

National Environmental Science Programme



Shark Bay Bandicoot Management

(Preliminary report subject to further sensitivity testing)

Population modelling for optimising strategies for the Shark Bay bandicoot translocation program phase 1 – Dirk Hartog Island and Mt. Gibson

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Recommendations

Based on our Population Viability Analysis (PVA) models it appears that Shark Bay bandicoots (SBB, formerly western barred bandicoots) are well suited for a translocation program. Our modelling predicts that survival probabilities are relatively high for all source populations unless survival and reproduction is reduced by, for example, an environmental stochastic event on average once every 5 years. In the absence of any further supplementation, long-term (50 years) predicted survival probabilities of both Dirk Hartog Island and Mt. Gibson populations fall below that of their source populations. This is likely driven by smaller populations in our models not surviving environmental stochasticity. Although SBBs are well adapted to surviving harsh environmental conditions, we recommend ongoing monitoring of translocated populations. Reinforcement from source populations, along with other mitigation measures, may improve survival probabilities. The final report will provide recommendations regarding optimal supplementation strategies given realistic logistical constraints. The final report will also recommend the smallest translocated population size required to maximise the probability of long-term survival of all translocated populations. In the models, population growth is restricted by a stochastic environmental event that reduces survival to 35% and reproduction by 80% occurring at a frequency of 1 in 5 years compared to a frequency of 1 in 10 years. Of the source populations, Faure Island shows greatest sensitivity to the greater frequency, which is likely driven by the bottleneck through Heirisson Prong and compounded by its smaller population size. Contemporary genetic data will better inform ongoing management of Faure Island.

Mixing of source populations achieves highest genetic diversity in translocated populations, as observed with the Arid Recovery populations (1). New comprehensive genetic data recently attained will be incorporated into future models for confirmation. However, the PVA models show that Mt Gibson is unlikely to have as high diversity as Dirk Hartog Island even though it did have three source populations (Dorre, Bernier and Faure) compared to two for Dirk Hartog (Dorre and Bernier). This is likely due to Faure Island, which is itself a translocated population. Faure was established with founders sourced solely from Dorre via Heirisson Prong, thereby biasing the allelic frequencies of the Mt. Gibson population in favour of the Dorre population. The genetic analysis of contemporary samples from Dorre, Bernier and Faure islands that is currently being undertaken will better inform the PVA models for the final report.

Based on our PVA models we recommend the following:

- Phase 1 of both DBCA and AWC translocation programs can occur concurrently without risk of population decline in Bernier and Dorre populations unless severe conditions are occurring;
- Risk of population decline in all 3 source populations is seen at higher frequencies of reduced survival and reproduction, so managers should take environment conditions into account when harvesting;
- To achieve highest genetic diversity in translocated populations mixing of source populations as part of the same relocation is recommended, preferably with an equal contribution from both Dorre and Bernier Island populations;
- The genetic diversity of the Mt. Gibson translocation could be increased by including a greater number of Bernier individuals, possibly in place of Faure individuals; and
- Investment in the collection of life history data to better inform the models is essential. The models are currently based on a number of assumptions and as such this report such be treated as a guide. Life history data required includes, but is not limited to:
 - % of females breeding at any given time on all islands
 - Relationship between % females breeding and mean inbreeding coefficients at all three source populations (Dorre, Bernier, Faure)
 - Estimates of mortality, particularly juvenile mortality (the models are particularly sensitive to mortality estimates)

Caveats

Data provided for the parameterisation of the models was collected between 2006 and 2013 (2), and late 1980s/early 1990s (3, 4). Genetic data for the models was collected between 1995 and 2005, using only six variable microsatellite markers (5). More contemporary samples and survey data is required to reduce variability in the models.

