Science for Saving Species

Research findings factsheet

Project 4.1.6.2

Threatened Species Recovery Hub

National Environmental Science Programme

Genetic management and population modelling to benefit translocated mammals

In brief

Many threatened species are becoming increasingly isolated due to habitat loss and degradation, which can lead to loss of genetic diversity and increased extinction risk. Translocating animals between locations is one way of facilitating much-needed gene flow and improving conditions for population growth.

This project focused on the genetic management of three threatened mammals: the banded hare-wallaby (*Lagostrophus fasciatus*), the dibbler (*Parantechinus apicalis*) and the Shark Bay bandicoot (*Perameles bougainville*). Two of these – the banded hare-wallaby and the Shark Bay bandicoot – are now largely restricted to islands. All three species are being translocated to Dirk Hartog Island in Western Australia as part of a major restoration project led by the WA Department of Biodiversity, Conservation and Attractions. We aimed to devise strategies to maximise the retention of genetic diversity in translocated populations, while minimising detrimental impacts of 'harvesting' animals for translocation on the wild source populations.

We conducted population viability analysis (PVA) modelling, incorporating both demographic and genetic information for each species. We devised optimal translocation strategies for each species, which all included sourcing founders from multiple island populations to maximise genetic diversity. The PVA models for the Shark Bay bandicoot and banded hare-wallaby indicated that translocations should be avoided during drought, and that translocation of the dibbler to much larger islands is required for the survival of the island dibbler populations. Consequently, moving dibblers to the 630 km^2 Dirk Hartog Island, via an intermediary captive breeding program, will facilitate population recovery, and should enhance resilience to environmental fluctuations and retention of genetic diversity. We have shown how PVA models can provide important insights into the genetic management of a species and offer a framework for planning future translocations and captive breeding programs.

Dibbler. Image: Perth Zoo

The University of Western Australia

Murdoch University

australian wildlife conservancy

Department of Biodiversity, Conservation and Attractions

The University of Sydney

Background

Habitat fragmentation, predation from introduced pests and anthropogenic-driven environmental events such as fire and drought put further pressure on already fragile ecosystems, and lead to increasingly isolated animal populations. Small, isolated populations can lose genetic diversity and may become inbred, and if the population declines below sustainable thresholds, the species can become locally extinct.

Given the major threats to Australia's remaining mammal species, interventions are necessary to support healthy levels of genetic diversity. Translocating animals between locations is one way of facilitating gene flow to prevent the erosion of genetic diversity. However, translocations are resource intensive, and their success is not guaranteed. Translocation success depends on many factors including the life history of the animal (e.g. fecundity and mortality), external factors such as drought and disease, and the number of founding individuals. How such factors interact is hard to predict. Furthermore, when assessing if a translocation should take place, it is also important to consider the impact of removing animals from small, remnant wild populations.

Maintaining genetic diversity is a key component of successful translocation programs and is heavily influenced by the source(s) of translocated animals. It is important to understand the genetic diversity of the founder population(s). Gaining access to ideal, genetically diverse founder populations may not be possible if a species is restricted to offshore islands, as island populations are usually isolated with no immigration, and their small effective population sizes lead to low genetic diversity. Consequently, strategies need to be investigated to optimise the selection of founders from multiple source populations to maximise genetic diversity of founder groups. Captive breeding is a useful tool for translocations as it can assist in boosting founder numbers when remnant source populations are of limited or uncertain size, as well as mitigate the inherent risk of extinction due to over-harvesting for wild-to-wild translocations.

The distribution of the Vulnerable banded hare-wallaby (*Lagostrophus fasciatus*), Endangered dibbler (*Parantechinus apicalis*) and Endangered Shark Bay bandicoot (*Perameles bougainville*) have all been drastically reduced as a result of multiple, interacting threatening processes occurring on mainland Australia. As remnant populations of these species are predominantly on offshore islands, there are concerns these populations have low genetic diversity, may be reaching critically low population sizes, and may have enhanced extinction risks in the long-term. Translocations are required to establish further insurance populations to expand population numbers and buffer against future population declines.

Aim of the research

This project focused on the genetic management of the banded hare-wallaby, dibbler and Shark Bay bandicoot, which are being translocated to Dirk Hartog Island in Western Australia, as part of the 'Return to 1616' project managed by the Western Australian Department of Biodiversity, Conservation and Attractions (DBCA). Return to 1616 is an exciting and ambitious project aiming to restore Dirk Hartog's biodiversity to what it was before European arrival, following the removal of livestock (sheep, goats) and feral predators. At the time of the project, two species (the hare-wallaby and bandicoot) were also being translocated into predator-free mainland sanctuaries managed by Australian Wildlife Conservancy. The three subprojects aimed to devise strategies to maximise the retention of genetic diversity in the translocated populations, while minimising the detrimental impacts of harvesting on the wild source populations.

LEFT: Shark Bay Bandicoot. Image: Saul Cowen, DBCA WA

What we did

The research was led by the University of Western Australia in close collaboration with DBCA. Australian Wildlife Conservancy (AWC), the University of Sydney and Murdoch University were also involved in providing samples, expertise and genetic datasets.

