

The ecology and evolution of invasive
Potamopyrgus antipodarum in Australia

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A thesis submitted for the degree of
Doctor of Philosophy

February 2016
Institute for Applied Ecology
University of Canberra
Australia

Abstract

The spread of invasive organisms is one of the greatest threats to ecosystems and biodiversity worldwide. Understanding the evolutionary and ecological factors responsible for the transport, introduction, establishment and spread of invasive species will assist the development of control strategies.

The New Zealand mudsnail, *Potamopyrgus antipodarum* (Gray 1843) (Gastropoda: Hydrobiidae), is a global freshwater invader, with populations established in Europe, Asia, the Americas and Australia. While sexual and asexual *P. antipodarum* coexist in the native range, invasive populations reproduce by parthenogenesis, producing dense populations that compete for resources with native species. *Potamopyrgus antipodarum* is a natural model system for the study of evolutionary and ecological processes underlying invasion.

This thesis assesses the invasion history, genetic diversity and ecology of *P. antipodarum* in Australia, with particular focus on: a) potential source populations, b) distribution and structure of populations, and c) species traits related to the establishment, persistence and spread of invasive *P. antipodarum*. Genetic analyses were carried out on specimens collected for this study from New Zealand and Australia, along with existing museum samples. In combination with published data, the analyses revealed low genetic diversity among and within invasive populations in south-eastern Australia, relative to New Zealand populations. Phylogenetic relationships inferred from mitochondrial sequences indicated that the Australian populations belong to clades dominated by parthenogenetic haplotypes that are known to be present in Europe and

the US. These ‘invasive clades’ are likely to originate from the North Island of New Zealand, and suggest a role for selection in determining genetic composition of invasive populations.

The genotypic diversity of Australian *P. antipodarum* was low, with few, closely related clones distributed across south-eastern Australia. The pattern of clone distribution was not consistent with any assessed geographical or abiotic factors; instead a few, widely-distributed clones were present in high frequencies at most sites. Differences in clone frequencies were found, which may indicate differential success of clonal lineages.

A range of traits have been proposed as facilitators of invasion success, and within-species variation in these traits can promote differential success of genotypes. Using laboratory-based experiments, the performance of the three most common Australian clones was tested across a suite of invasion-relevant traits. Ecologically-relevant variation in traits was found among the clones. These differences may have determined the spatial distribution of clones, and may continue to do so into the future.

This thesis found that the *P. antipodarum* invasion of Australia is the result of few introductions of a small number of globally-invasive genotypes that vary in ecologically-relevant traits. From a source of considerable genetic diversity in the native range, very few genotypes have become invasive. Those that are invasive appear to be very successful at continental scales. These findings highlight a capacity in asexual invaders to successfully invade, and potentially adapt to, a broad range of ecosystems. The *P. antipodarum* invasion system is amenable to research using combinations of field-based studies, molecular and laboratory approaches, and is likely to yield significant, broadly-applicable insights into invasion.

Acknowledgements

I would like to acknowledge all those that have given me support and encouragement throughout my PhD. First and foremost, I would like to thank my three supervisors: Professor Ross Thompson, Professor Paul Sunnucks and Associate Professor Dianne Gleeson. Ross's passion and enthusiasm for science is infectious and I have used this as a constant source of motivation. I appreciate the independence Ross has given me during my candidature, seemingly maintaining his faith while I shaped a project and even made (occasional!) mistakes. His encouragement for me to frequently present my work at conferences and engage in "postgrad life" has greatly enriched my PhD experience. From the outset Paul has challenged me to broaden my thinking, helping to get the most out of my research. I thank Paul for introducing me to genetics, and for his patience as I found my feet. Dianne has assisted me through the majority of my lab tribulations (and triumphs!), maintaining her encouragement throughout. I am grateful for the way Di has made seemingly insurmountable tasks appear straightforward. I would also like to thank Dr. Maurine Neiman from the University of Iowa. Maurine is an inspiring biologist, I am very fortunate to have had access to her insightful input for much of my work. I appreciate Maurine's generosity with her time, data, samples, expertise and support.

My PhD experience has been greatly enriched by the opportunity to regularly present my research at international and domestic conferences. This was made possible by the generous financial support of the Australian Society for Limnology, the Institute for Applied Ecology (IAE) and the Australian Centre for Biodiversity.

In the early stages of my PhD I spent considerable time examining the Hydrobiid specimens at the Museum Victoria and the Environment Protection Authority Victoria, I thank these institutions and their staff for accommodating me. Samples collected during my fieldwork were supplemented by contributions from the EPA and from Toni Furlonge, to whom I am very grateful. Many thanks to Dr. Dorota Paczesniak for generously contributing her data and expertise over numerous (doubtless inconvenient!) Skype calls.