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Cover page photo: Shark Bay Bandicoot. Image: DBCA, WA

Executive Summary

The range of the Shark Bay bandicoot (SBB; *Perameles bougainville*) has been drastically reduced due to a range of threatening processes including feral predators, land development, habitat fragmentation, fire and drought. There are currently only two remaining wild populations of SBB on Dorre and Bernier islands in Shark Bay, Western Australia. Translocation is an important conservation strategy for this species' recovery. To date, SBBs have been translocated three times including Heirisson Prong, WA (1995, 1996), Arid Recovery, SA (2000, 2009) and Faure Island, WA (2005) with only the Arid Recovery and Faure Island populations still persisting. To prevent any further loss of SBBs, this species has been targeted for translocation to several locations, including to Mt. Gibson (131,710 hectare AWC sanctuary located north-east of Perth) and to Dirk Hartog Island, Shark Bay, WA (part of the Return to 1616 project) between 2017 and 2019. Future translocation locations also include Sturt Desert, Pilliga, and Mallee Cliffs. The extinction probability of harvesting Dorre and Bernier Islands has been quantified using population viability analysis (PVA) modelling. The modelling has been undertaken using parameters collected from the published literature and collected from unpublished WA Department of Biodiversity, Conservation and Attractions (DBCA) reports.

The objective of this report was to use Population Viability Analysis (PVA) modelling to provide guidelines for phase 1 of the SBB translocation program, i.e. the movement of animals to Dirk Hartog and Mt. Gibson from Bernier, Dorre and Faure Islands between 2017 and 2019. The following three areas were assessed: 1) the optimal translocation strategy to Dirk Hartog Island only; 2) the implications on population viability of the planned translocation strategy to Mt. Gibson; and 3) combining 1 and 2 to re-assess the impact on source populations of multiple harvest events. Molecular genetic data created by Smith and Hughes (5) was used as a starting point for the island populations. It should be noted that the majority of parameters, including genetic data, are based on data collected more than ten years ago. More recent survey data and genetic samples have been requested from DBCA to improve the models into the future. The occurrence of a stochastic environmental event that leads to reductions in survival and reproduction was also built into the model, occurring 1 in 5 years and 1 in 10 years. This was to simulate the range and possible frequencies of population size fluctuation associated with periodic fluctuations in rainfall (2). For convenience from hereon this event is referred to as a drought, although true droughts are likely to have more complex outcomes, for example arising from unknown species interactions. A summary of the results from the PVA modelling translocation scenarios for 50 calendar years are provided. PVA modelling results show that the planned Phase 1 translocations can occur without risk of population decline at either source (Bernier or Dorre) location, unless drought is occurring at a frequency of 1 in 5 years. The probability of population decline at all 3 source populations increases if harvested in a drought year. Mixing the populations of Bernier and Dorre Islands will improve the genetic diversity of the receiving population in the long term. New genetic data using single nucleotide polymorphisms (SNPs) will permit the calculation of genome wide heterozygosity to ascertain genetic diversity retention. This SNP analysis will be concluded in late 2018 and incorporated into future models.

Results Summary

A summary of the results from PVA modelling translocation scenarios for 50 calendar years are provided in Tables 1 to 4.

Tables 1 and 3 show results for target populations and source populations, respectively, when drought frequency is set to 1 in 10 years. Survival probability for target populations fluctuate from 0.67 to 0.81 (Table 1). Further sensitivity testing of the source individuals and empirical genetic data should improve the resolution around this, as well as increasing the number of iterations to 1000. Translocations of 100 individuals in one year, have a slightly lower probability of survival than 50 individuals per year over two years. Target population sizes are constant across all the scenarios when drought frequency is 1 in 10 years (Table 1; Figure 1), and the lower final N of Mt Gibson is predominantly driven by its smaller carrying capacity. The probability of survival of the source populations remains high (Table 3); and final population sizes of Bernier and Faure are lower than initial sizes, likely due to conservative carrying capacity estimates of these islands (Table 3).

The trends seen for a drought frequency of 1 in 10 years were mostly repeated for a frequency of 1 in 5 years, although final population sizes were reduced for all populations (Tables 2 and 4). The survival probabilities of translocated populations were markedly reduced in all scenarios (see Table 2). Reductions in long-term source population sizes appear to be driven by the 1 in 5 drought frequency rather than the harvest as the downward trend is apparent in high frequency drought years without any form of harvest (Figure 2a versus 2b).