The initial focus was to assess the current genetic variation within species to fully understand the number of genetically distinct populations, inter-population dynamics and the diversity harboured within them. The three projects then used population viability analysis (PVA) modelling to support the development of optimal translocation strategies for each of the three species.

PVA modelling is an informative tool that allows managers to make robust predictions around population survival and retention of genetic diversity under differing management and environmental scenarios, simultaneously for source and translocated populations. We used an individual-based simulation approach, which incorporates both intrinsic and extrinsic factors at the individual level, to construct stochastic population models using Vortex software.

Baseline PVA models were developed that accurately reflected the life history of each species and included genetic data. To do this, life-history parameters such as reproduction and mortality rates, as well as the frequency of stochastic events such as drought, were carefully selected from primary sources, as well as expert elicitation – the more accurate these parameters are, the more accurate are the model projections. We then constructed and trialled various translocation scenarios aimed at optimising translocation programs. For example, the number of individuals needed, over what timeframes, and how frequently animals should be moved are all questions that can be answered. Further, the value of mixing populations to improve genetic diversity can be assessed, as can the impact of harvesting on critical source populations.

Dirk Hartog Island, Western Australia. Image: DBCA WA

What we found

Banded hare-wallaby (*Lagostrophus fasciatus*)

The banded hare-wallaby has remnant wild populations only on Bernier and Dorre Islands off the Western Australia coast. These island populations have been used as source populations for conservation translocations, including new translocations to Dirk Hartog Island and Mt Gibson Sanctuary (AWC), but source populations regularly fluctuate in size due to cyclical drought conditions on the islands. Harvesting for translocations during drought periods has the potential to reduce the population sizes and could lead to further reductions in genetic diversity.

We used a limited microsatellite marker panel (7 markers) to quantify genetic variation across the two islands and incorporated this data into PVA models. Crucially, we included the impacts of regular periods of low rainfall in our models, and tested for the impacts to source and translocated population viability of increases in drought frequency expected due to climate change.

Our findings showed that the genetic diversity of the banded hare-wallaby was very low compared to that of mainland populations of the co-occurring rufous hare-wallaby (*Lagorchestes hirsutus*), and that both remnant island populations possibly underwent genetic bottlenecks in the 1990s. Interestingly, genetic differentiation of banded hare-wallaby was lower than that observed for rufous hare-wallaby across the two islands but indicated a lack of contemporary gene flow.

Banded hare wallaby. Image: Colleen Sims, DBCA WA

Based on the genetic data, our models showed that when establishing new populations, 25 founders may be sufficient to avoid a lasting bottleneck effect under favourable environmental conditions, but that risks multiply for founder sizes of less than 20 animals. PVA modelling suggests that 100 founders should lead to high survival probabilities and genetic diversity retention in newly translocated populations. We recommended mixing both source islands as opposed to harvesting from a single source to maximise genetic diversity. Increasing drought frequencies strongly impacted both survival and growth of new populations, and so we recommended that translocations are avoided during extended periods of drought.

Dibbler (*Parantechinus apicalis*)

The dibbler now only occurs naturally on mainland Australia in the Fitzgerald River National Park and on two small islands, Boullanger and Whitlock Islands in Jurien Bay off the west coast of Western Australia. The island populations are at risk of extinction with consistently low population numbers observed over the past decade. Dibblers are currently being harvested from Boullanger and Whitlock Islands for captive-breeding at Perth Zoo, which can enhance founder numbers on Dirk Hartog Island. However, due to low population sizes on Boullanger and Whitlock Islands there is a risk of over-harvesting leading to irreversible population declines.

We described the genetic diversity of the remnant island populations,

What we found (continued)

and the established translocated population on Escape Island from 2013 to 2018, using 14 microsatellite markers. Our data showed a trend of decreasing genetic diversity over time, with current genetic diversity in island dibblers being very low. The Whitlock Island population had the lowest genetic diversity whereas the admixed population on Escape Island had the highest. We found two distinct genetic clusters in the Jurien Bay Islands and supported an earlier observation of uneven mating success on Escape Island.

The PVA model predicted further declines in genetic diversity in the future, as well as a steady decline in population sizes for all islands. Based on modelling projections, and without any other intervention, the harvesting of animals from Whitlock and Boullanger Island is recommended to initiate captive breeding and to provide founders for the Dirk Hartog Island population to maximise genetic diversity in the Dirk Hartog Island population. Escape Island may be used as a surrogate for Boullanger Island. We found that the optimal translocation scenario, to Dirk Hartog Island, considering retention of genetic diversity and impact to source populations, includes founding the captive population with six mate pairs from Whitlock Island and 14 from either Boullanger or Escape Islands and releasing at least 80 animals from the captive breeding population onto the island over two years.

