Evaluating success of translocations in maintaining genetic diversity in a threatened mammal

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ABSTRACT

The effectiveness of fauna reintroduction programs has been limited by the availability of source animals and the lack of follow up monitoring to assess whether viable populations have been successfully established, particularly in terms of conserving genetic diversity. Here we present genetic assessment of the translocation of golden bandicoots (Isoodon auratus) from a large source population on Barrow Island off the north-west coast of Western Australia to two other island sites and a mainland fenced enclosure. We assessed the genetic diversity of animals translocated to each site and their wild-born progeny, and whether wild-born animals showed evidence of genetic bottlenecks or genetic drift from the source population. Encouragingly, we found no significant loss of genetic diversity in any of the wild-born populations compared to the source population and no significant increase in inbreeding or relatedness amongst wild-born individuals compared to founder populations two years post-translocation. However, we detected an approximately 10-fold reduction in effective population size between founding and wild-born populations. We found no apparent differentiation between wild-born populations and the original source population, or between wild-born animals and their respective founders. Population viability modeling predicts that each of the translocated populations is susceptible to loss of genetic diversity over time. Taken together these results suggest that the golden bandicoot reintroduction program has been initially successful as a result of large founding sizes and high reproductive rates; however, ongoing augmentation will be required to prevent genetic erosion and maintain evolutionary potential in the long-term.

1. Introduction

The reintroduction of extirpated fauna to parts of their former native range is a key conservation tool used by wildlife managers to increase effective population size and spatial representation of threatened species, and reduce the risk of extinction. Reintroductions are also expected to have a greater benefit on ecosystems by restoring some level of ecosystem function in the species' former habitat; for example, bandicoots are considered 'ecosystem engineers', having an important role in soil turnover and nutrient cycling (Valentine et al., 2012). The ultimate aim of reintroduction programs is to establish viable, self-sustaining populations (IUCN, 2012), though the criteria used to judge their success or failure are often not clearly defined, such that there is still no clear agreement on what constitutes a successful reintroduction (Moseby et al., 2011; Seddon, 1999). For example, Bajomi (2010) summarises four different definitions of success, including breeding of the first wild-born generation, positive population growth rate over three generations or 10 years, the use of population viability analysis indicating a self-sustaining population and population persistence over a defined period of time.

Globally, reintroductions have been attempted for a large number of vertebrate species (primarily mammals and birds) but have had only what is viewed as limited success in establishing viable, self-sustaining populations in the medium to long-term (Fischer and Lindenmayer, 2000; Sheean et al., 2012; Short, 2009). Habitat suitability and quality, and the failure to control or remove threatening processes (such as predation) are frequently identified as the reasons for the failure of reintroduced populations (Moseby et al., 2011; Sheean et al., 2012), though others may include naivety of

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captive-reared individuals, too few individuals released or disease (Short, 2009). Whether successful or not, the genetic viability of reintroduced populations is rarely investigated despite widespread recognition of the negative impacts of inbreeding and genetic drift in small populations (but see Jamieson, 2011; Mock et al., 2004; Reynolds et al., 2013; Weiser et al., 2013). To avoid or ameliorate these effects it is important that genetic issues be incorporated early in the design of reintroduction strategies, and also in the post-release monitoring, since they are key aspects of both short-term (e.g. inbreeding depression) and long term (e.g. erosion of genetic diversity) population sustainability. These issues have been highlighted recently, with consideration of the selection of founders, maintaining genetic diversity and monitoring genetic diversity in reintroduced populations included within the IUCN species reintroduction guidelines (IUCN, 2012).

Typically, reintroduced populations are established from small numbers of founder individuals due to the rarity of wild populations and the high costs associated with translocation and captive breeding programs, leading to a founding population of small effective size that may be genetically bottlenecked (Fischer and Lindenmayer, 2000; Jamieson, 2011; Tracy et al., 2011). Further, it is becoming more commonplace to establish conservation sites that physically separate vulnerable species from their threatening processes, such as on predator- or disease-free islands or in fenced enclosures (Abbott, 2000; Hayward and Kerley, 2009), resulting in the isolation of these populations from extant ones. Small, isolated populations such as these are likely to be highly susceptible to the loss of genetic variation through random genetic drift and inbreeding, which can impact on long-term population adaptation and persistence (Brook et al., 2002; Frankham, 2005; Jamieson et al., 2006). In addition, in the shorter term, inbreeding depression resulting in lower survival or fitness of offspring may further reduce demographic population sizes contributing to population decline or failure (Gilpin and Soule, 1986). The rate of inbreeding is likely to be affected by the mating patterns and dispersal behavior of the species, which determines the within-population spatial genetic structure. Low density of founding populations may contribute to non-random mating if animals have low dispersal and mate more frequently with closely-located individuals. Thus, ideally, founding populations should be large and genetically diverse to overcome small population inbreeding effects and to retain longer-term adaptive capacity.