Table 1. Summary of PVA results for *target* populations after 50 years with a drought probability of 2.5% (which equals 1 in 40 generations or 1 in 10 calendar years). P: probability of survival; N: mean number of individuals in extant populations; H_{e} : expected heterozygosity; DHI: Dirk Hartog Island; MG: Mt. Gibson. Scenarios in bold are the optimal scenarios for DHI only, MG only and DHI & MG combined.

Target Pop.	Scenario #	Description	Ρ	N	Η _ε
DHI only	1	50 individuals from Dorre in year 1 and 50 individuals in year 2	0.77	2986	0.270
	3	100 individuals from Dorre in year 1	0.72	3058	0.276
	5	50 individuals from Dorre in year 1 and 50 individuals from Bernier in year 2	0.78	2932	0.493
	7	50 individuals from Bernier in year 1 and 50 individuals from Dorre in year 2	0.81	2845	0.461
	9	25 individuals from each of Bernier and Dorre in year 1 and year 2	0.79	2995	0.496
Mt. Gibson	11	14 individuals from Dorre and 10 individuals fromFaure in year 1; 2 individuals from Bernier,8 from Dorre and 7 from Faure in year 2;40 individuals from Bernier in year 3	0.73*	496	0.450
DHI & Mt. Gibson	13	Combination of scenarios 9 and 11 (see Table 6 for more details)	DHI 0.79 MG 0.67	DHI 2717 MG 464	DHI 0.485 MG 0.446

* Note this includes a measure of inbreeding depression (3.14 lethal equivalents) based on the fact that Faure Island was founded by 20 individuals from Heirisson Prong in 2005 (founded on 14 individuals from Dorre Island in 1995). Contemporary empirical genetic data will inform current levels of inbreeding on Faure which may change the use of inbreeding depression in the models over time.

Table 2. Summary of PVA results for *target* populations after 50 years with a drought probability of 5% (which equals 1 in 20 generations or 1 in 5 calendar years). P: probability of survival; N: mean number of individuals in extant populations; H_F : expected heterozygosity; DHI: Dirk Hartog Island; MG: Mt. Gibson.

Target Pop.	Scenario #	Description	Р	Ν	H _e
DHI only	2	50 individuals from Dorre in year 1 and 50 individuals in year 2	0.33	1078	0.250
	4	100 individuals from Dorre in year 1	0.23	1651	0.267
	6	50 individuals from Dorre in year 1 and 50 individuals from Bernier in year 2	0.41	1200	0.461
	8	50 individuals from Bernier in year 1 and 50 individuals from Dorre in year 2	0.36	1520	0.453
	10	25 individuals from each of Bernier and Dorre in year 1 and year 2	0.27	1130	0.478
Mt. Gibson	12	14 individuals from Dorre and 10 individuals from Faure in year 1; 2 individuals from Bernier, 8 from Dorre and 7 from Faure in year 2; 40 individuals from Bernier in year 3	0.26	315	0.418
DHI & Mt. Gibson	14	Combination of scenarios 10 and 12 (see Table 6 for more details)	DHI 0.24 MG 0.14	DHI 1912 MG 389	DHI 0.439 MG 0.428

Table 3. Summary of PVA results for *source* populations after 50 years with a drought probability of 2.5% (which equals 1 in 40 generations or 1 in 10 calendar years). P: probability of survival; N: mean number of individuals in extant populations; H_E : expected heterozygosity; D: Dorre Island; B: Bernier Island; F: Faure Island. Scenarios in bold are the optimal scenarios for DHI only, MG only and DHI & MG combined.

Target Pop.	Scenario #	Description	Р	Ν	H _E
DHI only	1	50 individuals from Dorre in year 1 and 50 individuals in year 2	D 0.98	D 1118	D 0.292
	3	100 individuals from Dorre in year 1	D 0.96	D 1058	D 0.296
	5	50 individuals from Dorre in year 1 and 50 individuals from Bernier in year 2	D 0.97 B 0.93	D 1053 B 635	D 0.291 B 0.207
	7	50 individuals from Bernier in year 1 and 50 individuals from Dorre in year 2	D 0.97 B 0.95	D 1122 B 661	D 0.292 B 0.214
	9	25 individuals from each of Bernier and Dorre in year 1 and year 2	D 0.97 B 0.91	D 1073 B 645	D 0.291 B 0.208
Mt. Gibson	11	14 individuals from Dorre and 10 individuals fromFaure in year 1; 2 individuals from Bernier,8 from Dorre and 7 from Faure in year 2,40 individuals from Bernier in year 3	D 0.97 B 0.96 F 0.85	D 1108 B 651 F 310	D 0.298 B 0.203 F 0.247
DHI & Mt. Gibson	13	Combination of scenarios 9 and 11 (see Table 2 for more details)	D 0.98 B 0.94 F 0.88	D 1098 B 681 F 302	D 0.293B 0.199F 0.248