Shark Bay bandicoot (*Perameles bougainville*)

Only two remaining wild populations of the Shark Bay bandicoot exist on Dorre and Bernier Islands in Shark Bay, Western Australia. Prior to this study, Shark Bay bandicoots had been translocated three times, with two of the translocated populations persisting. To reduce the extinction risk for this species, at the time of this study it was targeted for further translocation to several locations, including to Mt. Gibson (an AWC sanctuary, reintroduction now complete) and to Dirk Hartog Island.

We conducted PVA modelling using demographic data from published literature and expert elicitation, and projections of historical molecular genetic data (Smith and Hughes 2008). The impacts of periodic fluctuations in rainfall on bandicoot food sources were included in the model.

PVA modelling results showed the planned translocations can occur without risk of population decline at either source location, Bernier or Dorre Island, unless drought occurred at a frequency of 1 in 5 years or more, an increase from current estimates of around 1 in 7 years. At this higher drought frequency, population decline occurs in all three source populations with or without harvesting. Our results showed that mixing the populations from Bernier and Dorre Islands will improve the genetic diversity of the newly established populations in the long-term.

New genetic data using single nucleotide polymorphisms (SNPs) will allow us to determine if genetic diversity is retained in the translocated populations. These SNP data can be incorporated into future PVA models, using the models developed here as a baseline.

General implications and recommendations

Our research shows how analysis of genetic variation combined with population modelling can be used to inform the management of small animal populations by simulating the sensitive trade-offs involved in translocating threatened species. This is a key finding for species with few remnant populations remaining, as previously little was known about the impact on source populations of harvesting for translocations. PVA modelling can also be used to assess the cost-effectiveness of various translocation strategies.

The results from this research are already having an impact on decision-making for the target species in terms of how many individuals can be safely harvested from source populations, and how many are needed to maximise the chance of survival and retention of genetic diversity that will be vital for their long-term viability. In addition, the inclusion of PVA modelling in translocation proposals for other species is now strongly encouraged by the Western Australian DBCA, and encouraged by AWC for suitable species, to assist in evaluating translocation scenarios.

As monitoring of translocations of the dibbler, Shark Bay bandicoot and banded hare-wallaby are currently underway on Dirk Hartog Island, using the approximate recommendations from this

General implications and recommendations (continued)

project, it will be valuable to compare monitoring data to the population dynamics we simulated using PVA. Genetic monitoring of translocated populations at Dirk Hartog Island and Mt Gibson is also ongoing and we recommend genetic monitoring of source populations at regular intervals to determine the impacts of harvesting, as well as natural stochastic events, on population genetic diversity. In the instance of translocated populations, it will be important to evaluate patterns of admixture to detect potential mating bias such as has occurred in dibblers.

A clear trade-off exists in conservation translocation programs between maximising the viability of new populations and minimising the negative impact on the precious source populations. With many threatened Australian species experiencing increased fragmentation and subsequently elevated extinction risk, devising translocation strategies that maximise genetic diversity is increasingly being considered for long-term management. The use of PVA models can provide important guidance for the genetic management of a population and a framework for planning translocations and captive breeding programs.

Cited material

Aisya Z., White D.J., Thavornkanlapachai R., Rick K. and Mitchell N.J. (In Press) Using PVA and captive breeding to balance trade-offs in the rescue of the island dibbler onto a new island ark. *Scientific Reports.*

Smith S. and Hughes J. (2008) Microsatellite and mitochondrial DNA variation defines island genetic reservoirs for reintroductions of an endangered Australian marsupial, *Perameles bougainville*. *Conservation Genetics* 9:547-57.

White D., Ottewell K., Spencer P.B.S., Smith M., Short J., Sims C. and Mitchell N.J. (2020) Genetic consequences of multiple translocations of the banded hare-wallaby in Western Australia. *Diversity* https://doi.org/10.3390/d12120448

White, D. and Ottewell, K. (November 2020). Genetic management and population modelling of translocated fauna: Banded hare-wallaby (*Lagostrophus fasciatus*). NESP Threatened Species Recovery Hub Project 4.1.6.2 report, Brisbane.

White, D. and Aisya, Z. (November 2020). Genetic management and population modelling of translocated fauna: Dibbler (*Parantechinus apicalis*). NESP Threatened Species Recovery Hub Project 4.1.6.2 report, Brisbane.

White, D. and Hogg, C. (November 2019). Shark Bay Bandicoot Management: Population modelling for optimising strategies for the Shark Bay bandicoot translocation program phase 1 – Dirk Hartog Island and Mt. Gibson. NESP Threatened Species Recovery Hub Project 4.1.6.2 preliminary report, Brisbane.

Further Information

Daniel White - daniel.white@uwa.edu.au

The authors would like to thank Saul Cowen (DBCA) for valuable comments and additional images, Nicki Mitchell (UWA) for project support and Jennifer Anson (AWC) for reviewing this factsheet.

Threatened Species Recovery Hub
National Environmental Science Programme

Cite this publication as NESP Threatened Species Recovery Hub. 2021. Genetic management and population modelling to benefit translocated mammals, Project 4.1.6.2 Research findings factsheet.

This project is supported through funding from the Australian Government's National Environmental Science Program.