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Genetic assessment for conservation of rare and threatened fauna

Animal Science

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Project Team	granted
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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. Genetic information can aid resolution of the taxonomic identity of species and sub-species to determine whether they have appropriate conservation listing. At a population level, analysis of the genetic diversity present, and its distribution across extant populations, provides information on the genetic 'health' of threatened species. Concurrent analysis of some of the proximal drivers of genetic change can identify appropriate management responses for declining populations to improve conservation outcomes. Further, emerging genomic technologies are enabling novel genetic monitoring approaches, expanding the available toolbox for threatened species monitoring.

Aims

- Resolve taxonomic boundaries of Western Australian bandicoots (*Isoodon* sp.), particularly *I. auratus*, *I. fusciventer* and *I. obesulus*, and their subspecies, to determine appropriate conservation rankings and management units.
- Investigate genomic diversity of island and mainland populations of golden bandicoots (*I. auratus*) and assess success of reintroductions in WA and NT.
- Develop molecular identification of golden and northern brown bandicoots to assist in morphological identification of bandicoots in the field in the Kimberley.
- Assess long-term genetic change in the reintroduced population of golden bandicoots at Matuwa.
- 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.
- Assess the genetic diversity and patterns of introgression of boodies translocated to Matuwa.
- Contribute to assessment of sub-species boundaries within northern quolls (*Dasyurus hallucatus*) using genomic sequencing of museum and contemporary specimens.
- Investigate genetic diversity of translocated brushtail possums (*Trichosurus vulpecula*) and their source populations at Matuwa.
- Contribute to taxonomic assessment of brushtail possums, including resolution of Western Australian sub-species.
- Assess genetic diversity, genetic structure and monitor cave use of ghost bat (*Macroderma gigas*) populations in the Pilbara, and develop high-throughput genotyping array and molecular sexing markers for individual identification of ghost bats from faecal DNA.
- Assess species composition and individual relatedness of Hamelin Bay pilot whale stranding.
- Assess whether collection of blow from humpback dolphins using drones is suitable for non-invasive DNA sampling
- Assess genetic diversity across wild, translocated and historical populations of Gilbert's potoroo to inform a population management strategy
- Assess genetic diversity and genetic connectivity amongst Pilbara leaf-nosed bat roosts and patterns of sex-biased dispersal
- Assess use of faecal DNA sampling to estimate population size of mala at Matuwa
- Provide wildlife species identification using DNA barcoding

Progress

- Mitochondrial and microsatellite analysis of *I. obesulus*, *I. fusciventer*, *I. auratus* and *I. macrourus* has been completed, with one manuscript published and another close to submission. Mitochondrial and microsatellite analysis support elevation of *I. fusciventer* from sub-species of *I. obesulus* to full species.

Additional sampling has resolved greater distinction between *I. fusciventer* and *I. auratus*, supporting their current taxonomy, although analyses were insufficient to fully resolve the taxonomic relationship with South Australian *I. obesulus*. Genomic analyses are underway on museum skins and contemporary samples to provide further resolution.

- Genomic analysis of island, mainland and reintroduced populations of *I. auratus* is underway.
- Species identification of field-collected samples of golden and northern brown bandicoots is ongoing.
- Genomic analysis of temporal samples of golden bandicoots at Matuwa is underway with a student to be recruited for the project in 2021.
- Analysis of quenda using fauna underpasses has not progressed as collaborator is no longer at UWA.
- Microsatellite analysis of genetic diversity and structure of wheatbelt and mid-north west rock wallaby populations has been completed, including analysis of all individuals translocated to Kalbarri National Park from 2016 to 2018 and new recruits to 2019 with a manuscript currently in preparation (Kristen Nillson leading). A further project to undertake genomic analyses (whole genome sequencing, exon capture, ddRAD) of historical (museum) and contemporary populations of black-flanked rock wallaby is currently underway in collaboration with Australian Museum and ANU researchers.
- Two manuscripts have been published on Matuwa boodies, one detailing patterns of mtDNA and microsatellite diversity and introgression amongst Shark Bay and Barrow Island boodies two years post-translocation and the second using genome-wide SNP data to assess hybrid structure and fitness outcomes of different hybrid classes.
- Genomic analysis of museum specimens and contemporary samples of northern quolls is underway with type specimens sourced from the Natural History Museum for sequencing, in collaboration with Western Australian Museum.
- A manuscript detailing the genetic diversity of the translocated brushtail possum population at Matuwa has been published indicating a signature of a genetic bottleneck associated with translocation, although genetic health of the population is currently reasonable.
- Taxonomic assessment of brushtail possums has not progressed with collaborators at Adelaide University.
- Genetic monitoring of ghost bats at West Angelas, the Robe Valley and South Flank mining precincts have been completed. Additional populations in these studies will contribute to a Pilbara-wide population genetic study. Whole genome sequencing has been completed on a male and female ghost bat and markers for molecular sexing have been identified and validated. A manuscript detailing the use of microsatellite and molecular sexing markers for faecal DNA analysis in ghost bats has been published. A reduced SNP array for high throughput analysis of scats has been designed and is now operational with a manuscript currently in preparation.
- Preliminary analysis of DNA barcoding and microsatellite data from pilot whales stranded at Hamelin Bay has been completed. Further analysis will be undertaken as part of a Masters project developing molecular ageing methods for the species (Matt Heydenrych, Curtin University).
- DNA analysis of dolphin blow samples from drone sampling has been completed and a manuscript published, demonstrating that collection of blow is possible although no DNA was able to be extracted from the collection vessels.
- Tissue samples from wild, translocated and historical populations of Gilbert's potoroo have been sourced and DNA extractions are currently underway.
- Genomic data have been generated for Pilbara leaf-nosed bat populations and preliminary data analyses are underway.
- Faecal DNA analysis and population size estimation for mala has been completed as part of a Masters project (Shannon Treloar, ECU)
- DNA barcoding of wildlife species is ongoing, as required.

