

**Project Plan SP 2021-008**

**Building resilience to change for mammals in a  
multi-use landscape: identifying refugia and  
landscape connectivity for small mammals in the  
Pilbara**

**BCS Animal Science**

**Project Core Team**

X X **Supervising Scientist** Kym Ottewell

**Data Custodian** Kym Ottewell

**Project status as of Feb. 5, 2024, 4:08 p.m.**

X X Update requested

**Document endorsements and approvals as of Feb. 5, 2024, 4:08 p.m.**

X X

**Project Team** granted

**Program Leader** granted

**Directorate** granted

**Biometrician** granted

**Herbarium Curator** not required

**Animal Ethics Committee** not required



# Building resilience to change for mammals in a multi-use landscape: identifying refugia and landscape connectivity for small mammals in the Pilbara

## Program

BCS Animal Science

## Departmental Service

Service 7: Research and Conservation Partnerships

## Project Staff

X X X **Role Person Time allocation (FTE)**

Supervising Scientist Kym Ottewell 0.2

Research Scientist Lesley Gibson 0.1

Research Scientist Margaret Byrne 0.05

Research Scientist Janine Kinloch 0.1

Research Scientist Katherine Zdunic 0.05

Research Scientist Bart Huntley 0.05

## Related Science Projects

## Proposed period of the project

Oct. 1, 2018 – Dec. 31, 2022

# Relevance and Outcomes

## Background

Identifying and protecting core habitat and dispersal corridors is the cornerstone of best-practice conservation in multi-use landscapes. Globally, the conservation community is recognising that a static, fragmented protected area system is, in many cases, inadequate to conserve populations and species in large areas, over long time-scales and given current rates of environmental change (Hannah et al. 2007, Moritz and Agudo 2013). This recognition has motivated a paradigm shift in conservation thinking away from managing species at a local scale to a broader spatial and temporal perspective: managing species and ecological processes at a whole-of-landscape scale (Pressey et al. 2007) and incorporating evolutionary processes to build species' capacity for adaptation to environmental change (Sgrò et al. 2011).

There are three key foci in this species' resilience conservation approach: (i) identifying historical refugia, areas of the landscape that offer temporally stable, climatically buffered habitat that species can retreat to, persist in and expand from under changing environmental conditions, and which represent potential reservoirs of genetic diversity for adaptation to change (Moritz 2002, Byrne 2008, Byrne et al. 2008, Keppel et al. 2012); (ii) protecting key habitat in species' current distributions; and (iii) promoting population connectivity to maintain metapopulation viability and to retain species' evolutionary potential (Sgrò et al. 2011, Christie and Knowles 2015).

Frameworks exist for the identification of refugia (Keppel et al. 2012) and their incorporation into conservation planning including Australian examples (Keppel et al. 2015, Rosauer et al. 2016). Tools also exist for predicting current habitat and translating this information into the design of nature reserve networks (Villero et al. 2017). Efforts to characterise landscape connectivity, however, are frequently hampered by the lack of empirical data on species dispersal with which to inform mechanistic models (Huntley et al. 2010). Emerging landscape

genetics approaches that quantify gene flow as a proxy for realised dispersal to assess landscape connectivity hold promise to infer dispersal corridors, but to date there has been little uptake in conservation planning, both here and internationally (Keller et al. 2015). Single-species case studies are available (Braunisch et al. 2010, Harradine et al. 2015), however, to be useful as a landscape-scale conservation prioritisation tool, connectivity expectations across a range of species with different movement characteristics and/or habitat requirements is required for robust conservation decision-making (Harradine et al. 2015).

Characterising the landscape features that modify or promote connectivity is critical information for landscape-scale conservation planning. Further, in much the same way that the spatio-temporal stability of refugia are assessed, the stability of species' dispersal corridors should be evaluated under past, present and predicted future environmental conditions to inform crucial dispersal routes. Application of a spatio-temporal landscape genetics approach to multi-species conservation planning therefore represents a novel and significant advancement in this field and provides a means to move beyond a simple pattern- to process-based approach to species conservation (Sgrò et al. 2011, Moritz and Agudo 2013, Keller et al. 2015).

