An assessment of the current taxonomic and genetic status of Barrow Island vertebrate fauna

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December 2017

GOVERNMENT OF
WESTERN AUSTRALIA

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The recommended reference for this publication is:
Moro, D. (2017). An assessment of the current taxonomic and genetic status of Barrow Island vertebrate fauna. Report to the Barrow Island Threatened and Priority Species Translocation Program Advisory Committee. Department of Biodiversity, Conservation and Attractions, Perth.

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Acknowledgments

The project was supported by the Gorgon Threatened and Priority Species Translocation and Reintroduction Program Advisory Committee. Drafts of this report were reviewed by Dr Peter Kendrick, Paul Connolly, Dr Manda Page, and Keith Morris.

Summary

A desktop assessment of the current status of 11 threatened or priority mammal species, two bird species and one reptile species on Barrow Island suggests the taxonomic status for many of these taxa remains equivocal. There are inadequate data to support or deny the current taxonomic and genetic level of island uniqueness for most of the fauna assessed based on molecular and/or morphological patterns.

While species nomenclature remains a legacy of past morphological assessments, contemporary research using molecular approaches has not addressed the fundamental questions that conservation practitioners require to manage these island species. The research to date suggests most taxa require a formal reassessment of their relationships to mainland populations to resolve their taxonomy and therefore their conservation value.

Gaps in knowledge are primarily related to a formal taxonomic reassessment to resolve species-subspecies boundaries, and molecular studies to resolve or reassess contemporary versus historical (evolutionary) population structure and relationships to reference populations. Resolving these boundaries may alter the formal conservation listing of a species or, alternatively, identify unique taxa that require conservation listing. These decisions become relevant in the context of translocation and conservation and management prioritisation.

1 Context

Barrow Island was set aside as a nature reserve in 1908 in recognition of its outstanding flora and fauna values. It is a Class A nature reserve for the purpose ‘Conservation of Flora and Fauna’. The island is vested in the Conservation and Parks Commission and is managed by the Department of Biodiversity, Conservation and Attractions (DBCA).

The biodiversity values of Barrow Island are unique and significant on a national and international scale. Barrow Island contains a high diversity of flora and fauna species and communities that have been isolated from the mainland for approximately seven thousand years, resulting in taxa now endemic to the island, and they have not been exposed to the same threats that impact mainland flora and fauna. Under the State’s Wildlife Conservation Notice 2016, and Commonwealth’s EPBC Act 1999, Barrow Island supports six listed threatened terrestrial vertebrate subspecies: five mammal species and one bird species, in addition to several listed subterranean fauna. Barrow Island is also a nesting site for four species of marine turtle, and for two of these species the nesting is regionally significant.

The Gorgon Gas Development Revised and Expanded Proposal: Barrow Island Nature Reserve was approved in 2009 by the Western Australian Government subject to a number of conditions and a commitment by the Gorgon Joint Venture participants to fund a series of “Additional Gorgon Joint Venture Undertakings”. One of these programs was a Threatened and Priority Species Translocation and Reintroduction Program:

‘…..an ongoing program to be developed by the DCLM CEO and implemented by DCLM to translocate and reintroduce selected threatened species of fauna from Barrow Island to other suitable habitat within Australia including monitoring and management of such fauna populations and habitats.’

This program was to be developed and implemented by the Department of Conservation and Land Management (now Department of Biodiversity, Conservation and Attractions) and would translocate selected threatened and priority fauna species from Barrow Island to suitable sites in Australia. Translocations commenced in January 2010, and a strategic plan guides the implementation of the Threatened and Priority Species Translocation and Reintroduction Program (Morris and Yates 2015). This strategic plan reviews the initial processes involved in selecting fauna species for translocation and the translocation sites. It also clarifies the Program’s objectives and provides direction for further work in this program.

The overall aim of the Translocation Program is to increase the distribution and abundance of selected fauna found on Barrow Island by translocating animals to suitable habitat on other islands and/or areas of the mainland where threatening processes are effectively managed (ie reconstructing fauna communities). The Program’s specific objectives are to:

1. Implement translocations of selected Barrow Island terrestrial fauna to suitable island and mainland areas of Australia to increase their distribution and abundance, and/or to attempt to reconstruct local fauna assemblages.
2. Manage threatening processes at translocation sites to improve translocated species persistence.
3. Determine and better understand the genetic, demographic and ecological factors that influence the success of fauna translocations through adaptive management.
4. Develop partnerships within Parks and Wildlife, and with traditional owners, universities and industry to implement the program.

Since 2010, several of these listed threatened species have been translocated to other secure mainland and island sites. However, to assist with prioritising species for future translocations, or to supplement the genetic resource of translocated populations, it is necessary to understand the uniqueness of the fauna on Barrow Island relative to those on the mainland and other island populations of the same or similar species.

