Science for Saving Species

Research findings factsheet

Project 4.1.6.3



Genetic rescue of the Victorian eastern barred bandicoot to improve conservation outcomes

In brief

Genetic variation is essential for survival; however, many of Australia's threatened marsupials occur in small, fragmented populations. This can lead to a lack of genetic diversity and other genetic problems. Genetic rescue is potentially a powerful strategy for increasing population fitness and resilience in threatened marsupials.

A captive-breeding program began for the Victorian eastern barred bandicoot (*Perameles gunnii*) in 1988 to prevent extinction of this species on mainland Australia. While the program was successful, the low number of founding animals and ongoing captive breeding resulted in a significant loss of genetic diversity for this species.

To counter this loss of genetic variability, we bred Victorian eastern barred bandicoots with genetically diverse Tasmanian populations of the subspecies Perameles gunnii gunnii at the Mt Rothwell Conservation Reserve in Victoria. The Tasmanian populations were able to successfully cross with the Victorian population to produce three generations of healthy offspring. The offspring developed rapidly and have been released into large fenced areas at Mt Rothwell. The mating led to a significant increase in genetic diversity for

both the first (F1) and second (F2) generational offspring and a reduction in genetic issues such as jaw malformations.

The results have been so promising for the eastern barred bandicoot that we now have the confidence to continue outbreeding across other mainland populations at Phillip Island, Woodlands, Hamilton Conservation Reserve, French Island and Tiverton Sanctuary. Our results show how genetic mixing can benefit threatened species; however, it is essential that it be carefully coupled with habitat restoration and threat mitigation.







Background

Genetic variation is essential for survival; it allows species to adapt and evolve so they can overcome threats and avoid the negative consequences of inbreeding. However, many of Australia's threatened marsupials occur in small, fragmented populations, and inbreeding becomes inevitable. This leads to a decrease in their ability to fight threats - otherwise known as a loss of "population fitness". In large, healthy populations, natural selection weeds out recessive "deleterious alleles", which are gene variants that when expressed can lower an animal's fitness. Deleterious alleles are more frequently expressed when inbreeding occurs, however, meaning small

populations can become poorly adapted to their environment, which can lead to extinction.

Interest is increasing in using genetic translocations as a means of recovering small populations of threatened species. In an ideal genetic rescue, individuals from a healthy large population are introduced into a small recipient population to recover fitness and restore lost genetic variation. This can lead to population growth as well as increasing the potential for adaptive evolutionary changes to altered environmental conditions.

The eastern barred bandicoot (*Perameles gunnii*) was abundant in central and western Victoria before European colonisation but has dramatically declined due to land clearing for agriculture and introduced predators. In 1988, a captive-breeding program was initiated with animals from the last wild mainland population at Hamilton in Victoria to prevent the species' extinction. The program was successful, but genetic analysis highlighted that the low number of founding animals and ongoing captive breeding has resulted in a significant loss of genetic diversity. Physical abnormalities, such as jaw malformations, found in some captive and fenced populations also indicate possible inbreeding effects. These genetic issues are likely to compromise the future viability of the Victorian eastern barred bandicoot.



Research aims

The aims of the research were to determine whether Victorian eastern barred bandicoots could be crossed with Tasmanian eastern barred bandicoots, and whether any negative genetic effects were associated with the crossbreeding. Our long-term goal was to restore lost population fitness and genetic variation to the Victorian eastern barred bandicoot and create healthy populations of bandicoots that could be released into predatorfree areas.

LEFT: Lack of genetic diversity in the Victorian eastern barred bandicoot population had led to genetic issues such as jaw deformities. Image: Andrew Weeks.