Table 4. Summary of PVA results for source populations after 50 years with a drought probability of 5% (which equals 1 in20 generations or 1 in 5 calendar years). P: probability of survival; N: mean number of individuals in extant populations; H_e : expected heterozygosity; D: Dorre Island; B: Bernier Island; F: Faure Island.

Target Pop.	Scenario #	Description	Р	Ν	H _e
	2	50 individuals from Dorre in year 1 and 50 individuals in year 2	D 0.57	D 572	D 0.275
DHI only	4	100 individuals from Dorre in year 1	D 0.58	D 688	D 0.277
	6	50 individuals from Dorre in year 1 and 50 individuals from Bernier in year 2	D 0.64 B 0.56	D 560 B 327	D 0.264 B 0.186
	8	50 individuals from Bernier in year 1 and 50 individuals from Dorre in year 2	D 0.61 B 0.48	D 613 B 410	D 0.272 B 0.202
	10	25 individuals from each of Bernier and Dorre in year 1 and year 2	D 0.60 B 0.54	D 655 B 367	D 0.272 B 0.192
Mt. Gibson	12	14 individuals from Dorre and 10 individuals from Faure in year 1; 2 individuals from Bernier, 8 from Dorre and 7 from Faure in year 2; 40 individuals from Bernier in year 3	D 0.64B 0.52F 0.36	D 717 B 469 F 235	D 0.259 B 0.184 F 0.238
DHI & Mt. Gibson	14	Combination of scenarios 10 and 12 (see Table 2 for more details)	D 0.57 B 0.50 F 0.31	D 732 B 438 F 205	D 0.266 B 0.196 F 0.243



Figure 1. Population trajectories for 3 source populations and 2 translocated populations in the combined translocation scenario, at a drought frequency of 1 in 10 years. 'Year' on the x-axis is a SBB breeding period, equal to 3 months.



Figure 2a. Population trajectories for 3 source populations in the combined translocation scenario, at a drought frequency of 1 in 5 years. 'Year' on the x-axis is a SBB breeding period, equal to 3 months.



Figure 2b. Population trajectories for 3 source populations in the combined translocation scenario with no harvesting, at a drought frequency of 1 in 5 years. 'Year' on the x-axis is a SBB breeding period, equal to 3 months.

Background

The Shark Bay bandicoot (*Perameles bougainville*) is a long-nosed bandicoot from Western Australia. Formerly referred to as the western barred bandicoot, its former range was believed to have extended from mid-western Australia to NSW and Victoria, including South Australia, inhabiting semi-arid bush and scrubland (6, 7). However, a recent analysis of museum samples suggests that P. *bougainville* was one of five related species that occupied this wider distribution (8). Nonetheless, the only remnant populations of this widely distributed species complex occur on just two islands in Shark Bay: Dorre Island and Bernier Island. The combined estimated size of these populations fluctuates between seasons, ranging from several hundred to 3000 (2).

The drastic reduction in range and numbers has been influenced, like many other small Australian mammals, by anthropogenic-driven factors such as land development, habitat fragmentation, fire and drought. With adult males and females weighing in at around 200 g, western barred bandicoots fall inside a critical weight range of mammals that have undergone substantial range reduction since European arrival (9). They are particularly susceptible to predation by introduced cats (*Felis catus*) and foxes (*Vulpes vulpes*) (7). These pressures have led to a current national conservation classification of 'Endangered' under the Environmental Protection and Biodiversity Conservation Act 1999.