1.1 Project scope and objective

1. To review the genetic uniqueness of terrestrial vertebrate fauna, particularly mammals, on Barrow Island to inform future activities of the Threatened and Priority Species Translocation and Reintroduction Program and the ongoing management of fauna on Barrow Island.
2. Undertake a desktop literature review (including grey literature and expert knowledge) including:
    a) Review the current knowledge regarding the level of uniqueness that warrants management intervention for Barrow Island species potentially at risk from development.
    b) Consult with subject matter experts (SME) in relation to species-specific uniqueness.
    c) Provide recommendations for future research and/or management approaches for Barrow Island species potentially at risk from development.
    d) Provide recommendations for future management actions.
    e) Identify custodians of tissue samples that may be available for analysis.

2 Approach

- Review literature from Murdoch University library database catalogue, and the DBCA library.

- Consult with SME for taxa requiring specific queries regarding unpublished data and findings, and in relation to the storage location of Barrow Island tissue samples.
- Summarise information currently available with a view to identifying knowledge gaps and recommendations for future work in relation to the Threatened and Priority Species Translocation and Reintroduction Program.

3 Results

Results of the assessment have been summarised in tabular format for ease of reference.

Species	**Taxonomic identity (June 2017)**	**Assigned conservation status (October 2017)**			**Taxonomy & genetic knowledge**	**Reference**	**Subject Matter Experts consulted**	**Barrow Island Tissue samples location**	**Gaps**	**Recommendations for future work** (no assigned priority)
		Wildlife Cons. Notice (2016)	**EPBC Act**	**IUCN**						
Mammals										
Northern brushtail possum	*Trichosurus vulpecula arnhemensis** *OR* *T.v. hypoleucus***			T.v.h LC	Kerle *et al.* (1991): provide evidence to support separation of *T.v.arnhemensis* from *T.v.vulpecula* based on skull morphometrics, allozymes, karyotypes (including Barrow Is showing affinity to the northern group). Collins (2003): mtDNA control region genetics showed that Barrow Island possums grouped with those of SW WA more so than those of NW WA, and suggest these should be considered *T.v. hypoleucus.* Taylor and Foulkes (2004). Genetics of mtDNA cyt-b support species status. Genetics showed that Barrow Island possums grouped with those of SW WA more so than those of NW WA. Morphological analyses also failed to separate Barrow Island and SW populations. Woinarski et al. (2014): 3 subsp currently recognised: *T v. arnhemensis, T. v. hypoleucus, T. v. vulpecula*. Listed as *T.v.hypoleucus* in Action Plan based on genetic mtDNA phylogeographic study of Collins (2003), & Taylor and Foulkes (2004).	Kerle et al. (1991) Collins (2003) Taylor and Foulkes (2004) **Woinaski et al. (2014) *Jackson and Groves (2015)		Peter Spencer (Murdoch Uni) (n=3) Kenny Travouillon (WAM) (n=1)	Genetic diversity unknown for island population. No understanding of phylogeographic structure based on nuclear markers. Based on genetic data, clarify taxonomy of Barrow Island population.	1. Undertake phylogeographic study of island population to compare it to mainland populations using nuclear markers. 2. Assess level of genetic variation and structure within Barrow Island population. 3. Review taxonomic status based on contemporary information. 4. Management: Ensure purpose of translocation proposals of this species is clarified given low or no conservation status. Genetic distinction between island and mainland populations unclear at present. Recommend any translocation proposal await further nuclear genetic evidence or collect source animals only from one location (i.e. no mixing of founders).
Water rat	*Hydromys chrysogaster*	P4		LC	Hinds *et al*. (2002): Primers available for microsatellite work for water rat. Bettink (2016): Genetic study of mtDNA (cyt-b) found shared common ancestor between southwest WA and Barrow Island. Shallow divergence of 0.3% between these 2 areas	Hinds et al. (2002) Bettink (2016)	Karen Bettink (DBCA)	Karen Bettink (DBCA)	Current taxonomy may require reassessment given the recent molecular data collected by Bettink 2016 and suggestion of ESU relative	1. Review taxonomic status with consideration of a subspecies status based on current microsatellite information. [Ecological, morphometric and phenotypic data by Bettink 2016 supports reinstatement of subspecies

