

Long-term genetic consequences of mammal reintroductions into an Australian conservation reserve

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ABSTRACT

Reintroduction programs aim to restore self-sustaining populations of threatened species to their historic range. However, demographic restoration may not reflect genetic restoration, which is necessary for the long-term persistence of populations. Four threatened Australian mammals, the greater stick-nest rat (*Leporillus conditor*), greater bilby (*Macrotis lagotis*), burrowing bettong (*Bettongia lesueur*) and western barred bandicoot (*Perameles bougainville*), were reintroduced at Arid Recovery Reserve in northern South Australia over the last 18 years. These reintroductions have been deemed successful based on population growth and persistence, however the genetic consequences of the reintroductions are not known. We generated large single nucleotide polymorphism (SNP) datasets for each species currently at Arid Recovery and compared them to samples collected from founders. We found that average genetic diversity in all populations at the Arid Recovery Reserve are close to, or exceeding, the levels measured in the founders. Increased genetic diversity in two species was achieved by admixing slightly diverged and inbred source populations. Our results suggest that genetic diversity in translocated populations can be improved or maintained over relatively long time frames, even in small conservation reserves, and highlight the power of admixture as a tool for conservation management.

1. Introduction

Reintroduction programs aim to establish self-sustaining populations that do not require significant long-term management. Successful reintroductions generally increase a species' population size and geographic range, and restore ecological function to the area from which it was extirpated (Armstrong et al., 2015). Measuring an increase in population growth and size is most often how these reintroduction programs are judged to have succeeded (Ewen et al., 2012; Moseby et al., 2011). However, the ability of a population to persist in the long-term will also be strongly influenced by levels of genetic diversity (Cochran-Biederman et al., 2015; Weeks et al., 2015).

Reintroduced populations are susceptible to loss of genetic diversity due to founder effects, the isolated nature of reintroduction sites, and small population size (Frankham et al., 2010). These circumstances result in unavoidable inbreeding and genetic drift, leading to reduced fitness through the accumulation of deleterious alleles (genetic load),

and the increased expression of recessive deleterious traits (inbreeding depression). Additionally, loss of genetic diversity will diminish the adaptive capacity of a population and limit its ability to cope with environmental change (Groombridge et al., 2012).

Thus, most reintroduction programs adopt the preservation of genetic diversity as an explicit goal. Several guidelines can be followed to maximise genetic diversity in reintroduced populations, such as using large numbers of genetically diverse individuals as founders and encouraging rapid population growth after establishment (Jamieson and Lacy, 2012). However, it may not always be possible to follow these guidelines and many other interacting factors, such as the life-history traits and demographic history of a species, may affect genetic diversity in cryptic ways. It is therefore important that genetic monitoring is used in all reintroduction programs to evaluate success and guide management actions to maximise the retention of genetic diversity (Schwartz et al., 2007).

