

Concept Plan SP 2022-035

# Island genomes: enhancing management of Australia's threatened mammals

BCS Animal Science

## Project Core Team

X X **Supervising Scientist** Kym Ottewell  
**Data Custodian** Kym Ottewell

**Project status as of July 20, 2023, 9:23 a.m.**

X X New project, pending concept plan approval

**Document endorsements and approvals as of July 20, 2023, 9:23 a.m.**

X X  
**Project Team** granted  
**Program Leader** granted  
**Directorate** required



# Island genomes: enhancing management of Australia's threatened mammals

## Program

BCS Animal Science

## Departmental Service

Service 7: Research and Conservation Partnerships

## Background

Small populations, particularly those on islands, lose genetic diversity as a result of strong genetic drift. A long history of fauna extinctions on mainland Australia means that conservation of our threatened mammals requires effective management of different types of “islands” – continental islands isolated for at least 8,000 years by rising sea levels, mainland remnants resulting from range collapse over the past century, and increasingly, recent translocates into predator-controlled environments (either fenced exclosures or pest-free islands). Populations subject to single or repeated reductions in size will rapidly lose genetic diversity. More insidiously, island populations, held at small sizes for thousands of generations, accumulate deleterious mutations – genetic load – because selection against these is overwhelmed by drift. This erosion of genetic diversity and accumulation of genetic load reduces the adaptability and viability of populations, hampering their long-term survival. The extent to which genetic load increases in small, recently translocated populations is relatively unknown. Comparing populations with different histories of isolation and size reduction will broaden our understanding of how genetic load accumulates, and whether this impacts on translocation success.

This project focuses on seven species (rufous hare-wallaby, boodie, woylie, dibbler, golden bandicoot, black-flanked rock wallaby, tammar wallaby) with extensive and well-documented histories of conservation translocations and where there is potential for mixing populations to reduce genetic load in ongoing management. These species have a history of range collapse but have multiple fragmented remnant populations where information on current/historical divergence will be critical to management decisions. These species have had multiple previous or ongoing translocations with documentation of translocation history and monitoring of translocation outcomes. We will assess (i) whether outcomes of past translocations can be predicted by genetic diversity or load of source and translocated populations, and ii) for mixed populations, whether genomic/phenotypic divergence among sources has positive or negative outcomes.

## Aims

The specific aims are:

1. To test for increased genetic load on islands as well as reduced genetic diversity on islands and in serially bottlenecked translocated populations, relative to pre-decline or remnant mainland populations.
2. To estimate historical population sizes, migration rates and divergence times, and also phenotypic divergence, between potential source populations in relation to now extinct, geographically intervening populations.
3. To test whether high diversity, low load or (for mixed populations) genetic similarity of source populations improves short-term outcomes of translocations after controlling for confounding factors.

## Expected outcome

Determining the impacts of genetic diversity and genetic load on translocation success for a suite of threatened species will assist in the development of broader guidelines for translocations on when it is necessary to mix populations to restore genetic diversity and reduce genetic load, and the relationship between degree of genetic and/or morphological divergence between populations and translocation success. Scientific findings will be communicated through scientific manuscripts, reports and presentations to species recovery teams, external stakeholders and the general public.

## Strategic context

This project addresses many of the objectives of the Science Strategic Plan 2018-21:

- Conduct biological survey, including genetic survey, in priority management areas, and for key species and ecological communities.

- Effectively acquire and share knowledge of biodiversity.
- Undertake research to address knowledge gaps for threatened species and ecological communities.
- Assess conservation status of species and ecological communities.
- Provide scientific basis for monitoring of threatened species and ecological communities.
- Effective communication of scientific knowledge and information to policy and decision makers through appropriate processes.
- Undertake research and monitoring to address gaps in biodiversity knowledge and support decision-making.
- Identify and realise opportunities for adoption of technical advances and innovative approaches for conservation.
- Continue development of up-to-date, integrated and accessible data catalogues and databases.

## Expected collaborations

This SCP covers activities conducted on an externally-funded ARC Linkage research project. Collaborators on the project include Craig Moritz (Australian National University), Nicola Mitchell (University of Western Australia), Mark Eldridge (Australian Museum), Kenny Travouillon (Western Australian Museum), Steve Cooper (University of Adelaide) and Jenny Pierson (Australian Wildlife Conservancy).

## Proposed period of the project

July 19, 2022 – Dec. 31, 2023

## Staff time allocation

to	X	X	X	X
Role	Year 1	Year 2	Year 3	
Scientist	0.3	0.3	0.3	
Technical	0.1	0.1	0.1	
Volunteer				
Collaborator				

## Indicative operating budget

to	X	X	X	X
Source	Year 1	Year 2	Year 3	
Consolidated Funds (DBCA)				
External Funding	164,453,223,032	83,571		