					indicates they are closely related. However, the presence of reciprocal monophyly with other cyt-b lineages, and analysis of nuclear DNA showing very low genetic diversity (FIS=0.0) indicates that lack of gene flow between the two areas has occurred: southwest WA and Barrow Island populations were significantly differentiated in nuclear DNA microsatellites from each other and all remaining clusters, recording no admixture. Barrow Island was found to also have unique alleles and monomorphic microsatellite markers across all microsatellite markers sampled. Suggestion is that SW and Barrow Island form a genetically-defined Evolutionary Significant Unit (ESU), and Barrow Island is a genetically-defined Management Unit (MU) within this ESU.Genetic data alone may be evidence to support taxonomic reassessment though morphometric data suggests latitudinal changes. Similarity of body sizes between Barrow Island and SW populations suggest latitude through Bergmann's rule is a greater influence than the island rule. Both SW and Barrow Island forms are phenotypically differentiated from other regions in Australia.				to other populations in eastern Australia.	taxonomy collectively for the southwest/Barrow Island group.] 2. Management: Ensure purpose of translocation proposals of this species is clarified given the low conservation status. Suitable genetic information available to inform translocation proposals. Genetic data support founder animals may comprise individuals from island and SW mainland populations if this were the decision taken.
Western chestnut mouse	*Pseudomys nanus ferculinus ** *OR* *Ps. nanus***				White (2006): Study compared mtDNA control region with mainland samples and found little evidence for island-mainland separation. The mtDNA of island P. nanus has haplotypes that appear elsewhere on mainland and reflects a gene pool of a widespread species (i.e. no unique structuring of island population). Previously recognised as *P.n.ferculinus* but removed from threatened species list in 2006/2007 based on mtDNA genetic evidence. Weeks et al. (2015): Genetics of Barrow Island population using microsatellites shows high levels of heterozygosity and low levels of inbreeding comparable to mainland populations sampled in Pilbara. Genetics data support a species with high island variation in microsatellite DNA markers sampled.	White (2006) **Woinaski et al. (2014) *Jackson and Groves (2015) Weeks et al. (2015)		Kenny Travouillon (WAM) (n=58)		1. Review taxonomic status to remove subspecies status on Barrow Island and to align taxonomy with contemporary data. 2. Management: Ensure purpose of translocation proposals of this species is clarified given lack of a conservation status. Suitable genetic information available to inform translocations. Genetic data support founder animals may comprise individuals from island and mainland populations if this were the decision taken for translocation proposals.
Common rock rat	*Zyzomys argurus*			LC	Cooper and Schmitt (2005): morphological examination of 20 traits in nearly 400 specimens across its range. Identified distinct morphological differentiation between populations in four broad geographic regions – Pilbara, Kimberley, NT and Queensland. Barrow Island was at one margin of the Pilbara variation, individuals being larger than the other Pilbara localities examined (Kendrew Island, Rosemary Island, Dolphin Island and Woodstock) and all the other	Cooper and Schmitt (2005)	Linc Schmitt (UWA)	Peter Spencer (Murdoch Uni) (n=3)	No genetic work currently available to compare island with mainland populations, or to understand level of genetic diversity among island population.	1. Undertake island and mainland genetic phylogeography comparisons (with more Barrow Island samples). 2. Understand genetic diversity within Barrow Island population relative to mainland population.

					populations. Celeste Wale (UWA): currently investigating microsatellite and mtDNA structuring to assess phylogeography of species. n>730 tissue samples. Linc Schmitt (pers comm): Work underway to study morphology and genetics with a view to extending the analysis to encompass a broader geographic range.					3. Management: Ensure purpose of translocation proposals of this species is clarified given Least Concern conservation status and unknown genetic variation within island population relative to mainland populations. Genetic distinction of island and mainland populations unclear at present. Recommend translocation proposals await genetic evidence or collect source animals only from one location (i.e. no mixing of founders).
Barrow Island euro	*Macropus robustus isabellinis*** OR *Osphranter r.isabellinus **	VU	VU		Woinarski *et al.* (2014): Recognise the subspecies although state that Eldridge (unpubl. data) suggests *M. r. isabellinus* is not a valid subspecies. Eldridge et al. (2014): Compared phylogeography of *Macropus robustus* across their NT and Qld range using sequence variation for mtDNA (d-loop) and microsatellites. Included 1 sample from Barrow Island. Barrow Island showed minor divergence from mainland samples. Eldridge (unpubl. data): preliminary analyses of larger genetic dataset shows limited divergence between Barrow Island and mainland euros. Also low genetic diversity among island populations sampled. Jackson & Groves (2015): recognise the Barrow Is subspecies as a new separate genus (*Osphranter*) but state formal taxonomic revision is required.	**Woinaski *et al*. (2014) Eldridge *et al.* (2014) *Jackson and Groves (2015)	Mark Eldridge (Australian Museum) n=40		Analyse larger genetic dataset of Eldridge (unpubl. data)	1. Analyse larger genetic data by Eldridge. 2. Formally resolve taxonomy with mainland to consider contemporary molecular data collected (vs morphological data species concepts currently used). 3. Management Genetic distinction of island and mainland populations unlikely. However, recommend translocation proposals await analysis of larger genetic dataset or collect source animals only from one location (i.e. no mixing of founders).
Spectacled hare-wallaby	*Lagorchestes conspicillatus conspicillatus*	VU	VU	NT (full species)	Courtenay (1993): investigated skull morphology, allozymes, and karyotypes for species across Australia, including specimens from Barrow Island. Morphometrics suggested two different taxa occurred on mainland Australia and these differed to those from Barrow Island. Karotyping and allozymes remained inconclusive. Woinarski et al (2014): Include 2 subspecies (Barrow Island *L. c. conspicillatus* and *L. c. leichardti*). Presently the subspecies *L. c. conspicillatus* occurs on Barrow Island but has been	Courtenay (1993). Woinarski *et al*. (2014) Jackson and Groves (2015)	Jackie Courtenay (Earth Creations)	Peter Spencer (Murdoch Uni) (n=3)	Subspecies have not been subject to molecular comparison. No genetic work conducted on diversity within island population.	1. Compare phylogenetic differences between subspecies using current molecular tools. These can be used to clarify taxonomic novelty. 2. Management Genetic distinction of island and mainland populations unclear at present. Recommend translocation