There is urgent need to apply novel landscape-scale, multi-species approaches to conservation in Australian ecosystems. More mammal species have become extinct in Australia in the last 200 years than anywhere else on Earth (Woinarski et al. 2015). Small-medium sized mammal fauna, or 'critical weight range' mammals are recognised as being the most 'at risk' to human-associated disturbances (McKenzie et al. 2007). Mammal extinctions are overrepresented in Australia's arid and semi-arid regions (McDonald et al. 2015). These disturbance-prone ecosystems are understudied globally, despite having high levels of biodiversity. Furthermore, systems that are dynamic over space and time provide an opportunity for understanding how spatio-temporal heterogeneity impact microevolutionary and meta-population processes.

The Pilbara biogeographic region in arid Western Australia is a biodiversity hotspot with high rates of species diversity and endemism (Pepper et al. 2013). This vast and ancient landscape is also economically important, with significant mineral deposits making this region a mining hotspot. This creates conflict between the actions needed to protect biodiversity and those that support economic development. In 2017, the WA Government released the Pilbara Conservation Strategy, providing a framework for initiatives that protect biodiversity, while recognising that long-term conservation will be most effective at a landscape-scale across tenure boundaries. The strategy highlights that a landscape-scale, coordinated approach to development and biodiversity conservation is critical to ensure sustainable outcomes for government, industry and the environment.

This project is therefore significant in bringing together key government and industry stakeholders actively engaged in conservation management in the Pilbara bioregion to identify priority conservation management areas for small-medium sized mammal fauna. The project will capitalise on existing collections; both through tissue and DNA collections and occurrence records from State and national biodiversity record databases. This Project Plan provides details about the generation and collation of high resolution genomic and spatial environmental data, and statistical analyses to investigate patterns across the major mammal groups in the Pilbara (rodents, marsupials and bats). This unique data set will provide current and historical insight into how these animals utilise the Pilbara landscape, resulting in important conservation outcomes. Furthermore, the framework developed for integrating these findings into conservation prioritisations will be applicable for conservation management globally.

## Aims

This project aims to evaluate and apply novel spatio-temporal landscape genetic methods to explore historical refugia, identify current habitat and locate dispersal corridors that build evolutionary resilience for mammal fauna, essential for best-practice conservation under global change. Our approach is applied to spatial and genetic datasets assembled for eight small-medium sized mammal species. We will also incorporate datasets generated in aligned Pilbara mammal projects for an additional three species, resulting in a dataset of 11 species, including four that are endangered nationally. A key outcome is to identify strategic landscape-scale conservation priorities for habitat protection and threat management via systematic conservation planning (SCP). This project is significant in advancing new methodologies to incorporate connectivity modelling into multi-species conservation planning, identifying the major factors contributing to species landscape use and providing a framework for prioritising evolutionary resilient landscapes that can be applied to conservation management in multi-use landscapes globally.

We address our aims through the following objectives:

- Locate core habitat and connectivity pathways (corridors) for species under current environmental conditions by modelling habitat suitability and contemporary gene flow.

- Locate key areas for persistence under changing climates by inferring locations of evolutionary refugia from population genomic data and spatial modelling of range dynamics under historical and predicted future environments.
- Using SCP, identify cost-effective conservation strategies to enhance and protect these areas for optimal combinations of threatened and non-threatened species.

## Expected outcome

The key project outcome for this research is the development of an integrated approach to identifying and protecting dispersal corridors and core habitat in conservation planning. This knowledge product will be of significant interest and benefit to DBCA and a range of other relevant stakeholders. For example, systematic conservation prioritisation maps (incorporating historic refugia, species habitat suitability maps, landscape connectivity maps and future projections of the latter products) produced in this project will be of significant value to government and industry stakeholders. To disseminate these outcomes and ensure uptake and practicality for DBCA and other groups, we will deliver:

1. *Presentations* – Findings will be disseminated through presentations at local, national and international scientific conferences. Importantly, a stakeholder workshop in year 3 of the project will bring together industry, government, indigenous and conservation groups to ensure engagement and dissemination of research findings and uptake of key recommendations. Finally, a public seminar will be held at the completion of the project to promote research outcomes to interested stakeholders and to inform the broader community.
2. *Publications* – Research outcomes will be published in high-impact international peer-reviewed journals with these being open access where possible.
3. *Recommendations/tools* – specific advice will be provided on the representativeness of the current conservation reserve system and priority areas for landscape conservation management action under the Pilbara Conservation Strategy. This project will more broadly assist relevant stakeholders by generating information on priority areas for mammal conservation in the Pilbara that will be used to: 1) target on-ground management actions for threat mitigation (e.g. fire, feral animal control); 2) assess potential impacts of proposed future developments and inform strategies to alleviate, mitigate or compensate for these impacts; and 3) provide an expanded knowledge base regarding the processes that maintain ecological and genetic viability, connectivity and long term resilience and persistence of Pilbara fauna.

## Knowledge transfer

A major goal of the project is the translation of research outputs and transmission of knowledge products across anticipated users from DBCA (including regional offices), partner organisations (Murdoch University, Roy Hill Mining, WABSI, WAM, ANU, Biologic and CSIRO) and other stakeholder groups (e.g. NRM organisations, Dept Water and Environmental Regulation). Knowledge and technology transfer to groups wanting to follow our framework for integrating dispersal corridors, core habitat and refugia in conservation planning will be facilitated through publication of peer-reviewed manuscripts and presentations at conferences, public seminars and stakeholder workshops.

## Tasks and Milestones

### Year 1 (2019 – 2020): Collate and generate data

1. Carry out a literature review on the habitat requirements, dispersal characteristics, life history traits and conservation status of focal species in the project.
2. Catalogue tissue/DNA samples across all species. Perform a literature review of the statistical methods to be employed. Based on the literature and the spatial coverage of available material across the Pilbara, determine a robust sampling design.
3. Perform DNA extractions (for tissues), quantification and quality control for all samples.
4. Send samples to Diversity Arrays Technology for SNP (Single Nucleotide Polymorphism) genotyping.
5. In collaboration with the Spatial Analysis and Remote Sensing Branch at DBCA, collate available spatial data, and determine new spatial products to be modelled for the Pilbara.
6. In collaboration with the Spatial Analysis and Remote Sensing Branch at DBCA and Biologic, determine methodology for generating a topoclimate layer for the Pilbara using iButton data [data contributed by Biologic].

7. Design honours projects and recruit students for 2020 academic year.

## **Year 2 (2020 – 2021): Population genetics and Species Distribution Models (SDMs)**

1. Support two honours projects: (i) “A landscape genetic approach to understanding landscape connectivity in small ground-dwelling mammals in the Pilbara, Western Australia”; (ii) “Population genetics of small mammals in the Pilbara: Finding evolutionary refugia”
2. Design a pipeline for SNP filtering, creating reproducible workflows. Complete filtering for all SNP datasets.
3. Complete population genetic analyses, including genetic clustering analyses (for isolation-by-barrier hypothesis), tests for isolation-by-distance, estimates of genetic diversity and fine-scale patterns of relatedness.
4. Confirm methodology for landscape genetic analyses and SDMs. Complete preliminary analyses and use the quoll as a model for the full workflow.
5. Present preliminary findings at an Australian conference.

## **Year 3 (2021 – 2022): Systematic Conservation Planning**

1. Complete landscape genetic analyses and SDMs for all species.
2. Prepare publications for SDMs and population/landscape genetics findings. Work with honours students to publish studies on historical refugia and landscape genetic comparative analyses.
3. Incorporate population genetic results, landscape genetic results, SDMs and historical refugia into a Systematic Conservation Planning framework.
4. Determine key areas of habitat important as refugia and for landscape connectivity for individual species and guilds of species.
5. Present findings at a stakeholder workshop in the Pilbara. Gather input from partner organisations and other stakeholders to ensure uptake of conservation recommendations generated during the project, and provide training for using the products as a tool for management. Collect feedback to assess feasibility, accuracy and practicality and incorporate into outputs.
6. Present a public lecture, and at an international and Australian conference.
7. Create predictions under future climate change scenarios and search for adaptive loci.

