

Final Report to Nature Foundation SA-The Roy and Marjory Edwards Scholarship

Project: Conservation Genetics of an Endangered Marsupial, the Southern Brown Bandicoot

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Introduction

Habitat loss and fragmentation are major threats to the world's biodiversity. Throughout Australia, land has been extensively cleared and modified through agriculture, forestry and urbanisation. In South Australia, less than 20% of native forests and woodlands remain and many of these have been severely fragmented into smaller and isolated patches. Species inhabiting fragmented habitats can suffer from decreased population size, reduced or inhibited dispersal and a series of genetic risks, including inbreeding, reduced genetic diversity, increased genetic differentiation among populations and potentially increased extinction risk. The southern brown bandicoot (*Isoodon obesulus*), the focus of the current project, is a rabbit-sized ground-dwelling marsupial, which has declined in number dramatically over the last 220 years. The subspecies *I. o. obesulus* is listed as nationally endangered under the Australian Environment Protection and Biodiversity Conservation Act 1999. Habitat loss and fragmentation has become one of the main processes threatening the survival of *I. obesulus*, leading to a contracted distribution and local population extinctions throughout Australia. In this project, a combination of microsatellite, nuclear and mitochondrial markers have been applied to investigate several questions relating to population genetic structure, gene flow, dispersal and genetic distinctiveness of populations of *I. o. obesulus* in southern Australia. The results obtained in this project have increased our knowledge of the genetic connectivity of *I. o. obesulus* populations in fragmented landscapes and provided valuable baseline genetic information for the conservation management of the species. This project consists of four parts as explained below.

Part One

Nine polymorphic microsatellite markers were developed using a next generation sequencing approach. The markers were genotyped in 59 individuals from two distinct locations (the Mount Burr Range and the Mount Lofty Ranges) in South Australia. These markers, in addition to six microsatellite markers from a previous study, were used for the following analyses and provide a valuable resource for future molecular ecological studies of *I. obesulus*.

The data of this part has been published:

Li Y, Lancaster M, Cooper SB, Packer J, Carthew S (2013) Characterization of nine microsatellite loci from the endangered southern brown bandicoot (*Isoodon obesulus*) using 454 pyrosequencing. *Conservation Genetics Resources* **5**, 105-107.

Part Two

Population structure and gene flow/dispersal of *I. o. obesulus* within a fragmented forest system in south-east South Australia – the Mount Burr Range (Fig. 1) were investigated. In this fragmented habitat, native forest patches are surrounded by matrices of either *Pinus radiata* plantations or cleared agricultural land. A total of 147 samples from 14 native forest patches were genotyped at 15 microsatellite loci. The results showed significant population genetic structuring at a fine spatial scale, with strong genetic differentiation among patches. Gene flow and dispersal was limited and generally only among neighbouring patches. The findings contribute valuable information on the positioning of habitat corridors in this area, and enable the effectiveness of these corridors to be assessed in the future.

The data of this part has been submitted to the journal Conservation Genetics in April 2014 and the manuscript is in review at the moment.

Part Three

In this part, 14 microsatellite markers were utilised to genotype 284 individuals from 15 sites in a heavily modified peri-urban landscape in South Australia – the Mount Lofty Ranges (Fig. 2). The results showed significant genetic differentiation among sites. Sites in the central Mount Lofty Ranges were also more genetically differentiated than sites distributed over a similar spatial scale in the Mount Burr Range, with evidence for a dispersal threshold of 1km (the Mount Burr populations had a ~2.5 km dispersal threshold), and with two sites appearing to be genetically isolated. These analyses suggested that gene flow/dispersal was limited to a higher degree in the Mount Lofty Ranges compared to Mount Burr, possibly due to the heavily modified landscape in the former area (e.g. a mixture of matrix of urban constructs and agricultural land).

The data of this part has been submitted to the journal PlosOne in July 2014 and the manuscript is in review at the moment.