					translocated to Hermite Is (Montebello Is). Jackson & Groves (2015): recognise 2 subspecies: *L.c.conspicillatus* and *L.c. leichardti*			Kenny Travouillon (WAM) (n=1)		proposals await genetic evidence or collect source animals only from one location (i.e. no mixing of founders).
Black-flanked rock-wallaby	*Petrogale lateralis lateralis*	EN	VU		Eldridge et al. (1999) and Eldridge et al. (2001): show that island populations of *P. lateralis* have exceptionally low levels of neutral genetic diversity compared to mainland populations. Assessed level of genetic diversity at 11 microsatellite loci from island and mainland populations of *P. l. lateralis*, including Barrow Island population, supports low-level divergence with the other *P. lateralis* sequenced. Results show evidence that Barrow Island individuals are less polymorphic than mainland samples. Eldridge *et al.* (2004): evidence that genetically depauperate translocated populations do successfully establish, but their genetics tend to remain unrepresentative of their source population, and genetically atypical of their species. Mason *et al*. (2011): show there is low genetic diversity at the nuclear (MHC) gene under selection compared to mainland populations sampled, suggesting populations remain highly vulnerable to environmental changes. They suggest pooling individuals from multiple populations for translocation programs. Potter *et al*. (2012): phylogeographic study of *Petrogale* across Australia using 2 nuclear and 3 mtDNA genes with the aim of screening representatives of the species for chromosomal and morphological variation and to reassess their taxonomy. No samples collected from Barrow Island for *P. l. lateralis. P. l. lateralis* (mainland) cluster together and with the 'West Kimberley' race of *P. lateralis.* Woinarski *et al*. (2014): Recognise that this taxon occurs as a variety of subspecies and 'races' due to disjunct populations: *P. l. lateralis, P. l.* 'West Kimberley' subspecies (*sensu* Briscoe *et al*. 1982), *P.l.hackettii, P.l.pearsoni, P.l.*'MacDonnell Ranges' subspecies (sensu Briscoe et al. 1982). State that populations from Barlee Range (Ashburton) may or may not represent *P. l. lateralis* based on early genetic data [M Eldridge, pers comm, although see Potter et al 2017 which supports separation of groups]. Subspecies also occurs as discrete populations at several other locations including Salisbury Is.	Eldridge *et al*. (1999) Eldridge *et al*. (2001) Eldridge *et al*. (2004) Mason *et al*. (2011) Potter *et al*. (2012) Woinaski et al. (2014) Eldridge et al. (2014) Jackson and Groves (2015) Potter et al. (2017)	Mark Eldridge (Australian Museum) n=30			1. Management: Suitable genetic information available to inform translocation proposals. Genetic distinction of island and mainland populations low. Genetic data support founder animals may comprise individuals from island and mainland *lateralis* populations.

					Potter *et al*. (2017): compare gene divergence across *Petrogale* species (including Barrow Island) using a genomics approach. The data show some, but not exceptional, divergence between Barrow Island and mainland populations. *P. l. lateralis* is widespread (as isolated populations) on the mainland and most populations are genetically recently diverged and distinct, however, Barrow Island is no more divergent than any other population. They suggest the species reflects an example of a taxon that has undergone chromosomal changes that are acute signatures of speciation. Eldridge (pers comm) has a larger unpublished dataset although this shows a similar pattern (some, but not exceptional divergence between Barrow Island and mainland lateralis populations). Jackson and Groves (2015): recognise Barrow Island population as *P. l. lateralis.*					
Pseudantechinus	*Pseudantechinus roryi*				Cooper et al. (2000): study of allozymes and morphology (including Barrow Island samples) recognises *P. roryi* on Barrow Island. Westerman et al. (2008): compare phylogeny analyses from sequences of 3 mtDNA and 3 nuclear loci of *Pseudantechninus* (including *P. roryi*). They suggest there is no clear genetic boundary between *P. macdonnellensis* and *P. roryi,* but some diversity does occur among the sequence data of populations from Cape Range, Barrow Island, and Port Hedland (Abydos-Woodstock) areas; whether these subdivisions represent species boundaries or geographically structured intraspecific variation can only be determined with more extensive geographic sampling of animals than has been undertaken. Only 2 specimens sampled from Barrow Island, and <10 from across their range. Woinarski et al. (2014): suggest *P roryi* naming is premature based on study by Westerman et al (2008) and possibly represents a complex within *P. macdonnellensis-P.roryi* because of high geographic variation. Suggest more research required into taxonomic boundaries. Recommend *P. roryi* be synonymised with *P. macdonnelensis*. Jackson and Groves (2015): recognise separation of *P. roryi* from *P. macdonnellensis* primarily based on morphological distinguishing features.	Cooper et al. (2000). Westerman et al. (2008) Woinaski et al. (2014) Jackson and Groves (2015)		Peter Spencer (Murdoch Uni) (n=34)	Taxonomy remains ambiguous and unresolved. More samples required across range of *P. roryi* and *P. macdonnellensis* to clarify Westerman *et al*. (2008) and Cooper *et al*. (2000) findings as to whether preliminary subdivisions represent species boundaries or geographically structured intraspecific variation.	1. Repeat molecular analyses for *P.roryi* for Barrow Island and other Pilbara locations using additional and more extensive sampling. 2. Resolve taxonomy based on findings. 3. Management Ensure purpose of translocation proposals of this species is clarified given lack of a conservation status. Genetic distinction of island and mainland populations unclear at present. Recommend any translocation proposal await genetic evidence or collect source animals only from one location (i.e. no mixing of founders).