Management implications

- An Australia-wide phylogenetic assessment of *I. obesulus* and related species/subspecies has enabled a more informed evaluation of taxonomic boundaries in this group as well as evaluation of threat status, particularly for the eastern and Tasmanian sub-species of *I. obesulus*.
- Genetic assessment of the diversity of wild and reintroduced populations of golden bandicoots will enable future management decisions regarding translocations to other mainland and island sites, as well as identifying whether existing translocations require genetic management (e.g. reduce inbreeding, reduce genetic erosion). Molecular identification of golden and northern brown bandicoots in the Kimberley will

assist development of additional characters for field identification.

- Genetic and genomic analysis of rock wallaby populations will assess the genetic health of extant and historical populations, including an assessment of the effectiveness of past management interventions to inform planning of future conservation actions. Assessment of the Kalbarri National Park translocation of rock wallabies showed establishing founder populations from mixed divergent sources increased genetic diversity relative to the source populations. Analysis has also confirmed successful reproduction between extant Kalbarri animals and introduced animals, suggesting no pre-zygotic reproductive barriers are present.
- Mixing divergent source populations of boodies in a translocation to Matuwa has increased genetic diversity of the reintroduced population, but there is trend of asymmetrical introgression towards crosses between smaller-sized Barrow Island males and larger-sized Shark Bay Island females. Assessment of survivorship and fecundity of introgressed individuals relative to their ancestry indicated no fitness impacts of introgression.
- Genetic and population viability analyses 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 faecal DNA has proven to be an effective, non-invasive method to assess genetic diversity of ghost bat populations as well as to monitor movement of individual bats in space and time. Monitoring projects have indicated individual bats remain in caves over multiple years and most frequently use caves within ~10km. Information on ghost bat cave use is informative for environmental impact assessment. Development of high-throughput SNP genotyping methods has enabled more rapid and reproducible screening of faecal DNA samples for monitoring.
- Genetic analysis of Gilbert's potoroo will inform a population management strategy to ensure genetic diversity is conserved in this highly endangered species.

Future directions

- Phylogenomic analysis of *Isoodon* spp. is being 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.
- Analysis of genomic data from island, mainland and reintroduced populations of *I. auratus* will be progressed to evaluate the genetic health of current populations and inform future translocations. Genomic resources developed for this project will be used to design a reduced SNP array for high throughput identification of *I. auratus* and *I. macrourus* field samples.
- High-resolution genomic analyses will be undertaken to document the genetic impacts of management interventions on rock wallaby populations, while analyses of historical and contemporary diversity will document the recent evolutionary history of the species. Methods for non-invasive sampling of rock wallabies will be investigated.
- Further genomic and morphological analyses of the admixed population of boodies at Matuwa will be undertaken by UWA PhD candidate Kate Rick to explore the genomic consequences of introgression.
- Further sampling of Pilbara ghost bat populations will be conducted through ongoing monitoring of populations in BHP and Rio Tinto mining precincts. Further improvements to the SNP genotyping array will be undertaken to include sexing markers and a project to evaluate optimal sampling protocols for ghost bats to quantify population size to enable impact assessment.
- Genomic analysis of Gilbert's potoroo will be undertaken and information contributed to the population management strategy.
- Genomic analysis of Pilbara leaf-nosed bat will be undertaken and information provided to stakeholders.