

Progress Report SP 2012-034

Genetic assessment for conservation of rare and threatened fauna

Animal Science

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Project status as of Aug. 21, 2018, 8:10 a.m.

Update requested

Document endorsements and approvals as of Aug. 21, 2018, 8:10 a.m.

Project Team	granted
Program Leader	granted
Directorate	required

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.
- Investigate the role of fauna underpasses in providing connectivity between quenda (*I. obesulus* ssp. *fusciventer*) populations impacted by main road construction.
- 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 DNA barcoding to confirm species identifications.
- Investigate genetic diversity of translocated brushtail possums and their source populations at Matuwa (Lorna Glen).
- Contribute to taxonomic assessment of *Trichosurus vulpecula*, including resolution of WA sub-species.
- Assess genetic diversity, genetic structure and cave use of ghost bat (*Macroderma gigas*) populations in the Pilbara.
- Assess species composition and individual relatedness of Hamelin Bay pilot whale stranding.

Progress

- Initial mt DNA sequencing of *I. obesulus*, *I. auratus* and *I. macrourus* was insufficient to fully resolve taxonomic issues and genomic analyses are being undertaken in collaboration with South Australian Museum. A population genetic analysis was conducted to designate 'management units' in Western Australian bandicoots using microsatellite data and a draft manuscript is being prepared.
- Population viability analyses of urban quenda populations impacted by road construction have been completed. This explored the long-term trajectory of populations with and without fauna underpasses, and impacted by an additional range of threats (fire, urban expansion, inbreeding). A manuscript has been published in *PLoS One* 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 west rock wallaby populations has been completed. Genetic and population viability analyses of the first two translocations of wheatbelt wallabies to Kalbarri National Park has been completed. Genetic analysis of a third Kalbarri translocation is currently being undertaken.
- Microsatellite analysis of ghost bat populations across the Pilbara indicated high connectivity with a low level of genetic structuring between the Hamersley and northern Chichester regions. Spatial analyses indicated ghost bats were detected most frequently between caves located within ~10 km. Temporal analyses indicated a small number of individuals used the same cave over a two year time period.
- Assessment of the genetic diversity, genetic structure and cave use by Pilbara ghost bats has been completed, and two reports have been prepared.
- DNA barcoding and microsatellite analysis of pilot whales stranded at Hamelin Bay has been completed.
- DNA barcoding was used to confirm species identity of several stranded cetaceans.

- Assessment of the genetic diversity of brushtail possums translocated to Matuwa compared with their source populations has been completed, including development of a population viability model. A scientific manuscript is currently in review.
- Tissue samples of Western Australian brushtail possums have been sent to the South Australian Museum for phylogenomic analysis

Management implications

- An Australia-wide phylogenetic assessment of *Isoodon. 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. This information has informed an evaluation of threat status by the Commonwealth for the eastern and Tasmanian sub-species of *I. obesulus*.
- Population viability analysis of quenda populations provides information to inform management of populations in the urban interface and demonstrates that 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. Assessment of the 2016-17 translocation of rock wallabies to Kalbarri National Park showed that establishing mixed populations of Mt Caroline and Nangeen animals at Kalbarri increased their genetic diversity relative to either source population, and genetic analysis of a juvenile animal in 2017 indicated successful reproduction between a Kalbarri male and a wheatbelt female, indicating no genetic barriers to reproduction and that mixing founder animals from different populations is an effective management strategy
- Genetic analyses and a Population Viability Analysis (PVA) of brushtail possums at Matuwa showed that low genetic diversity or inbreeding are not likely contributing to the small population numbers. Modelling suggests that if population size remains small then augmentation is required to maintain genetic diversity.
- Microsatellite genotyping of ghost bat scats has been successful and represents a novel approach to population monitoring of this species that is difficult to monitor with traditional methods. Genetic analysis indicated high connectivity of ghost bat populations across the Pilbara, with a low level of genetic structuring between the Hamersley and northern Chichester regions, providing information for environmental impact assessment. Spatial analyses indicated ghost bats were detected most frequently between caves located within ~10 km providing information on home range and dispersal distances.

Future directions

- Phylogenomic analysis of *Isoodon* spp. will be undertaken to formally resolve the species boundaries across the group. Analyses of historical (using museum skins) and contemporary genetic diversity will be used to document their recent evolutionary history.
- Quenda mating system manuscript will be finalised.
- Comparison of historic and contemporary population genetics of wheatbelt rock wallaby populations will be finalised to monitor genetic change and investigate impact of past management actions. Monitoring of the Kalbarri National Park translocated rock wallaby populations will be completed and a manuscript prepared.
- Manuscript on brushtail possum translocation to Matuwa will be finalised.
- Assessment of the taxonomy of brushtail possum subspecies will be completed in conjunction with South Australian Museum.
- Further sampling of Pilbara and Kimberley ghost bat populations will be conducted to extend analyses.
- Genetic analyses of the Hamelin Bay pilot whale stranding will be completed.