7 Genetics of Invasive Species in New Zealand

D. Gleeson, H. Harman and T. Armstrong

7.1 Introduction

The genetic architecture of invasive species is now considered to be an important factor governing the long-term success of colonization in a new environment, as this is critical for the subsequent ability of invasives to respond to natural selection (Lee 2002). A clearer understanding of the genetics of invasive species has the potential to provide insights into the mechanisms of invasions as well as determining the genetic changes associated with the process of invasions. Genetic information may also be used to determine factors such as the origin and relative success of invasive species, and provide potential for investigating novel methods of control.

New Zealand offers opportunities to investigate the genetic processes underlying invasive species. Mainly this is due to a significant number of invasive species in New Zealand being deliberately introduced and, as a consequence, having well-documented introduction histories that enable post-colonization genetic investigations to be carried out. In addition, New Zealand is a heterogeneous landscape that possesses many natural barriers along with varying climatic conditions, facilitating multiple founder events, as well as providing colonizers with a range of selection pressures. Given these factors, relatively few studies have taken advantage of the opportunities presented by such introductions. This chapter reviews the research that has attempted to address the genetics of alien species in New Zealand, and suggests potential future research directions that can take advantage of these systems.

7.2 Genetics of Colonization

The principles of colonization genetics have been well documented through a range of publications that have investigated these in relation to classical models of founder events and allopatric speciation (Mayr 1963; Baker and Steb-
bins 1965; Carson 1971; Barton and Charlesworth 1984). Generally, invasive alien species experience the same effects as do natural colonizers, in that there is an initial establishment phase followed by rapid growth and subsequent invasion. The genetic consequence of such founder events has been one of the central tenets of allopatric speciation (Barton and Charlesworth 1984). The predicted genetic outcomes following a dramatic reduction in population size associated with founder events are a reduction in genetic variability, and, if species experience several independent founder events, this can result in genetic divergence among founding populations. Random genetic drift (Wright 1931) is the chance process most often advocated as the cause of the observed genetic change.

The extent of genetic change following founder events is predicted to be highly contingent on the size of the initial founding population. If the founding population is large, then there may be no substantial loss of genetic variability (i.e., allelic diversity) in the newly established range, as there is a high probability of all the genetic variants in the parental population being represented in the founder population (Kambhampati et al. 1990). Alternatively, if the initial founding population is small and subsequent establishment in the new range results in even smaller isolated subpopulations, then random genetic drift will play an increasingly important role in the loss or restructuring of variation. Thus, the effects of founding events and subsequent genetic drift are often difficult to distinguish (Barton and Charlesworth 1984).

The most recognized genetic consequence of colonization is the loss of genetic variability, due to founding individuals representing only a subset of the species’ variability. Recessive alleles have a higher probability of becoming homozygous and being exposed to the effects of selection, with many alleles potentially becoming disadvantageous due to the new imbalance in the epigenotype or change in selective value (Mayr 1963). From the perspective of colonizing ability, genetic changes can either facilitate this or have a negative effect. An extreme example of where a reduction in genetic diversity post-colonization has resulted in significant changes in behavior in an invasive species is the Argentine ant, *Linepithema humile* (Tsutsui et al. 2000, 2001; Tsutsui and Case 2001). This species becomes a successful invader due to the loss of both self-recognition and aggressive territoriality, enabling the formation of “supercolonies” extending up to thousands of kilometers. However, there have been few studies that have addressed the importance of genetics in the establishment and early success of invasive species (Roderick and Howarth 1999). Rather, most studies have used genetic markers to investigate the origins and population genetic structure of invasive species.