I owe a debt of gratitude to my many helpers in the field and laboratory. Katherine Harrison and Dr. Sam Venables were the epitome of patience while guiding me up the steep learning curve in the genetics lab. Dr. Valerie Caron donated many weekend hours of expert assistance in processing my samples; no doubt I would still be slaving over a hot gel were it not for Val's selfless help. Thanks to Laura, Darren, Chantelle, David, Teresa, Mel, Clarissa, Paula,

James, Lucie, Sally, Alan and Evan for helping to collect water, clean tanks and go on grand snail hunts.

I would like to thank the administrative staff at Monash University's School of Biological Sciences, and the research support unit at the IAE, especially Barbara Harriss, for helping me deal with my mild admino-phobia (fear of paperwork!).

I have enjoyed being part of various lab groups: my thanks to the Sunnucks Lab at Monash Uni, the Wildlife Genetics Lab at the IAE, and the freshwater crews at both Monash and the IAE. Particular thanks to Professor Jenny Davis and Associate Professor Carlo Sgrò for their constructive comments on my early project proposals.

To my friends at the IAE and Monash Uni, along with the many friends made at conferences, thank-you for helping to make this such a rewarding experience. A PhD could potentially be an isolating experience, but I have been lucky to share it with a group of supremely interesting, talented and adventurous friends. Particular thanks to Dr. Giselle Perdomo, Dr. Lucie Bland and Teresa Gonzalez, with whom I have had many stimulating conversations. My gratitude goes to Dr. David Hartley for his close friendship, the odd beer or three during our candidatures and his support during our many hard years following the capricious Richmond Tigers.

I am particularly indebted to Laura Caffrey and Dr Darren Giling. Loz and Daz often sacrificed their time and other commitments to accompany me on snail hunts and help out in the snail dungeon. For this they each thoroughly deserve, at last, the title "Snail Hunter: Grand Master." Our many shared experiences have built an irrevocable bond.

My gratitude to the Trappist monks of Scourmont Abbey for the occasional reminder that producing something complex over a long period of time can be highly enjoyable.

Thank-you to my family for your support and interest in all I do. My deepest thanks go to my parents for sparking, at a very young age, my interest in nature, science and how things work. My heartfelt thanks to my wife, Chantelle, for organising a wedding single-handedly, for her unconditional support, and for my regular use of her exceptional intelligence as a sounding board.

This thesis would not be possible without everyone mentioned above. My thanks again to all who have supported me, and in so doing endured my punny sense of humour. Hopefully it is some consolation that we have done our little bit to prevent *P. antipodarum* becoming simply another snail in the coffin of biodiversity.

Foreword

This thesis represents work carried out under the supervision of Professor Ross Thompson, Professor Paul Sunnucks and Associate Professor Dianne Gleeson. The thesis is composed of a series of connected but independent units, each of which is intended for publication. Each chapter is written as a separate entity, with a full complement of the sections required by a manuscript and there may be some overlap of material among chapters. Some chapters have used data published in previous studies and the authors contributing these data are acknowledged in-text. When such chapters come to be submitted as papers for publication, these collaborators will be recognised as co-authors, and are identified as such below.

Chapter 1. *General introduction*. This chapter provides a background on asexual reproduction in invasion and a summary of existing knowledge of the ecology of the clonal invader, *Potamopyrgus antipodarum*. It will be combined with components of my general discussion to be submitted as a co-authored paper with my supervisors.

Chapter 2. *Reconstructing the invasion history of Potamopyrgus antipodarum in Australia*. This chapter uses genetic markers to explore the global movement of *P. antipodarum* and infer potential source populations. This chapter will be submitted as a paper co-authored with Dr. Maurine Neiman (University of Iowa), Dr. Dorota Paczesniak (Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)), and my supervisors.

Chapter 3. *The distribution of invasive clones of Potamopyrgus antipodarum in south-eastern Australia.* This chapter identifies the distribution patterns of different *P. antipodarum* genotypes across south-eastern Australia. This chapter will be submitted as a paper co-authored with Dr. Maurine Neiman (University of Iowa), Dr. Dorota Paczesniak (IPK), and my supervisors.

Chapter 4. *Differential performance among genotypes in a clonal invader.* This chapter compares the performance of three *P. antipodarum* genotypes across a suite of invasion-relevant traits. This chapter will be submitted as a paper co-authored with my supervisors.

Chapter 5. *General discussion.* This chapter provides an overview and synthesis of my findings, and proposes future research directions.

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