Most studies assessing genetic diversity in reintroduction programs

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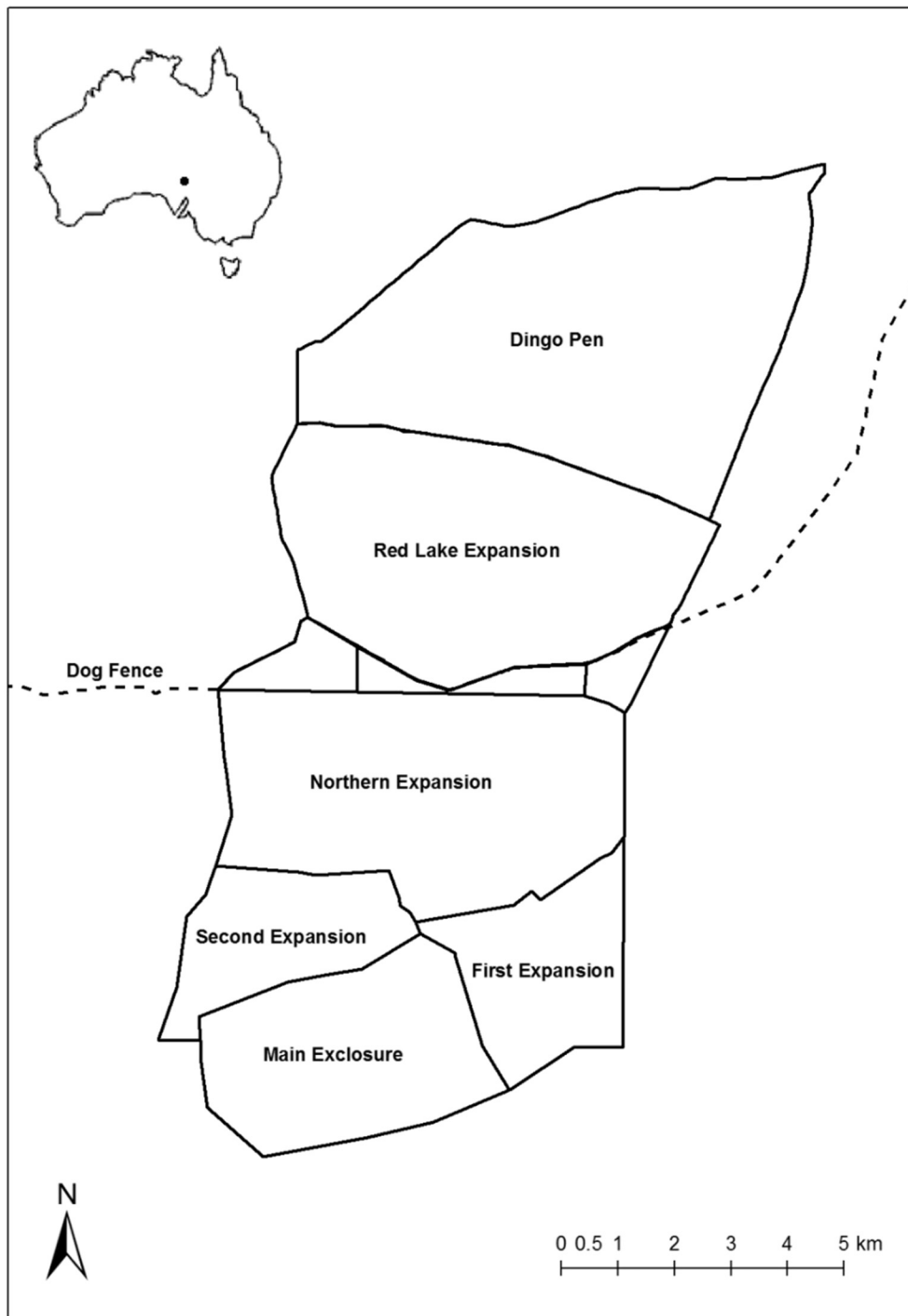


Fig. 1. Location and lay-out of Arid Recovery reserve. Rabbits, cats and foxes have been removed from the four southern paddocks of the Reserve.

have sampled the source and reintroduced populations simultaneously a number of years after release—for example *Gongylomorphus bojerii* (Michaelides et al., 2015) and *Notionmystis cincta* (Brekke et al., 2011)—or sampled just the reintroduced population at multiple time-points—such as *Vulpes velox* (Cullingham and Moehrenschrager, 2013) and *Mustela nigripes* (Cain et al., 2011). In contrast, relatively few studies have explicitly tested changes in genetic diversity from founders to descendants over multiple generations (e.g. Moraes et al., 2017). Such data is crucial for validating and establishing guidelines for maximising genetic diversity in reintroduced populations.

The Arid Recovery Reserve reintroduction program provides a model system in which to compare founder and descendant genetic diversity, as tissue samples were taken from founding individuals at

time of release and stored explicitly for later genetic analysis. The reserve is a 123 km² fenced enclosure situated 20 km north of Roxby Downs in arid South Australia (Fig. 1). A netting fence surrounds the reserve, and all European rabbits (*Oryctolagus cuniculus*), cats (*Felis catus*), and foxes (*Vulpes vulpes*) have been removed from a 60 km² sector at the southern end (Moseby and Read, 2006). Since 1998, this has allowed four species of locally extinct mammals to be reintroduced within the enclosure (Moseby et al., 2011), namely the greater stick-nest rat (GSRN, *Leporillus conditor*), greater bilby (*Macrotis lagotis*), burrowing bettong (*Bettongia lesueur*), and western barred bandicoot (WBB, *Perameles bougainville*). These species were all once widespread across the Australian arid zone, but their geographic ranges have been severely reduced due to competition with grazing stock and rabbits, and

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