There have been extensive declines in the mammal fauna of Australia since European settlement began in 1788 (Burbidge et al., 2008a), with 94 species currently listed as critically endangered, endangered or vulnerable under Australian legislation (*Environment Protection and Biodiversity Conservation* (*EPBC*) *Act* 1999). Today, several of these species persist only on islands or in remote areas where exotic predators (foxes, cats, rats) or competitors (goats, rabbits) are absent. Barrow Island is a large island (23 400 ha) approximately 70 km off the north-western coast of Western Australia that is free of exotic predators. This important nature reserve supports 13 native mammal species that are extinct or rare on the mainland, including the golden bandicoot (*Isoodon auratus*) that is currently listed as Vulnerable under the *EPBC* Act. Golden bandicoots were once widespread across Australia's arid zones prior to European arrival but have suffered severe declines throughout much of their range as a result of predation by exotic predators and loss of habitat (Burbidge et al., 2008b). In Western Australia, golden bandicoots occur in large numbers (estimated population size of 20 000–50 000) on Barrow Island, with smaller and sparser populations on the mainland and coastal islands of the Kimberley region (McKenzie et al., 2008). The Barrow Island population was used as the source population for translocation of golden bandicoots to three conservation sites: to two nearby islands, Doole and Hermite Island, and to the Australian mainland

within a fenced enclosure at Lorna Glen proposed conservation reserve (DEC, 2010, 2011). The translocations to Hermite Island and Lorna Glen are considered reintroductions as there is sub-fossil evidence of golden bandicoots at these locations in the recent past (Baynes, 2006; Montague, 1914); however, golden bandicoots are not known from Doole Island and this site is considered a conservation introduction. Due to the large size of the Barrow Island population, large numbers of animals (92–165 animals) were able to be sourced and released to each translocation site; greater numbers than are typically used in threatened species reintroduction programs (Fischer and Lindenmayer, 2000; Short, 2009).

This operational scale translocation of golden bandicoots from a large population to two smaller islands and a fenced reintroduction site provides an ideal opportunity to explore the interacting effects of founder population size on maintenance of genetic diversity and long-term persistence in effectively closed populations. We surveyed the genetic diversity of source and reintroduced populations of the golden bandicoot to determine whether a large founder size contributed to the initial success of reintroductions and to predict future patterns of genetic diversity. Specifically our aims were to: (1) compare the genetic diversity of founding and wild-born offspring at each translocation site to assess how diversity was conserved during the establishment phase; (2) determine whether there was any evidence for inbreeding in the established populations, which may lead to a reduction in fitness in the longer term; (3) assess effective population size of source and reintroduced populations and whether there is any evidence of genetic drift amongst populations; and (4) use modeling approaches to determine whether founding numbers were sufficient to maintain genetic diversity over time or whether further intervention (genetic augmentation) is required to maintain genetic diversity in these populations.

2. Material and methods

2.1. Study species and location

Two subspecies of the golden bandicoot *I. auratus* have previously been recognized (McKenzie et al., 2008). *Isoodon a. auratus* is currently restricted to four islands and several mainland sites along the north-west Kimberley coast of Western Australia, and Marchinbar Island in the Northern Territory. The Barrow Island subspecies, *I. a. barrowensis,* was until recently restricted to Barrow and Middle Islands off the Pilbara coast of Western Australia. The two sub-species are differentiated on morphological grounds though there appears to be little genetic support for the division (Westerman and Krajewski, 2000). *Isoodon a. barrowensis* is slightly smaller and has slightly darker fur than the mainland subspecies, and weighs between 250 and 600 g when mature (McKenzie et al., 2008). The species is mainly solitary, although home ranges overlap and may alter by seasons, usually increasing in size in drier seasons (McKenzie et al., 2008). Females give birth throughout the year, with up to five pouch young possible, though typically only one to two young may survive to weaning (J. Dunlop, pers. comm.).

2.2. Translocation history

The Western Australian Department of Parks and Wildlife (DPaW) have successfully established populations of *I. a. barrowensis* at three locations within their former range that are free of exotic predators: Lorna Glen proposed conservation reserve, Hermite Island and Doole Island (Fig. 1). Animals were sourced from the large Barrow Island population (BI, 20°51′ S, 115°24′ E) by trapping several areas on the island over a four week period. Animals were sexed, weighed and measured before being transported to each