The role of wildlife rehabilitation in ameliorating the loss of genetic diversity in isolated inbred populations

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Abstract

Many small isolated population fragments of wildlife species are suffering from inbreeding and loss of genetic diversity and have elevated extinction risks. These can often be genetically rescued by outcrossing to another population within the species, especially if the two populations are adapted to similar environments and have the same chromosome numbers and structures. However, there have been only ~ 30 genetic rescue attempts worldwide, yet about 1.4 million populations of threatened species would likely benefit from them. Rehabilitated wildlife represent an important, underutilised source of animals for outcrossing to genetically rescue isolated inbred population fragments with low genetic diversity. Such use of rehabilitated wildlife is likely to result in a higher survival and reproductive success of rescued wildlife as they will typically experience lower population densities and less-competitive inbred residents, than when returned to the density saturated habitats they often derive from.

Keywords: conservation, genetic rescue, heterosis, hybrid vigour, inbreeding, island populations, loss of genetic diversity, outbreeding depression, rehabilitated wildlife, threatened species

Introduction

Very large numbers of rehabilitated wildlife are returned to the wild each year in Australia, as a result of the efforts of dedicated wildlife rescuers, often with support from veterinarians. From statistics published in 2000, around 11,500 rehabilitated wildlife were being re-released per year in New South Wales in the 1990s, and ~3,300 in Victoria, and the numbers may be higher now [1].

Rehabilitated wildlife are typically returned to sites very near to where they were collected [2]. This often means that they have to re-establish in density saturated sites where they face stiff competition from highly fit residents to establish and breed. Is this always the most effective use of these animals? In 2008, Derek Spielman [2] came up with the novel suggestion that rehabilitated wildlife be used to genetically rescue isolated, inbred populations. Thus, rehabilitated wildlife would, where appropriate, be returned to another site where there was an isolated wildlife population of the same species that was suffering from loss of genetic diversity and inbreeding, meaning it had low reproductive fitness, compromised ability to evolve, and elevated extinction risk.

In this presentation, I will re-evaluate Derek Spielman's proposal in the light of evidence that has accumulated in the last 10 years. The issues I will address are:

- How serious are problems due to inbreeding and loss of genetic diversity in isolated populations?
- What are the risks and benefits of crossing populations?

- From where can donor animals be sourced for genetic rescues?
- What are the benefits and costs of using rehabilitated wildlife for genetic rescues?
- How can genetic rescues be implemented?

In brief, recent evidence has greatly strengthened the case for using rehabilitated wildlife for genetic rescue purposes, where isolated fragmented populations suffering genetic problems exist. Rehabilitated wildlife also provide useful animals for re-founding of extinct populations, provided the original cause of the extinction has been addresses, but that issue is not discussed further in this contribution.

How serious are problems due to inbreeding and loss of genetic diversity in small isolated populations?

Inbreeding, the production of offspring from parents related by descent, has been known since Darwin’s work in the 1870s to have overwhelmingly harmful effects on all aspects of reproduction and survival (reproductive fitness) [3]. This is referred to as inbreeding depression. However, it is only in the last 20 years that the full impact of this across the whole life cycle has become clear [4]. The effects of a brother-sister mating have devastating impacts, reducing lifetime reproductive output of the progeny by 55-99% across red deer, collared flycatcher, great tits and song sparrows, and similar harmful effects are expected in other outbreeding species [4]. Given sufficient inbreeding, the extinction risk is increased [4].

For most outbreeding wildlife species, inbreeding occurs more slowly due to finite size, accumulating over generations in genetically isolated populations [4, 5]. However, this inbreeding is also harmful, but somewhat less than for the same cumulative inbreeding due to faster inbreeding [4, 5]. In closed populations, inbreeding increases at a rate inversely dependent on the genetically effective size ($1/[2N_e]$. Thus, in a closed population with an effective population size of 25 (a size typical of many endangered species), inbreeding increases by 2% per generation initially, and after 14 generations the inbreeding coefficient is the same as in the progeny of a brother-sister mating (25%). All genetic effects of small populations (inbreeding, loss of genetic diversity and genetic drift) depend on the genetically effective population size and this is typically much less than the census size, averaging only about 13% of it [4]. Thus a population with 100 potentially breeding adult has, on average a genetically effective population size of only 13.

The second harmful effect occurring in small closed populations is loss of genetic diversity, and a consequent reduce ability to evolve, especially in response to new threats such as new or changed diseases, global environmental change, pollution, or introduced predators or competitors [5]. For example, some populations of the northern quoll have evolved tolerance to toxic cane toads, but many populations have not [6, 7]. Further, some amphibian species have evolved resistance to the chytrid fungus that has devastated amphibians across the planet [8]. In approximately random mating species, including most wildlife, the proportionate loss of genetic diversity is closely related to the increase in inbreeding [4, 5].

How many isolated, inbred population fragments with low genetic diversity are there? For threatened species there are ~ 1.4 million population fragments that would likely benefit from genetic rescue attempts, and if we include non-threatened species the number climbs to ~ 150 million population fragments with genetic problems [4].

What are the risks and benefits of outcrossing populations?
Populations that are inbred and have low genetic diversity can have these effects reversed by outcrossing to another population of the same species [4] – this is also referred to as augmenting gene flow. The effects on reproductive fitness are usually beneficial (genetic rescue), but in a minority of cases they can be harmful (outbreeding depression). Fortunately, the risk of outbreeding depression is predictable [4, 9]. Population that are adapted to similar environments, have the same chromosome numbers and structures (karyotypes), and have been isolated for 500 years or less have a low risk of outbreeding depression [4, 9]. Conversely, populations that are different species, and/or adapted to different environments for many generations, and/or have fixed chromosomal difference have an elevated risk of outbreeding depression when crossed [4, 9]. For example, crossing of horses and donkeys results in sterile mules: horses and donkeys are separate species, they have many fixed chromosomal differences, were adapted to different continents, and have been isolated for ~ 2 million years [4].