Planigale	*Planigale sp.* *OR* **Planigale sp. 1*				Archer (1976). Identified Barrow Island specimen as a 'non typical' form of *P. maculata* based on morphology. Painter et al. (1995): show that mtDNA cyt-b sequences from two specimens collected in the Pilbara region of WA are highly divergent from other planigales and from each other and may represent previously unrecognised species. Suggest the Pilbara specimen was collected from Millstream (not Barrow Island). Hintz (2016): compared *Planigale* across their range using 3 mtDNA genes and 3 nuclear genes but with limited samples from the Pilbara. Barrow Island sample was grouped with other Pilbara specimens (albeit with a low likelihood of divergence from other groups). Westerman et al. (2016): compare *Planigale* across multiple mtDNA and nuclear markers, including specimens (n=4) from Barrow Island. Suggest there is no significant population genetic structure between the Barrow Island samples and the Pilbara mainland, and the animals on Barrow Island fall within the genetic differentiation observed for *Planigale* 'species 1'. L. Umbrello PhD (current): study has incorporated more individuals (n=230 specimens across island and mainland) and re-assessed the phylogeographic variation of *Planigale* sp.1 across Pilbara using mtDNA (control region and cyt-b) and nuclear markers (omega-globin), and found a pattern of isolation-by-distance is more likely to explain the little variation observed by Westerman *et al*. (2016) (i.e. no phylogeographic structure). L Umbrello and colleagues are also undertaking a species morphological description of the two Pilbara *Planigales.* ABRS: Known previously in ABRS as *'Planigale* sp 1. (Pilbara WA)'. The Barrow Island specimens are one of the two *Planigale* species that occur in the Pilbara region and the larger, more common species of the two (L. Umbrello pers comm).	Archer (1976) Painter et al. (1995) Hintz (2016) *van Dyck et al. (2013) *Westerman et al. (2016)	Linette Umbrello (WAM) Ric How	Peter Spencer (Murdoch Uni) (n=7) Kenny Travouillon (WAM) (n=1)	Lack of formal taxonomy to island population based on recent molecular information.	1. Resolve taxonomy of island population. 2. Management Ensure purpose of translocation proposals of this species is clarified given lack of a conservation status. Genetic distinction of island and mainland populations unlikely but awaiting formal completion of genetic and morphological analyses to support translocation decisions within a genetic context.
Barrow Island boodie	*Bettongia lesueur* unnamed subspecies (Barrow Island)	CD	VU	NT (full species)	Woinarski *et al*. (2014): recognise 3 subspecies although state that these have not been compared using modern molecular genetic analyses (though see unpubl ms below). Jackson and Groves (2015): synonymise all subspecies as *B. l. lesueur*, although recognise the identity of the subspecies	Woinarski et al. (2014) Jackson and Groves (2015)	Kym Ottewell (DBCA)	Linc Schmitt (UWA) (n=265)	Morphometric data is too preliminary and requires further investigation.	1. Undertake a wider genomic study (using 1000s of loci) to compare the phylogeography of *B. lesueur* across Australia.