Translocation is an important conservation strategy for species recovery, and involves the movement of individuals from one location to another either as an introduction (previously un-colonised) or a re-introduction (previously or currently colonised). Whether a translocation is a success or failure depends on many factors including those intrinsic to life history such as fecundity and mortality, extrinsic factors like stochastic events such as drought and disease and, central to any translocation program, the number of founding individuals. How such factors interact is hard to predict. What's more, the long-term survival of a newly founded population can be dependent on how well genetic diversity is retained (1, 10, 11). Shark Bay bandicoots have been translocated three times to date including Heirisson Prong, WA (1995, 1996), Arid Recovery, SA (2000, 2009) and Faure Island, WA (2005) and only Arid Recovery and Faure Island have been successful.

To prevent any further loss of Shark Bay bandicoots, this species has been targeted for translocation to several locations, including initially between 2017 and 2019 to Mt. Gibson which is a 131,710 hectare AWC sanctuary located around 367 km north-east of Perth; and to Dirk Hartog Island, Shark Bay, WA as part of the Return to 1616 project. 'Dirk Hartog: Return to 1616' is an exciting project managed by the DBCA, the objective of which is to restore Dirk Hartog's biodiversity to what it was before European arrival. Further future translocation locations include Sturt Desert, Pilliga, and Mallee Cliffs. Since all translocations rely heavily on the two remnant populations - Dorre and Bernier - and since harvesting could occur at very similar times, especially to DHI and Mt. Gibson, it is vital to understand not just how many individuals are needed to make the translocations successful, but also to ensure source populations are not over-harvested.

Quantifying the probability of extinction is central to conservation management. Population viability analysis (PVA) modelling is a valuable conservation tool, as it allows various deterministic and stochastic factors to be considered so that robust predictions can be made about optimal translocation strategies that maximise survival and genetic diversity within newly founded populations, while simultaneously minimising impact on critical source populations. Our objective in this report is to use PVA modelling to provide guidelines for phase 1 of the Shark Bay bandicoot translocation program, i.e. the movement of animals to Dirk Hartog and Mt. Gibson from Bernier, Dorre and Faure Islands between 2017 and 2019. In particular we will address the following three points:

- 1. The optimal translocation strategy to Dirk Hartog Island only
- 2. The implications on population viability of the planned translocation strategy to Mt. Gibson
- 3. Combining 1. and 2. to re-assess the impact on source populations of multiple harvesting

Methods

Vortex software was used to develop a baseline PVA model for Shark Bay bandicoots (12). Vortex is an individual-based PVA approach that uses Monte Carlo simulations to emulate population trajectories based on intrinsic and extrinsic factors, which occur as discrete, sequential events and according to user-defined probabilities (13). Importantly, it allows the inclusion of genetic data. The parameters we used for the baseline model were sourced largely from Short et al (3), Short et al (4) and Chapman et al (2), and allowed for drought which is a realistic source of demographic stochasticity. Parameters are described in Table 5.

Once a baseline model was developed, various translocation scenarios were trialled involving the relocation of 100 individuals to Dirk Hartog Island by DBCA, and the planned 81 individuals to Mt. Gibson by AWC. Scenarios 1 to 4 consider a translocation from Dorre Island only to Dirk Hartog, scenarios 5 to 10 consider translocations to Dirk Hartog Island that involve mixing Dorre and Bernier Islands, scenarios 11 and 12 consider the translocation program planned by AWC to Mt. Gibson from Dorre, Bernier and Faure Islands and scenarios 13 and 14 include the Mt. Gibson translocation and an optimal translocation to Dirk Hartog Island. A full description of scenarios is presented in Table 6.

Table 5. Parameters used for population viability analyses of the Shark Bay bandicoot. Parameters extracted from (2-4).SBB: Shark Bay bandicoot; DDR: density dependent reproduction function.

