

NEWS AND VIEWS

PERSPECTIVE

Evolutionary, behavioural and molecular ecology must meet to achieve long-term conservation goals

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Founder populations in reintroduction programmes can experience a genetic bottleneck simply because of their small size. The influence of reproductive skew brought on by polygynous or polyandrous mating systems in these populations can exacerbate already difficult conservation genetic problems, such as inbreeding depression and loss of adaptive potential. Without an understanding of reproductive skew in a target species, and the effect it can have on genetic diversity retained over generations, long-term conservation goals will be compromised. In this issue of *Molecular Ecology*, Miller *et al.* (2009a) test how founder group size and variance in male reproductive success influence the maintenance of genetic diversity following reintroduction on a long-term scale. They evaluated genetic diversity in two wild populations of the iconic New Zealand tuatara (Fig. 1), which differ greatly in population size and genetic diversity, and compared this to genetic diversity in multiple founder populations sourced from both populations. Population viability analysis on the maintenance of genetic diversity over 400 years (10 generations) demonstrated that while the loss of heterozygosity was low when compared with both source populations (1–14%), the greater the male reproductive skew, the greater the predicted losses of genetic diversity. Importantly however, the loss of genetic diversity was ameliorated after population size exceeded 250 animals, regardless of the level of reproductive skew. This study demonstrates that highly informed conservation decisions could be made when you build on a solid foundation of demographic, natural history and behavioural ecology data. These data, when informed by modern population and genetic analysis, mean that fundamental applied conservation questions (how many animals should make up a founder population?) can be answered accurately and with an eye to the long-term consequences of management decisions.

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Fig. 1 Large adult male tuatara attacking a smaller male. Photo by Jeanine Refsnider.

In the late 1990s, fervent attempts were made to forge a collaborative link between the disparate disciplines of behaviour and conservation that would inform conservation planning and application. That effort, which included many of the World's top conservation and behavioural scientists, resulted in multiple edited books and review articles (see Angeloni *et al.* 2008), but the calls for a link between the disciplines has not resulted in increased collaboration or cross-fertilization (Caro 2007; Angeloni *et al.* 2008). In a recent review paper, Caro (2007) outlined a specific set of guidelines for how behavioural information could be more fruitfully employed to produce better conservation outcomes. He focused his guidelines rightly on descriptive and species-specific behavioural studies, as they have the most to offer on-the-ground conservation biologists. He painted a more cynical view for the contribution to conservation of behavioural ecology, which has always had a more evolutionary and theoretical focus. A stated goal of virtually every species-specific and broad-scale conservation programme is the preservation of evolutionary potential (Moritz 2002). If this goal is anything other than lip service, then is taking an evolutionary view really a luxury in conservation biology or is it a necessity?

Reproductive skew is a well-known aspect of mating system biology whereby some members of a population enjoy greater reproductive success than others, and many produce no offspring. The most common example is in mating systems where only a small proportion of adult males obtain most of the paternities, leaving many males out of the gene pool and thus reducing effective population size. Based largely on the revelations provided by direct paternity testing through molecular techniques, we now understand that reproductive skew is not the exception but the norm across many animals and plants. This fundamental

aspect of the natural history of species is of direct conservation interest because of the obvious influence on the long-term potential of founder populations; indeed this realization was one of the early drivers for a link between the disciplines (Caro 1999). None-the-less, from a broad perspective, comparatively few species-specific conservation programmes have detailed information on mating systems and reproductive skew. This can ultimately compromise long-term goals.

Tuatara, *Sphenodon punctatus*, are an iconic but endangered component of the New Zealand fauna and they also are of special evolutionary interest because they are the last remnants of the ancient Rhynchocephalian (Sphenodontine) radiation of reptiles, the sister clade to all lizards and snakes. Erased over the past century from mainland New Zealand by feral animals and habitat destruction, they now survive on approximately 30 offshore islands. There are two aspects of tuatara natural history that make them a special problem for conservationists that take a long-term view. First, they grow extremely slow, do not reach sexual maturity until they are ~14 years old, they may live to be over 100 years and females usually reproduce only every 4 years. Second, they have a polygynous mating system between years with extreme reproductive skew because reproduction is dominated by large males – as few as 30% of adult males obtain paternities (Moore *et al.* 2008b). Female mate choice also is influenced by disassortative mating based on MHC genotype (Miller *et al.* 2009b). These are natural history attributes that can have genetic consequences that must be considered in conservation planning.

Miller *et al.* (2009a) quantified the levels of genetic variation in two wild populations of tuatara. Stephens Island, only 150 ha in size, is home to 30 000–50 000 tuatara while North Brother Island, 4 ha, is home to approximately 350 adult tuatara. Both have been used as source populations for five reintroduction programmes, and three well-monitored reintroduced populations were included in this study. As predicted, Miller *et al.* (2009a) demonstrate that Stephens Island has much higher expected heterozygosity per locus (mean = 0.782) than North Brother Island (mean = 0.406) and also much higher allelic diversity (14.4 vs. 2.3). What does this mean for the maintenance of genetic diversity in reintroduced populations sourced from these two islands, given variation in reproductive skew levels and founder population size? To find out, Miller *et al.* (2009a) ran 10 models of a reintroduction of each founder group, from both low and high diversity source populations and under high and low densities, to examine the effects of male reproductive skew, and they modelled four different founder group sizes of translocations from both islands – all over 10 generations (about 400 years for tuatara). Their results show that larger founder populations are much better at retaining genetic diversity over 10 generations. Their results also demonstrate that male reproductive skew has a profound detrimental influence on genetic diversity over 10 generations, particularly when skew is high and founder population

size is small. However, the influence of male reproductive skew on loss of genetic diversity was minimal after population size reached approximately 250 animals. By modelling multiple scenarios, it is possible to evaluate the effects of source population choice, mating systems, and founder number on long-term outcomes. Ultimately, this approach will allow managers to design founder groups that will meet long-term management goals.

Almost by definition, founder populations in the vast majority of reintroduction programs are small for a very practical reason, and this, of course, also means that a comprehensive understanding of a target species mating system also may be very difficult to obtain. But when it is possible to include information on the mating system in a species of conservation concern, the study by Miller *et al.* (2009a) demonstrates how conservation and population genetic data and analytical techniques, when informed by a detailed understanding of the behavioural ecology of a target species, can provide real-world answers to real-world conservation problems. Will this always be possible? No. But when that opportunity is available, it must be taken to ensure long-term conservation goals. New Zealand scientists are leading by example (Moore *et al.* 2008a).

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