What we did

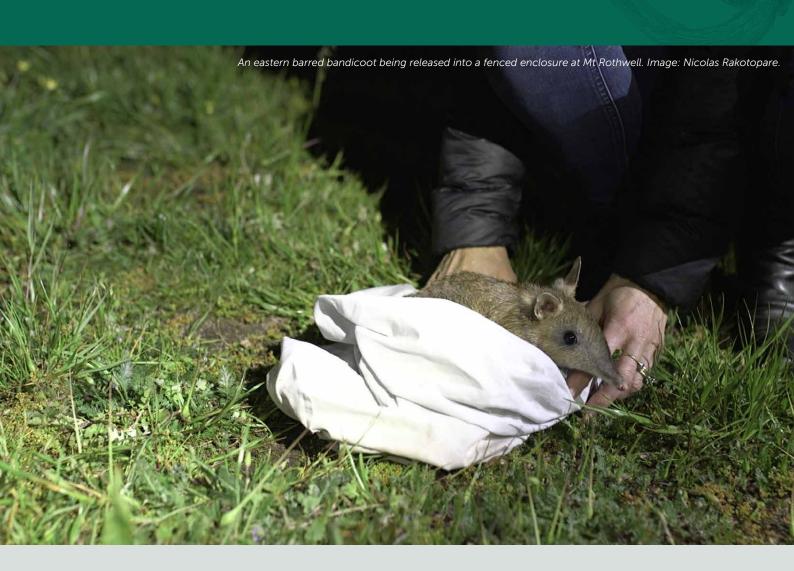
This research was carried out jointly by The University of Melbourne and Mt Rothwell Conservation Reserve. The gene pool–mixing experiments were undertaken at Mt Rothwell Conservation Reserve (Figure 1), a fenced, predator-free ecosystem located 45 km from Melbourne. Victorian eastern barred bandicoots have lived in the sanctuary for many years.

Previous research we had conducted showed that the Tasmanian subspecies *Perameles gunnii gunnii* featured a higher level of genetic diversity than the Victorian species. We therefore chose to conduct cross-breeding experiments between the Victorian and the Tasmanian subspecies. Tasmanian bandicoots were captured from several locations in the south of Tasmania and translocated to Mt Rothwell in 2017. A second cohort of Tasmanian eastern barred bandicoots were sourced in 2018 from the north and north-west of Tasmania. We targeted the north of Tasmania to capture unique genetic diversity found in this area and enable this diversity to be incorporated into the broader gene pool–mixing program.

The cross-breeding experiments between the Tasmanian and Victorian eastern barred bandicoots were conducted in special captive breeding pens at Mt Rothwell Conservation Reserve. We analysed the genetic fitness and genetic diversity of the first- and secondgeneration offspring. Genetic diversity was measured through analysis of genomic DNA from tissue samples, and we genotyped 20 microsatellite loci. Once offspring from the Tasmanian and Victorian crosses had matured (>120 days of age), we released some of the first (F1) and second (F2) generation bandicoots into large field enclosures (4–16 ha) at Mt Rothwell. We wanted to continue to build the population of outcrossed individuals. We regularly measured a range of different traits for each bandicoot in the captive pens and large enclosures, such as weight, tail length and number of pouch young.

We also conducted parallel genomic research, which included sequencing and assembling the entire genome for the eastern barred bandicoot, to compare the evolutionary distance between the Victorian and Tasmanian bandicoots.





Key findings

Our key finding was that the crosses between Tasmanian and Victorian eastern barred bandicoots were viable, and no negative effects of outcrossing for the first (F1), second (F2) and third generations (F3) were detected. We successfully bred 34 healthy eastern barred bandicoots in the captive pens over 2017 and 2018.

The genetic diversity of the bandicoots increased more than 50% in the first (F1) and second generation (F2) populations compared to the current Victorian population. The Tasmanian individuals contributed approximately 36 new alleles across the 20 microsatellite loci. The new Tasmanian individuals translocated to Mt Rothwell in spring 2018 have the potential to contribute another 21 unique alleles, further increasing genetic diversity by approximately 20%. These individuals, collected in the north of Tasmania, should be integrated into the outbreeding program to further enhance the founder size for Tasmanian genes.

We found no evidence of negative effects associated with outbred individuals in the large field enclosures. Importantly, we confirmed through genetic analyses the presence of third generation (F3) outbred individuals in the large enclosures.

Even though the Tasmanian and Victorian populations are likely to have been separated for more than 12,000 years, we found low levels of mitochondrial genetic differentiation between the two populations. These populations do not appear to have diverged to the point where there are any genetic, behavioural or ecological incompatibilities.

Implications and recommendations

This research has demonstrated no negative effects associated with crossing Tasmanian and Victorian eastern barred bandicoots, and provides strong evidence for using gene pool–mixing across all populations of Victorian eastern barred bandicoots.

