

# Conservation genetics of the endangered southern brown bandicoot (*Isoodon obesulus*) in South Australia



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Submitted for the degree of Doctor of Philosophy

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August 2013

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## Abstract

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 thesis, 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 thesis, 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 thesis 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 thesis was structured into four distinct data chapters as explained below.

Chapter Two comprises a published primer note, in which 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 thesis chapters and provide a valuable resource for future molecular ecological studies of *I. obesulus*.

In Chapter Three, I investigate population structure and gene flow/dispersal of *I. o. obesulus* within a fragmented forest system in south-east South Australia – the Mount Burr Range. 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.

In the fourth chapter I utilise 14 microsatellite markers to genotype 284 individuals from 15 sites in a heavily modified peri-urban landscape in South Australia – the Mount Lofty Ranges. 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 final data chapter (Chapter Five) 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*). This chapter 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.

## **Declaration**

I certify that this work contains no material which has been accepted for the award of any other degree or diploma in my name, in any university or other tertiary institution and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text. In addition, I certify that no part of this work will, in the future, be used in a submission in my name, for any other degree or diploma in any university or other tertiary institution without the prior approval of the University of Adelaide and where applicable, any partner institution responsible for the joint-award of this degree.

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## Acknowledgements

First of all, I would like to thank my supervisors Dr Melanie Lancaster, Professor Steve Cooper and Professor Sue Carthew for taking me in as their student and providing me with such an interesting project on the amazing bandicoot. Working with them and their students is a chance of a lifetime for me to get to experience the world of the incredible marsupials of Australia! I am deeply grateful to my supervisors for their patience, encouragement, enthusiasm, motivation, professional instructions and immense expert knowledge to walk me through the four-year's PhD. Massive thanks to them for quick and inspiring feedbacks on my thesis writing during the last couple of months before my candidature ends. Without their support and guidance, the completion of my PhD would not have been possible.

I would like to mention my colleagues. Thanks to Jasmin, with whom I experienced the first field trip of trapping bandicoots. She taught me all the skills I needed for trapping and handling and gave me an unforgettable memory. Thanks to Amanda who volunteered on my field trips whenever I needed her and provided excellent help in the field. Thanks to Nik for his patience and assistance with data processing. I also want to thank Bec and Casey for their amazing baking that always brought so much joy to the office. Their friendships have been invaluable and helped me through all the difficult times of my life in Australia.

I would like to thank all my volunteers who came to help me in the field. Thanks to Peter Hatcliff, Clive Carlyle and Catherine Carlyle, Janet Tan, Samuel Clarke, Kyle Holland, Jess Rowe, Jamie Kohler, Paula Bertsch, Nathan Stavridis, Amy White, Andrew Wiewel, Inta Chambers, Anthony Hay, Toni Bellingham, Orazio Cultreri, and Ben Stevenson and Michelle Le Duff from the Department of Environment, Water and Natural Resources (DEWNR) for their excellent field assistance. I also thank Troy Horn, Bryan Haywood and Robert Mengler from ForestrySA for their advice and assistance in the field. Thanks to Troy, who helped me get familiar with the bandicoot habitat in the south-east and rescued me once when the car got bogged in the mud and thanks to Bryan who provided his assistance whenever I needed. Thanks to Luke Price from DEWNR for sharing cage traps and bandicoot samples and his kind assistance with creating maps.

I would also like to thank Kathy Saint for laboratory assistance and Alison Fitch and Mike Gardner for their assistance with 454 sequencing data analysis.

A very special thanks to Sandy McConachy, who has been putting so much effort into developing collaborations between various universities in China and the University of Adelaide. Without her help and encouragement, my adventure in the fantastic Australia would not have been possible. I also want to thank Professor Richard Russell for taking care of me and other Chinese Scholarship holders during our life in Australia. I'm looking forward to seeing them in China in the future.

My special thanks is to my boyfriend Bo Li and my family. Thanks to Bo for accompanying and supporting me to get through all the difficulties and enduring the bad temper of me during the hard writing period. Thanks to my Mum, Dad and brother for caring and having faith in me.

Lastly, I would like to thank the China Scholarship Council for providing a living allowance. I also want to thank all my funding bodies: the University of Adelaide, the Australian Research Council Linkage grant (LP0668987), Native Vegetation Council, Wildlife Conservation Fund, DEWNR, the Department of Environment and Primary Industries (Victoria) and The Roy and Marjory Edwards Scholarship provided by Nature Foundation SA.

