequencing of *I. obesulus*, *I. auratus*, *I. macrourus* and their subspecies using mitochondrial and nuclear markers for taxonomic analysis has been undertaken. Preliminary analyses suggest further nuclear sequencing markers are needed to fully resolve species boundaries but that revision of *I. obesulus* sub-species designations is likely to be required.
- DNA analysis of quenda populations has been completed and population genetic analyses are currently being undertaken. Population viability analyses have been completed exploring the long-term trajectory of urban populations with and without fauna underpasses, and with an additional range of threats (fire, urban expansion).
- DNA analysis of rock wallaby populations has been completed and preliminary data analysis has investigated genetic diversity and structure of wheatbelt and northern WA populations.
- DNA barcoding was used to identify a stranded whale carcass as Omura's whale, constituting a new record for the species in WA

Management implications

- Resolution of taxonomic boundaries between *I. obesulus* and *I. auratus* and their broader relationships with eastern states bandicoots should enable revision of current threatened species status at state and commonwealth levels.
- Genetic and population viability analysis showed that quenda populations in small, isolated patches of remnant vegetation in the urban matrix are vulnerable to genetic erosion, inbreeding and population decline, particularly when connectivity within (fauna underpasses) or between (increased urbanisation) habitat patches becomes inhibited. The impact of fauna underpasses on population persistence is somewhat context-specific, but extinction risks are predicted to increase in the study populations without fauna underpasses.
- Genetic information on rock wallaby populations will enable a stocktake of the current status of nearly all extant populations, including the assessment of the effectiveness of past management interventions,

and will contribute to planning of future conservation actions, including translocations.

- The presence of the rare Omura's whale in Australian waters adds to our knowledge of the distribution of this species and has been updated on the state's fauna list.

Future directions

- Investigate potential of other nuclear markers for taxonomic analysis of bandicoots to further resolve species classifications. Investigate use of coalescent models to infer the evolutionary history of the genus.
- Complete analysis of population genetics and gene flow in urban quenda populations, including parentage assignment of individuals using fauna underpasses.
- Comparison of historic and contemporary population genetics of rock wallaby wheatbelt populations to monitor genetic change and investigate impact of past management actions. Develop population viability analyses to predict future trajectory of threatened populations.