					needs to be resolved: *B. l. graii* (Swan River), *B. l. harveyi* (Eyre Peninsula), *B. l.* 'undescribed subspecies' (Barrow Island and Boodie Island). F. Donaldson et al. (unpubl ms): compared genetic markers (microsatellites, mtDNA) of boodies on Barrow Island (n=229). Evidence from mtDNA suggests 2 major clades on the island, but with only one of these clades represented elsewhere (Dorre & Bernier Islands, Shark Bay). A large effective population size with little evidence of a bottleneck was also demonstrated on Barrow Island. R. Thavornkanlapachai et al. (unpubl. ms): compared genetic diversity and representation between source (Barrow Island, Dryandra) and (mixed) translocated populations. Estimates of genetic diversity were typically higher in the translocated population at Matuwa (Lorna Glen) than the source population samples at Dryandra, but there were no significant differences between samples from the translocation site and the Barrow Island source population. The study confirmed there is substantial phenotypic and genetic differentiation between the Shark Bay and Barrow Island populations of *B. lesueur*. Gene diversity on Barrow Island was comparably high to that among Dorre Is specimens at Dryandra. Despite high levels of genetic differentiation between source populations, *B. lesueur* translocated to a new site on the mainland were able to interbreed and produced viable offspring, with no detected fitness costs. Kym Ottewell and Mark Eldridge (unpubl data): Have a current proposal to resolve the taxonomy of Barrow Island and Shark Bay Island *B. lesueur* using genomic sequencing, and will include analysis of the extinct mainland subspecies *B. l. graii* and *B. l. harveyi* and related species, *B. anhydra*. Kenny Travouillon (unpubl. data): Preliminary morphometrics of skulls suggest a difference between Barrow Island boodie and those of the Nullarbor Plains.	F. Donaldson et al. (unpubl ms) R. Thavornkanlapachai et al. (unpubl. ms)		Peter Spencer (Murdoch Uni) (n=2) Kenny Travouillon (WAM) (n=2) Kym Ottewell (DBCA) (n=100+)	Subspecies have not been subject of taxonomic reassessment based on current molecular analyses.	2. Expand morphometric data to understand variation across taxon range. 3. Resolve taxonomic uncertainty of the Barrow Island population of *B. lesueur* as a valid species or subspecies. 4. Management Genetic distinction of island and mainland populations unclear at present. Recommend translocation proposals await genetic evidence or collect source animals only from one location (i.e. no mixing of founders).
Barrow Island golden bandicoot	***Isoodon auratus barrowensis* *OR*	VU	VU	VU	Thomas (1901): Morphology of skulls of Barrow Island specimens more similar to *I.obesulus* than *I.auratus*. Lyne and Mort (1981): Morphology of skulls of Barrow Island specimens more similar to *I.obesulus* than *I.auratus*.	Thomas (1901) Lyne and Mort (1981) Pope et al. (2001)	Kym Ottewell (DBCA)	Peter Spencer (Murdoch Uni) (n=8)	Level of genetic distinction between Barrow Island *I.auratus* and mainland conspecifics remains unclear based on various	1. Undertake a wider genomic study (using 1000s of loci) to compare the phylogeography of *I. auratus* and other *Isoodon* species across Australia.

	**Isoodon auratus*				Pope *et al*. (2001): Suggest *I.auratus* is conspecific to *I. obesulus* based on mtDNA control region and morphology studies. Zenger et al. (2005): Suggest *I.auratus* is conspecific with *I. obesulus*. Westerman *et al*. (2012): Suggest *I. auratus* is a distinct species to *I. obesulus*. Further, the subspecies *I. a. barrowensis* is genetically close to *I. a. auratus*. Woinarski *et al*. (2014): recognise species as *I. auratus* with no subspecies based on confusion about its taxonomy and whether it remains taxonomically justified as a subspecies (*I. a. barrowensis*) or full species only. Kenny Travouillon (unpubl data): preliminary skull morphometric data comparing island and mainland *I. auratus* suggests some differences between Barrow Island, Kimberley and central Australia. More samples required. Kym Ottewell and Steve Cooper (unpubl data): sequenced two mtDNA genes (control region, ND2) and several nuclear genes (vWF, BRCA1, RAG-1) of *I. auratus* and other *Isoodon* species across Australia. mtDNA suggests *I. auratus* is conspecific to *I. obesulus* but nuclear genes were equivocal due to low resolution. Current proposal underway to undertake a larger genomic assessment of *I. auratus* and other *Isoodon* species to understand phylogeographic patterns and resolve taxonomic units. Kym Ottewell (unpubl data): Microsatellite analysis (12 loci) of I. auratus populations from Barrow Island and the Kimberley region shows strong genetic structuring between the regions. This information supports some level of differentiation between the island and the mainland populations, however genomic analyses that involve analysis of many thousand loci is warranted to provide further resolution and support to these early findings.	Zenger et al. (2005) Westerman et al. (2012) *Woinarski et al. (2014) **Jackson and Groves (2015)	Kenny Travouillon (WAM)	Kenny Travoullon (WAM) (n=9) Kym Ottewell (DBCA) (n=300)	contradicting studies to date. Morphometric data is preliminary and requires more samples to support early findings. Taxonomy of species remains equivocal and reflects variable molecular data and morphological data collected to date.	2. Expand morphometric data to understand variation across taxon range. 3. Resolve taxonomic uncertainty of the Barrow Island population of *I.auratus* as a valid species or subspecies considering molecular and morphometric datasets. 4. Management Genetic distinction of island and mainland populations unclear at present. Recommend translocation proposals await genetic evidence or collect source animals only from one location (i.e. no mixing of founders).
Birds										
Spinifexbird	**Eremiornis carteri* *OR* ***Poodytes carteri*			LC	No molecular work known to have been conducted on this species. Apart from Barrow Is, the Spinifexbird has been recorded on more than a dozen other islands including Boodie, Dixon, Dolphin, Double, Long (Passage Islands), North Muiron,	*Schodde and Mason (1999) **BirdLife Australia (2017)	Allan Burbidge (DBCA)		Genetic diversity of Barrow Island population remains unknown. Level of morphological or genetic variation of	1. Understand genetic diversity of Barrow Island population, and phylogeographic variation of island with mainland specimens. 2. Management