Part Four

The final part investigates the phylogeography and population structure of the *I. o. obesulus* populations in South Australia and south-western Victoria using a combination of 14 microsatellite markers, two mitochondrial sequence markers (control region and *ND2*) and three nuclear sequence markers (*BRCA1*, *RAG1*, and *vWF*) (Fig. 3). This part aimed to identify any potential evolutionarily significant units (ESUs) in the study region. All markers supported two distinct genetic lineages of *I. o. obesulus* in South Australia and south-western Victoria. The first lineage consisted of individuals from the Mount Lofty Ranges and Kangaroo Island. Samples from the lower south-east of South Australia and south-western Victoria (the Grampians and Lower Glenelg) represented the second lineage. These two lineages should be considered as separate evolutionarily significant units and managed separately for conservation purposes. An expanded phylogenetic analysis was conducted using additional samples of *I. obesulus* from other regions in Australia and samples of *I. auratus* (the golden bandicoot, distributed in the Northern Territory and Western Australia). The results raise the issue of the taxonomic status of the two lineages and also suggest that current subspecies and species classification within *I. obesulus*/*I. auratus* may not adequately reflect the existing major genetic lineages.

The data of this part has been submitted to the journal Australian Journal of Zoology in June 2014 and the manuscript is in review at the moment.

