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Genetic assessment for conservation of rare and threatened fauna

Animal Science

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Genetic assessment for conservation of rare and threatened fauna

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Context

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

- Resolve taxonomic boundaries of Western Australian bandicoots (*Isodon* 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 and a preliminary report written and submitted. Further analyses using a more powerful genomics approach are required to fully resolve species boundaries between *I. obesulus* and *I. auratus*; however, a population genetic analysis is currently underway to designate 'management units' in Western Australian bandicoots.
- Population viability analyses of urban quenda populations impacted by road construction have been completed exploring the long-term trajectory of populations with and without fauna underpasses, and with an additional range of threats (fire, urban expansion, inbreeding). A manuscript has been submitted and a further manuscript documenting quenda mating patterns in remnant populations is being prepared.
- Preliminary data analysis of genetic diversity and structure of wheatbelt and mid-north rock wallaby populations has been completed.
- DNA barcoding was used to identify a stranded dolphin carcass as a Australian snubfin dolphin hybrid, most likely with a Indo-Pacific humpback dolphin.

Management implications

- An Australia-wide phylogenetic assessment of *I. obesulus* and related species/subspecies has enabled a more informed evaluation of taxonomic boundaries, showing that *I. o. obesulus* is restricted to eastern and southeastern Australia and identifying a range extension of *I. o. fusciventer* (Western Australia) into South Australia. The threat status is currently being evaluated at the Commonwealth level for the eastern and Tasmanian sub-species of *I. obesulus*.
- 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 is inhibited. The impact of fauna underpasses on population persistence is somewhat context-specific, but extinction risks are predicted to increase in populations without fauna underpasses.

- Genetic information on rock wallaby populations will enable evaluation 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 rare dolphin hybrids in Australian waters contributes to our knowledge of hybridization in the marine environment.

Future directions

- Continue phylogenomic analysis of the genus *Isodon* to formally resolve the species boundaries across the group.
- Complete manuscripts of urban quenda populations (population viability analysis and mating systems, including parentage assignment of individuals using fauna underpasses).
- Comparison of historic and contemporary population genetics of wheatbelt rock wallaby populations to monitor genetic change and investigate impact of past management actions. Develop population viability analyses to predict future trajectory of threatened populations.
- Utilize DNA barcoding to assist in fauna identifications when required.