					South Muiron, Scholl, Thevenard and about seven islands in the Montebello group. Although known from the Montebello Is historically, the species disappeared sometime after 1950, and were absent until some were translocated from Barrow Is in 2010-11. This translocation was conducted as part of the reconstruction of the Montebello Is fauna, not because of the conservation status of the species.				Barrow Island population relative to other island populations remains unknown.	Ensure purpose of future translocation proposals of this species is clarified given Least Concern conservation status and unknown genetic variation within island population relative to mainland populations. Genetic distinction of island and mainland populations unclear at present. Recommend translocation proposals await genetic evidence or collect source animals only from one location (i.e. no mixing of founders).
White-winged fairy-wren	*Malurus leucopterus edouardi*	VU	VU	VU	Burbidge et al. (2000): Surveys suggest the species was restricted to Barrow Island although may have occurred historically on nearby Trimouille and Hermite Islands. Driskell *et al.* (2002): sequenced 2 genes of the mtDNA from mainland and island (DHI n=10, Barrow Island n=8) populations. Birds on Barrow Island represented a strong monophyletic clade and were the most genetically distinct relative to other populations sampled. Barrow Island and Dirk Hartog Is specimens were not closely related relative to their relationship with mainland specimens sequenced. They concluded the Barrow Island and mainland populations are genetically isolated from other populations examined. Variation of mtDNA sequences within the Barrow Island population was low though within-population genetic diversity was comparable to that of other sampled populations elsewhere.	Burbidge et al. (2000) Driskell et al. (2002)			No understanding of phylogeographic structure based on nuclear markers.	1. Undertake phylogeographic study of island population to compare it to mainland populations using nuclear markers. 2. Assess level of genetic variation and structure within Barrow Island population. 3. Management Genetic distinction of island and mainland populations clear. Recommend Barrow Island birds should not be mixed with Dirk Hartog Is birds. However, within island gene diversity remains unknown and should be understood to support translocation proposals.
Reptiles										
Barrow Island leopard skink	*Ctenotus pantherinus acripes*				Storr (1975). First described holotype from Barrow Island based on morphology. Wilson and Swan (2010): use morphology to assign subspecies: *C. p. acripes* distinguished by mid body scale rows (36-40) more than other subspecies of *C. pantherinus*. Also has spinose scales on soles of feet and no dark ventral	Storr (1975) Wilson & Swan (2010) Cogger (2014)	Mark Cowan (DBCA) Roy Teal (Biota)	WAM	No molecular data for this taxon on Barrow Island. Unresolved taxonomy.	1. Collect and sequence tissues from Barrow Island specimens and compare phylogeographic variation across species range.

					stripe. Cogger (2014): identifies specimens as a subspecies based on morphology, distributed in arid NW Qld, NT and Barrow Island. D. Rabosky & A. Talpa (USA, unpubl. data): compared genetics of *C. pantherinus* (approx. 150 individuals) across their range and found little evidence for subspecies status, suggesting a relatively recent expansion of this species across the arid zone. No Barrow Island samples were used.		Daniel Rabosky (Uni Michigan USA)			2. Pending genetic results, reclassify taxonomy of Barrow Island subspecies (if required). 3. Management: Ensure purpose of translocation proposals of this species is clarified given lack of a conservation status and unknown genetic variation within island population relative to mainland populations. Genetic distinction of island and mainland populations unclear at present. Recommend translocation proposals await genetic evidence or collect source animals only from one location (i.e. no mixing of founders).

4 Discussion

A desktop assessment of the current status of 11 threatened or priority mammal species, two bird species and one reptile species on Barrow Island suggests the taxonomic status for many of these taxa remains equivocal. There are inadequate data to support or deny the current taxonomic and genetic level of island uniqueness for most of the fauna assessed based on molecular and/or morphological patterns. It is clear from this assessment that it is still relatively uncommon for genetic studies to lead to tangible, practical management strategies that are implemented in the field (the 'research–implementation gap'). There seems to continue to be a need to discuss and formulate questions that support on-ground conservation actions, improving the uptake of genetic management in species recovery.

Barrow Island has a number of fauna attributed with a subspecies status, and these taxa have an assumed level of uniqueness given the isolation of the island from the mainland. However, a resurgence in molecular techniques that compare the phylogeographic relationships of populations is making it unclear which taxa are taxonomically unique to Barrow Island, or whether they are an island variant of mainland congeners. Furthermore, species whose taxonomy remains ambiguous, or remains undescribed, makes for additional confusion about their significance from a conservation perspective.

While species nomenclature remains a legacy of past morphological assessments, contemporary research using molecular approaches suggests most taxa require a formal reassessment of their relationships to mainland populations to resolve their taxonomy and therefore their conservation value.