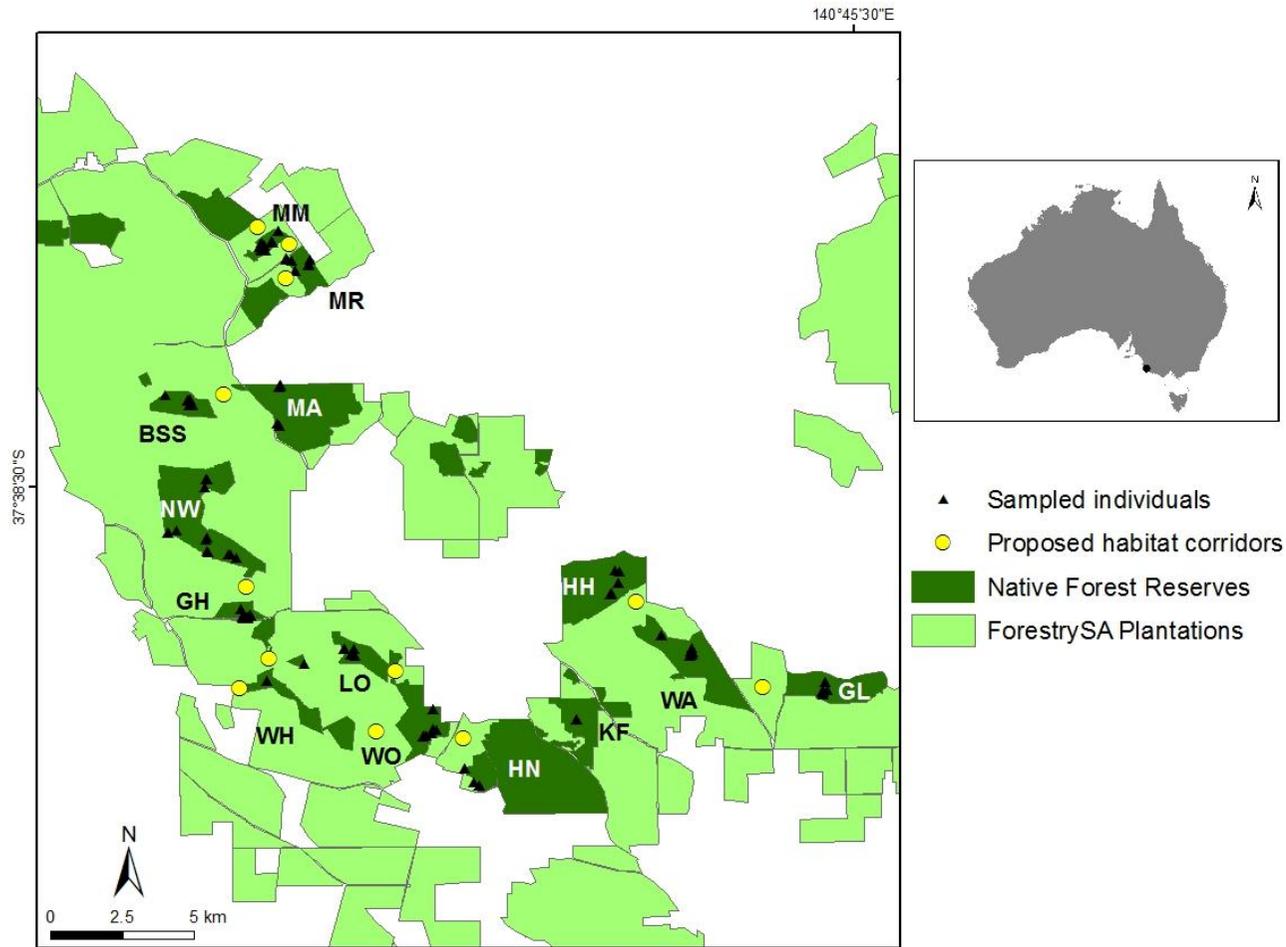


Fig. 1 Detailed map of the Mount Burr Range in the Green Triangle Forest in the south-east of South Australia, Australia. Native forest patches are represented in dark green, pine plantations are represented in light green, and agriculture lands are represented in white. Names of the 14 sampled patches were marked in or next to the corresponding dark green areas. Sampled bandicoot individuals were marked with dark triangles. Twelve habitat corridors were proposed in this area to connect proximate patches and they were marked with yellow circles in the map.