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## Study design

### Methodology

#### Study location

The Pilbara bioregion covers more than 17,800,000 hectares, with land use split primarily between pastoralism, mining, nature conservation, and indigenous reserves. The landscape is characterised by spinifex plains, rugged iron-rich ranges and deep rocky gorges. Annual rainfall varies from ~250 to 450 mm across the bioregion, mainly falling between December and March due to cyclonic events.

#### Study species and genetic samples

This project will focus on small-to-medium Pilbara mammals. Core focal species include Pilbara endemics (*Pseudomys chapmani*, *Ningau timealeyi*, *Dasykaluta rosamondae* and *Planigale* undescribed sp. 1) and several more widespread species (*Dasyurus hallucatus*, *Sminthopsis macroura*, *Sminthopsis youngsoni* and *Pseudomys hermannsburgensis*). We will also incorporate data generated from additional DBCA projects, including *Rhinonictis aurantia*, *Macrotis lagotis* and *Macroderma gigas*. There is also potential to include other species once the analytical framework has been developed.

Genetic datasets will be generated for the eight core focal species. Single nucleotide polymorphism (SNP) genotyping will be carried out by Diversity Arrays Technology (DART) Pty Ltd. DARTseq is a proprietary reduced representation next-generation sequencing method, which uses restriction enzymes optimised for the target species to achieve complexity reduction (Kilian et al. 2012, Cruz et al. 2013). Following DARTseq processing, we will filter SNPs to obtain an informative set of loci for genetic analysis, using R (R Core Team 2019). This will include the use of key filters to remove sex-linked SNPs, missing data and linkage disequilibrium. We will also filter on reproducibility (calculated using DART technical replicates), read depth and minor allele frequency.

Additional genetic datasets (mitochondrial DNA sequences, microsatellite genotypes) for many of the species are also available to the project and will be utilised where appropriate.

#### Environmental variables

Selecting appropriate environmental attributes that represent the spatial structure of the environment in a biologically relevant way is a major challenge of landscape genomics. To select the most appropriate spatial layers relevant to each species, we will review the literature and communicate with taxon and Pilbara experts. This information will be used to develop clear hypotheses about the landscape characteristics and environmental variables likely to be important for each species. These include Digital Elevation Models (and derivatives), fire, vegetation, hydrology, substrate, herbivore pressure and climatic variables (both present and future projections).

#### Statistical analyses

The bulk of statistical analyses will be carried out in R (R Core Team 2019), supported by the resources provided by the Pawsey Supercomputing Centre (with funding from the Australian Government and the Government of Western Australia). We describe the statistical methods we will use to address the major aims of this project below.

*Locate core habitat and connectivity pathways (corridors) for species under current environmental conditions by modelling habitat suitability and contemporary gene flow*

Species distribution models (SDMs) will be used to predict core habitat for each species. Many statistical models exist for predicting species distributions; we will use Maximum Entropy (MAXENT) through the dismo R package (Hijmans et al. 2017, Phillips et al. 2019), as well as an ensemble approach implemented at <http://www.bccvl.org.au/>. The results from these models will be used to create a multi-species SDM, which will be used to help weight conservation prioritisations by habitat patches that are important for a number of species. Locations with a high probability of occurrence for each species will also be used as 'nodes' for the CIRCUITSCAPE analysis (described below).

Landscape genetic models incorporating increasing complexity (Isolation-By-Distance [IBD], Isolation-By-Barrier [IBB], Isolation-By-Environment [IBE] and Isolation-By-Resistance [IBR]) will be evaluated for each species. A hypothesis of IBD will be explored using the dartR package (Gruber et al. 2018), to perform mantel tests. IBD will also be used as a null hypothesis in IBR models (support for IBD vs. IBR will be determined using an information-theoretic approach).



IBB will be tested using Principle Coordinate Analysis and genetic clustering methods. Following best practice, we will use multiple algorithms to confirm findings (including model-free and spatially explicit algorithms). We will use Tess3R (Caye and Francois 2016), sparse non-negative matrix factorization (sNMF, implemented through LEA; Frichot and François 2015) and Discriminant Analysis of Principle Components (DAPC, implemented through Adegenet; Jombart 2008, Jombart and Ahmed 2011).