For outcrosses of inbred populations to another population of the same species where the risk of outbreeding depression is low, 93% of the crossed populations have increased fitness (with almost all exceptions have low statistical power) and the median benefits are very large, based on a meta-analysis involving analyses on 156 data sets [10]. For outbreeding species (most rescued wildlife), the median benefit was 162% in wild/stressful conditions (i.e. the crosses have lifetime reproductive output ~ 2.6 times that of the inbred parent populations), and 51% in benign/captive ones, Further, most of the benefits persisted over subsequent generations, but this depends on the populations not becoming so small that they suffer new inbreeding [11].

Crossing of populations is widely used in agriculture and horticulture due to the benefits it confers – where it is typically referred to as hybrid vigour or heterosis. For example, crosses of inbred maize populations have grain yields that average about 190% greater than the inbred parents. Most of the commercial chicken and pig meat and some of the beef that we eat comes from population or breed crosses, as do the eggs [4]. Further, there are synthetic breeds of domestic livestock, such as Santa Gertrudis, Brangus and Australian milking zebus that derive from sub-species crosses, while crop and horticultural plants such as bananas, citrus, apples and roses are derived from pools of multiple species.

From where can donor animals be sourced for genetic rescues?
Up to this point, donor animals for genetic rescues in wildlife have to be captured from other populations and have their disease status checked, with the attendant financial costs, and the need for permits. By contrast, the use of rehabilitated animals for genetic rescues means that the costs of capture are avoided, and veterinary checks have often already been done, and it may be easier to obtain the required permits.

Most of the reintroduced rehabilitated wildlife are from non-threatened species [1], so only a few individuals will be available for genetic rescue of isolated population of threatened species. However, there are many more isolated fragmented populations of non-threatened species that would benefit from genetic rescue attempts [4], and very limited financial resources available for their conservation.

What are the benefits and costs of using rehabilitated animals for genetic rescues?
The following are the benefits and costs associated with using rehabilitated animals for genetic rescue purposes:
Benefits:

- Capture costs are eliminated
- The rehabilitated animals are more likely to survive and reproduce when re-introduced into wild habitats
- More isolated populations of wildlife will persist, resulting in lower extinction rates for species
- Isolated populations of non-threatened species (where there are very limited resources for conservation) can be saved, thus lowering the risk of species transitioning to a threatened status.

Costs:

- Risk of outbreeding depression: these largely predictable and avoidable
- Bureaucratic impediments – the protocols and regulations will often need to be revised
- Transport costs may be greater, as release may be at a greater distance from the rehabilitation centre
- Efforts are needed to identify populations requiring genetic augmentation. However, zoos and government conservation agencies (e.g. Office of Environment and Heritage in NSW) may already know of suitable populations. For example, populations enclosed by wildlife fencing, as for example conservation reserves in South Africa, and those in Australia used to isolate native wildlife from cats and foxes will need regular augmentation as population of species within them are small [12, 13].

In many circumstances the benefits will clearly outweigh the costs, resulting in a win-win situation.

How can genetic rescues be implemented?
Our book on *Genetic Management of Fragmented Animal and Plant Populations* provides details of how to implement genetic rescues, and we are currently writing a short, simpler *A Practical Guide to Genetic Management of Fragmented Animal and Plant* Populations that should be published in 2019. I emphasise that genetic issues must be considered in the context of other issues affecting the populations, as envisaged in the One Plan Approach [14]. You may be able to obtain assistance from zoos, government wildlife agencies and NGOs (e.g. WWF, Bush Heritage Australia, and Australian Wildlife Conservancy) who often have reintroduction programs and expertise in the area, and such consultation is recommended.

Discussion
There are currently bureaucratic impediments to genetic rescues, but the number of genetic rescues is increasing rapidly from a low base, and the attitude of scientists have changed markedly in recent years (especially since 2011 & 2015). The scientific impediments have been greatly reduced, and we are promoting a **paradigm shift** [4, 15]. “The times they are a changing!”

So what species would be candidates for genetic rescue? In general, this applies to any species with isolated inbred populations with low genetic diversity. From genetic data, we estimated that 29% of vertebrate species have genetically isolated populations [4]. In Australia, there are isolated island populations of many species of marsupials, rodents, reptiles, amphibians and birds, including euros, koalas, rock wallabies, native rodents, Capricorn silvereyes and Lord Howe Island golden whistler, and these typically have low genetic diversity and are inbred, and would often benefit genetically from genetic rescue attempts [16-18]. There are also isolated inbred populations on the mainland. For example, the mainland South Australian population of koalas derives from the French Island population that was founded with only 2-3 individuals and it has been through subsequent population bottlenecks, and has low genetic diversity and an elevated level of inherited disease (testicular aplasia) [5]. It would almost certainly benefit from gene flow from koalas, especially ones from non-bottlenecked populations in eastern Victoria.

Conclusions

- Many small isolated population fragments are suffering from inbreeding and loss of genetic diversity and have elevated extinction risks
- These can often be genetically rescued by outcrossing.
- Rehabilitated wildlife represent an important, underutilised source of animals for outcrossing
- Such use of rehabilitated wildlife is likely to result in a higher survival and reproductive success of rescued wildlife as they will typically experience lower population densities and less competitive inbred residents, than returning them to the density saturated habitats they often come from.

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