Vortex Parameter	Value
Scenario settings	
No. iterations	100*
No. "years"	200 SBB years (50 calendar years)
Duration of each "year" in days	90
Extinction definition	Only 1 sex remains
Number of populations in total	5 (Bernier, Dorre, Faure, DHI, Mt. Gibson)
Species description	
Inbreeding depression	
- Lethal equivalents	3.14
- % due to recessive lethal	50
EV concordance of reproduction & survival	0.5
EV correlation among populations	0.75 (or 0.9 if only Shark Bay populations)

Vortex Parameter	Value			
Catastrophes				
- Number of types of catastrophes	1 (drought)			
- Frequency	1 in 5 or 1 in 10 calendar years			
- Severity	65% reduction in survival; 80% reduction in reproduction			
Reproductive system				
Reproductive system	Polygynous			
Age of first offspring for Females/Males	2 SBB year/2 SBB years (3 months/6 months)			
Maximum age of female reproduction	17 SBB years (4 years 3 months)			
Maximum age of male reproduction	11 SBB years (2 years 9 months)			
Maximum lifespan	17 SBB years (4 years 3 months)			
Maximum number of broods/year	1			
Maximum number of progeny per brood	3			
Sex ratio at birth	50			
Reproductive rates				
% Adult females breeding	50 with DDR			
- EV in % breeding	5			
Distribution of broods per year				
- 0 broods	0			
- 1 broods	100			
Number of offspring per female per brood				
- Mean (<u>+</u> SD)	1.8 ± 1			
Mortality rates				
Females				
Mortality Age 0 to 1 (\pm SD)	50 <u>±</u> 10			
Annual mortality after Age 1 (\pm SD)	10 ± 3			
Males				
Mortality Age 0 to 1 (\pm SD)	50 ± 10			
Annual mortality after Age 1 (\pm SD)	10 ± 3			
Mate monopolisation				
% males in breeding pool	85			
% males successfully siring offspring	41			
Initial population size				
Bernier	800			
Dorre	1000			
Faure	437			
Carrying capacity, K (SD due to EV)				
Bernier	1000 (100)			
Dorre	1600 (160)			
Faure	500 (50)			
DHI	5000 (500)			
Mt. Gibson	800 (80)			
Genetic management				
Number of neutral loci to be modelled	5 empirical, 1 simulated			
Read starting allele frequencies from file	yes			

*Parameters run for 100 iterations. This will be increased to 1000 after agreement of parameters reached.

Target Pop.	Scenario #	Description			
DHI only	1	50 individuals from Dorre in year 1 and 50 individuals in year 2; cat prob 2.5%			
	2	50 individuals from Dorre in year 1 and 50 individuals in year 2; cat prob 5%			
	3	100 individuals from Dorre in year 1; cat prob 2.5%			
	4	100 individuals from Dorre in year 1; cat prob 5%			
	5	50 individuals from Dorre in year 1 and 50 individuals from Bernier in year 2; cat prob 2.5%			
	6	50 individuals from Dorre in year 1 and 50 individuals from Bernier in year 2; cat prob 5%			
	7	50 individuals from Bernier in year 1 and 50 individuals from Dorre in year 2; cat prob 2.5%			
	8	50 individuals from Bernier in year 1 and 50 individuals from Dorre in year 2; cat prob 5%			
	9	25 individuals from each of Bernier and Dorre in year 1 and year 2; cat prob 2.5%			
	10	25 individuals from each of Bernier and Dorre in year 1 and year 2; cat prob 5%			
Mt. Gibson	11	14 individuals from Dorre and 10 individuals from Faure in year 1; 30 individuals from Bernier, 36 from Dorre and 30 from Faure in year 3; cat prob 2.5%			
	12	14 individuals from Dorre and 10 individuals from Faure in year 1; 30 individuals from Bernier, 36 from Dorre and 30 from Faure in year 3; cat prob 5%			
DHI & Mt. Gibson	13	Mt. Gibson only scenario and optimal DHI translocation scenario; at cat prob 2.5%			
	14	Mt. Gibson only scenario and optimal DHI translocation scenario; at cat prob 5%			

 Table 6. The translocation scenarios. cat prob: probability of catastrophe occurring per generation (2.5% equals 1 in 40

 SBB breeding years or 1 in 10 calendar years, 5.0% equals 1 in 20 SBB breeding years or 1 in 5 calendar years).

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Further information: http://www.nespthreatenedspecies.edu.au/



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