The outcrossed eastern barred bandicoots could be integrated into current Victorian populations of eastern barred bandicoots to increase their overall adaptive potential and ensure their longerterm persistence. We recommend that the outcrossed individuals are included as founders for the new fenced reserve at Tiverton in western Victoria. We aim to produce a healthy population of at least 1000 individuals for future reintroductions.

We assume that genetic diversity as measured through microsatellites will generally reflect the increase in genetic diversity across the genome. We are currently undertaking different genomic analyses which will provide further clarity on the increases in diversity across the entire genome in the hybrid population.

A large number of other species could potentially benefit from genetic rescue, as many threatened species exist as small, isolated populations lacking genetic variation. Genetic rescue is a tool that could potentially benefit a broad range of other threatened animal and plant populations, especially if it is carefully coupled with habitat restoration. Critically, the threats that caused the population to decline in the first place – predators, competitors, habitat destruction – need to be removed at the same time as the genetic rescue is conducted.

When modifying populations to ensure some sort of rescue outcome, it is critical that other factors be taken into consideration and that the desired outcomes be clearly outlined. The potential for outbreeding depression is an important consideration where genetic mixing is proposed between source populations that are evolutionarily distant.

Genetic rescue in the mountain pygmy possum

The mountain pygmy-possum (Burramys parvus) is a small marsupial restricted to Australian alpine regions, where it hibernates under a cover of snow during winter. It is listed as Endangered under the Environment Protection and Biodiversity Conservation Act 1999, and less than 2000 wild adult individuals are likely to be left. The mountain pygmy possum occurs in three isolated regions in Victoria, and these populations have been isolated for at least 20,000 years. Threats to the possum include habitat destruction from ski resorts,

Mountain pygmy possum. Image: Flickr, CC Aust Alps effects of climate change on snow cover, competition with introduced species and predation by invasive predators, such as foxes and cats.

The Mt Buller population of the mountain pygmy-possum had undergone a rapid decline in genetic diversity. As the population was predicted to become extinct, a recovery program was implemented that involved habitat restoration, predator control, environmental protection and translocations. Wild-to-wild translocations were undertaken to boost the genetic diversity of the Mt Buller population. Six genetically healthy males from Mt Higginbotham were translocated to Mount Buller in 2010. This translocation occurred very late in the breeding season and while a successful hybrid was produced, the translocation was ultimately not successful; and another

translocation of six males from Mt Higginbotham was undertaken in 2011 at the start of the breeding season. This was followed by a further translocation of six males from Timms Spur early in the 2014 breeding season. Thirteen captivebred animals were also released into the Mt Buller population in 2013. We carried out genomic DNA analysis of tissue and hair samples from animals trapped from 2010 to 2017 to investigate the longerterm outcomes of this genetic rescue on animal fitness.

The possums from the two regions were able to interbreed, and produced viable offspring which had a higher genetic diversity than the original populations. The offspring were estimated to be at least twice as fit as their Mt Buller counterparts, and this advantage persisted through to the next generation. The hybrid animals had

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Genetic rescue in the mountain pygmy possum (continued)

a larger body size, and the female hybrids have produced more pouch young and lived longer than the Mt Buller population.

While environmental improvements may have influenced a small initial increase in population

size at Mt Buller, the rapid increase in population is most likely to have happened because of genetic improvements (Figure 1). This is based on the direct fitness estimates that we have made in the population and is also supported by the fact that similar environmental improvement programs for mountain pygmy-possums in another region have not resulted in large population increases.

There appear to be clear benefits associated with the introduction of genetic material from the Mt Higginbotham mountain pygmypossum population into the Mt Buller population. Our findings point to genetic rescue being a potentially useful option for the recovery of small, threatened populations of marsupials.

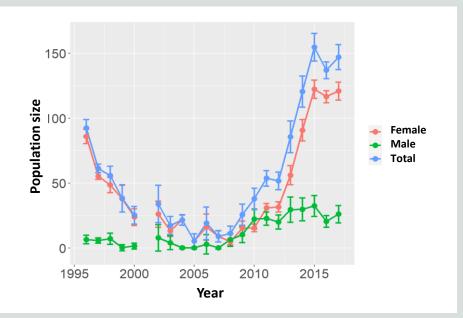


Figure 1. Mountain pygmy possum adult population size estimates based on modelling from capture–recapture data of the Mount Buller population. The blue line represents the total population size estimate while red and green lines represent female and male population size estimates, respectively. Error bars are standard error.

Citations

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Further Information

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