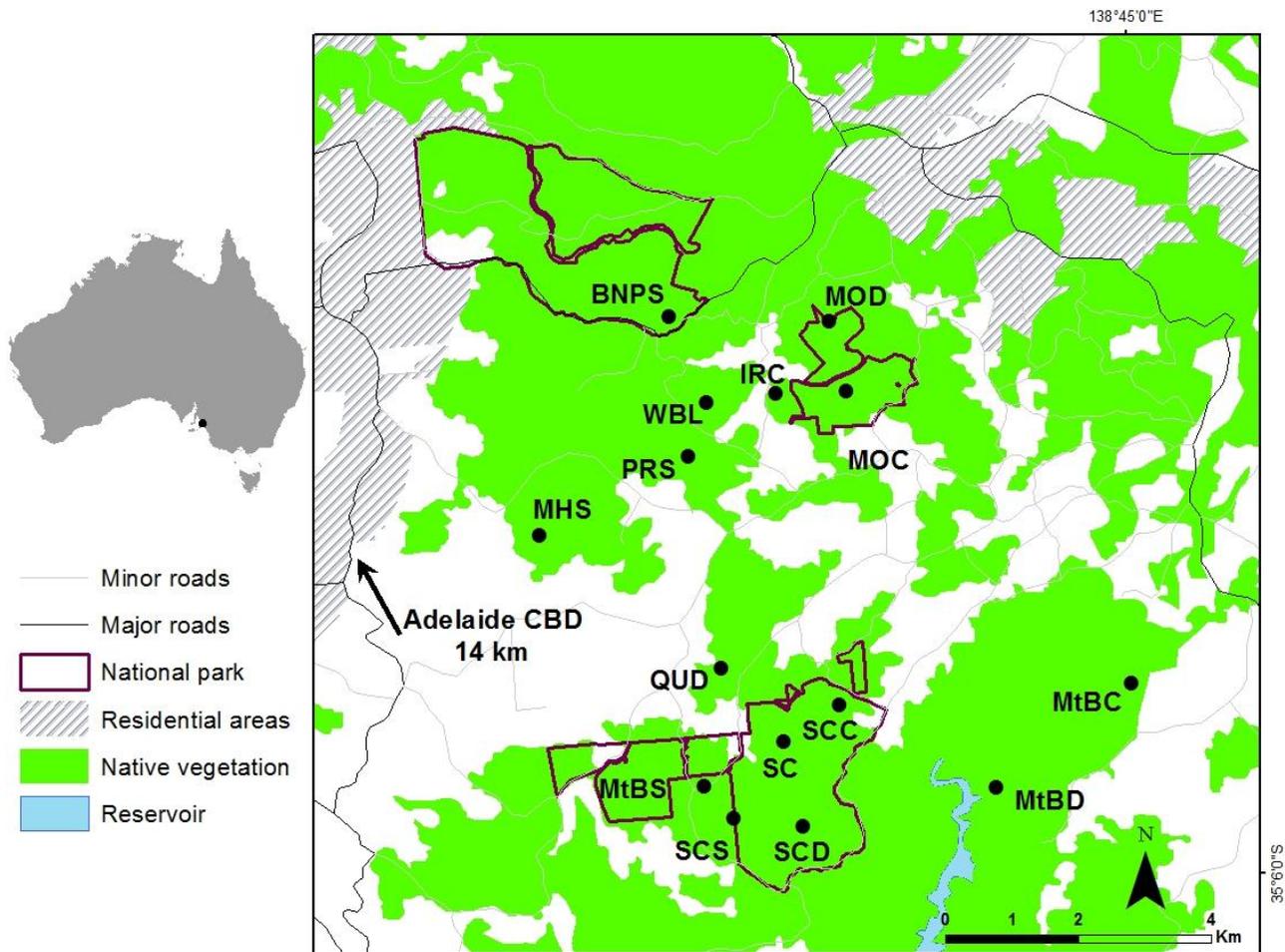


Fig. 2 Detailed map of the study sites in the central Mount Lofty Ranges of South Australia, Australia. Outlined areas in the map denote three national parks in our study area (Belair National Park, Mark Oliphant Conservation Park and Scott Creek Conservation Park). White areas denote agricultural land. Sampled sites were marked with dark dots and labelled with letters.

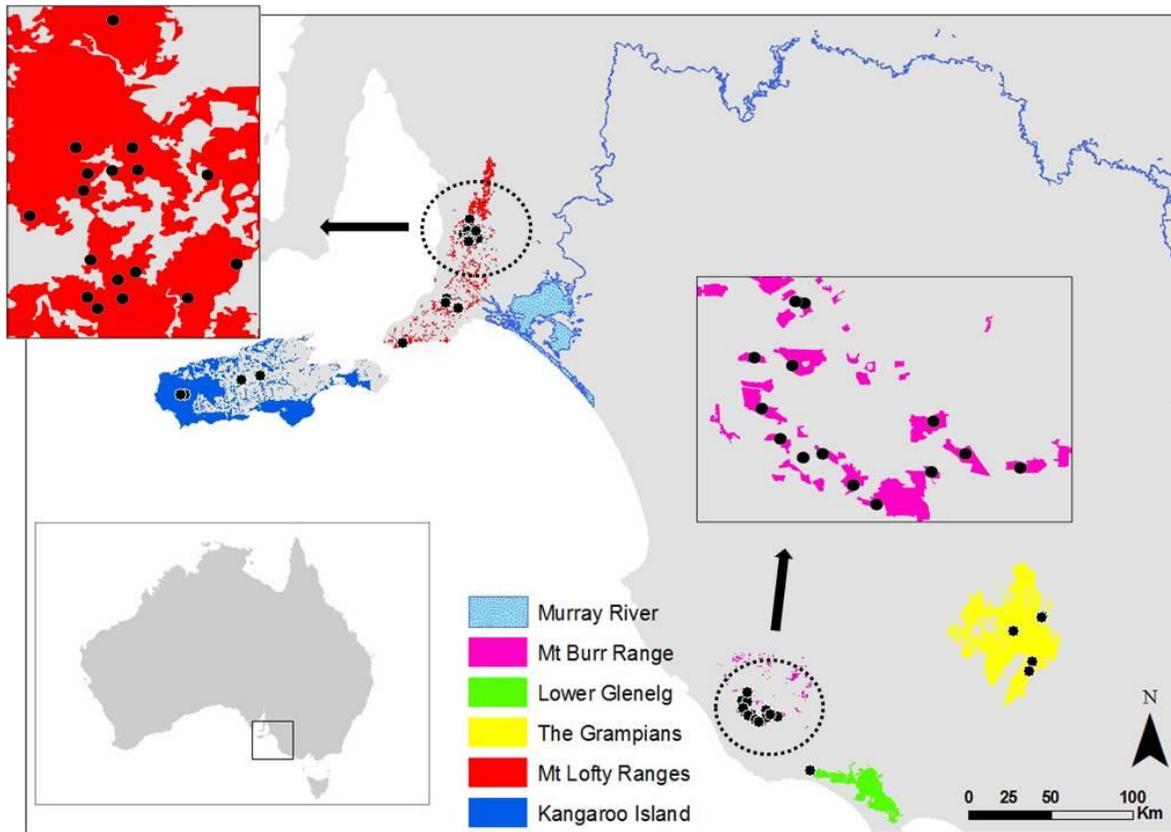


Fig. 3 Distribution of the five sampled regions of *I. o. obesulus* in southern Australia. Sampled locations in each region are labelled in black dots. The Mt Burr Range and core area of the Mt Lofty Ranges are enlarged for better visualising.