Gaps in knowledge are primarily related to a formal taxonomic reassessment to resolve species-subspecies boundaries, and molecular studies to resolve or reassess contemporary versus historical (evolutionary) population structure and relationships to reference populations (Table 2). Resolving these boundaries may alter the formal conservation listing of a species or, alternatively, identify unique taxa that require conservation listing. These decisions become relevant in the context of translocation and conservation and management prioritisation.

Based on the available data, there is adequate genetic information available for the water rat, chestnut mouse, and black-flanked rock-wallaby to understand their taxonomy and genetic structure with other populations.

Genetic information for the common rock rat, euro, planigale, boodie, bandicoot and white-winged fairy-wren remains unclear or limited at this time and awaits further analyses. Closing these gaps will help to resolve their taxonomy - and where deemed a conservation requirement -to assist with discussions about their future translocation and the required level of genetic augmentation of past translocations. At present, based on the available information, there is insufficient information to understand their taxonomy and genetic structure relative to other populations. It would not be recommended to establish new mixed-source populations.

No, or limited, phylogeographic information exists for the brushtail possum, spectacled hare-wallaby, pseudantechinus, spinifexbird and leopard skink. At present, based on the available information, there is insufficient information to understand their taxonomy and genetic structure relative to other populations. It would not be recommended to establish new mixed-source populations.

4.1 Management implications

Understanding the genetic diversity on the island for each species, and the level of sampling required to capture that diversity, will help to support translocation proposals.

Clarifying the objective of a translocation of island animals (indigenous genetic representation, refreshing the genetics of translocated populations) is an important necessity to tailor ongoing management to maximise the chances of long-term persistence. The Barrow Island Threatened and Priority Species Translocation and Reintroduction Program Strategic Plan (Morris and Yates 2015) describes four criteria that should be used to clarify which species should be targeted for future translocations:

1. Does the taxon contain unique genetic resources endemic to Barrow Island?
2. Is the taxon threatened or of conservation significance and will translocation reduce the risk of extinction?
3. Is there sufficient knowledge on the distribution and abundance of the taxon to ensure removal of animals for translocation does not threaten the Barrow Island population?
4. What is the likelihood of success?

Applying the available information on taxonomy and genetics (this report) to criteria 1 and 2, genetic information for many of the Barrow Island taxa investigated in this report is either lacking or remains unanalysed and of limited value within the context of threat status and translocation objective (Table 2).

One (subjective) finding of this assessment is a disconnect between the research conducted to date and its implementation as plain-language information with recommendations to help conservation practitioners understand the implications of the genetic studies, and their translation into useful management strategies, particularly at the population level.

Fundamentally, this report work highlights the need to develop research questions that can also target basic management needs: a taxonomy that remains clear and consistent with current data, and clear objectives to inform on translocation risk for each species.

A strategy suggested by Ottewell et al. (2015) - but modified for the genetic assessment of Barrow Island fauna populations relative to reference populations - may help with the decision-making process relevant to Barrow Island fauna and is worthy of adoption. Where conservation translocation is deemed a necessary option for species recovery, clarifying the taxonomy, the genetic differentiation between populations, genetic diversity within populations, and the level of inbreeding within populations on Barrow Island are important criteria to consider for understanding a suitable management objective. This information will help to clarify or reassess the genetic status and listing of many of these Barrow Island taxa. This resolution will also enable managers to understand whether a taxon contains unique genetic resources endemic to Barrow Island and worthy of focused attention. Existing tissue samples for completing genetic analyses could close these gaps for many taxa on Barrow Island.

Table 2. Summary of whether there is adequate information (subjectively assessed by author) currently available for each taxon on Barrow Island based on criterion 1 and 2 (Morris and Yates 2015).

Species	**Clarity on:**				**Information adequate for Criterion 1**	**Information adequate for Criterion 2**
	Taxonomy	**Morphology**	**mtDNA**	**nDNA**		
Northern brushtail possum	X	✓	✓	X	🟥	🟥
Water rat	X	X	✓	✓	🟩	🟩
Western chestnut mouse	X	X	✓	✓	🟩	🟩
Common rock rat	X	✓	IP	IP	🟧	🟧
Barrow Island euro	X	X	✓	IP	🟥	🟥
Spectacled hare-wallaby	X	✓	X	X	🟥	🟥
Black-flanked rock-wallaby	✓	X	✓	✓	🟩	🟩
Pseudantechinus	X	✓	L	L	🟧	🟧
Planigale	X	IP	IP	IP	🟧	🟧
Barrow Island boodie	X	X	IP	IP	🟧	🟧
Barrow Island golden bandicoot	X	L	IP	IP	🟧	🟧
Spinifexbird	X	X	X	X	🟥	🟩
White-winged fairy-wren	✓	X	✓	X	🟧	🟩
Barrow Island leopard skink	X	✓	X	X	🟥	🟥

✓ Information available; X Information unavailable or scant; IP: work in progress; L: limited samples from Barrow Island animals

Green: Adequate taxonomic and genetic information available to assist with translocation management decisions;

Orange: Taxonomic and genetic information partially available to assist with translocation management decisions;

Red: Insufficient taxonomic and genetic information available to assist with translocation management decisions.

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