To test for IBE, we will employ a novel use of generalised dissimilarity modelling (GDM) to assess genetic dissimilarity-environment associations (Ferrier et al. 2007), implemented in the gdm package (Fitzpatrick et al. 2020). Site-specific environmental variables will be extracted from high resolution spatial layers for analysis of genetic connectivity drivers.

IBR hypotheses will be tested using the R package ResistanceGA (Peterman 2018). Spatial environmental layers will be extracted for a number of Pilbara landscape subsets, and converted into resistance surfaces. ResistanceGA uses a genetic algorithm to objectively parameterise resistance surfaces, by comparing pairwise genetic data and effective distances with maximum likelihood population effects mixed effects models. Model selection is used to determine which resistance surface/s and cost-ratio/s best fits the observed genetic data (or whether a model of panmixia or IBD better explain the data). Effective distances are calculated using random-walk commute times (equivalent to CIRCUITSCAPE resistance distance).

Using a GIS platform and CIRCUITSCAPE (McRae et al. 2008), these landscape genetic models will be used to inform spatially explicit resistance surfaces to visualise landscape connectivity across multiple species. We will use these surfaces to identify 'dispersal corridors'; areas with high connectivity between habitat 'nodes'.

*Locate key areas for persistence under changing climates by inferring locations of evolutionary refugia from population genomic data and spatial modelling of range dynamics under historical and predicted future environments.*

SNP data for the eight focal species will be used to assess whether these species experienced population contractions during the Last Glacial Maximum (LGM) and to locate refugia. SDMs will be generated using MAXENT, with the 19 bioclimatic variables in the WorldClim archive (Hijmans et al. 2005). These will then be hindcast to the Pleistocene/LGM to assess regions of stability which may have acted as refugia. To investigate if range expansions occurred and locate possible LGM refugia, we will use the rangeExpansion package (Peter and Slatkin 2013). This method looks at the genetic patterns left from successive founder events during a range expansion. The loss of low frequency alleles during founder events results in allele frequency clines, with lower frequency at the origin of expansion, and frequency increasing in the direction of the expansion. These findings/models will also be used to forecast species distributions into the future, to compare likely distributions under a number of climate scenarios.

*Using Systematic Conservation Planning (SCP), identify cost-effective conservation strategies to enhance and protect these areas for optimal combinations of threatened and non-threatened species.*

The findings from the two previous objectives will be used in a SCP framework to develop conservation priorities that incorporate core habitat, refuges and landscape connectivity requirements across multiple species. This will include evaluating the performance of the current reserve system in protecting important refugia and dispersal pathways, identification of suitable conservation offset locations and areas for targeted threat management.

This will be achieved using the conservation planning software Marxan (Ball et al. 2009), to identify areas that maximise species habitat (as well as historical and future refugia), while ensuring these patches are sufficiently connected by dispersal corridors. We will then hold a Pilbara workshop involving partner organisations and relevant stakeholders to outline our findings, and demonstrate how systematic conservation planning can be used to address management challenges. Based on the feedback of participants in this workshop, we will revise data inputs and incorporate these into our SCP framework to come up with conservation prioritisations and recommendations for the Pilbara bioregion's mammal fauna.

## **Biometrician's Endorsement**

granted

## **Data management**

### **No. specimens**

### **Herbarium Curator's Endorsement**

not required

## Animal Ethics Committee's Endorsement

granted

## Data management

Tissue/DNA samples will be sourced from and returned to the relevant collections (including the DBCA Biodiversity and Conservation Sciences genetics lab, the WAM and the University of Western Australia). Genetic data will be routinely backed up on Google Drive, OneDrive and on the Pawsey and Australian National University servers. Data and documentation for published results will be uploaded to the DBCA Data Catalogue.

## Budget

### Consolidated Funds

to | X | X | X | X |

Source Year 1 Year 2 Year 3

FTE Scientist 69,18470,913 72,686

FTE Technical 19,177

Equipment

Vehicle

Travel

Other

Total 88,36170,913 72,686

### External Funds

to | X | X | X | X |

Source Year 1 Year 2 Year 3

Salaries, Wages, Overtime 110,730233,748 89,139

Overheads

Equipment

Vehicle

Travel 3,95813,929 9,416

Other 79,7501,690 8,390

Total 194,438249,367 106,945