

# The ecological and genetic risks of wildlife translocation

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Wildlife translocations have a low rate of success due to many factors including dispersal away from release site and low-quality habitat at release site. Additionally, some translocations are conducted without sufficient knowledge of the species, resulting in avoidable failure. On the other hand, some wildlife movements are not carried out due to perceived risks; risks without empirical data to assess those concerns. Translocations are used to both establish new populations and also to augment small, existing populations vulnerable to stochastic events such as bushfire or disease. It is important to know what effect this movement will have on resident species at the recipient site to ensure that efforts to conserve one species do not detrimentally impact others in the local area. My study is one of the first pre-emptive studies to quantify potential areas of risk so that should risk be detected, it can be mitigated. There is very little literature on this topic and this study is one of the first studies specifically planned, using an endangered species, to assess the genetic risks of translocation prior to management actions being taken. Here, I conducted an experimental translocation in enclosures built around an existing wild pygmy bluetongue population. I moved 24 individuals from two genetically distinct populations at the edges of the current species range and mixed them with a third recipient population. Through monthly monitoring over three consecutive activity seasons I was able to accurately, and repeatedly, assess the ecological and genetic risks associated with mixing source populations during population augmentation on both resident pygmy bluetongues and other lizards. I found that augmenting pygmy bluetongue populations does not negatively effect on the abundance and body condition of co-occurring lizard species in the recipient ecosystem.

Using polymorphic microsatellite loci, I genotyped each pygmy bluetongue and conducted parentage analysis to identify lineages of offspring according to the source population of the parents. I then used three fitness-related traits to compare those lineages in terms of growth (growth rate & body condition) and performance (bite force) to assess whether mixed lineages grew or performed differently to unmixed lineages. I found that genetically distinct populations do interbreed and do not discriminate based on source population which is a key finding if population augmentation is to be a conservation strategy for this species. Mixed-lineage offspring have similar levels of growth and performance to unmixed offspring suggesting that mixed-lineage offspring are unlikely to outcompete unmixed lineages for resource such as burrows or prey. I have also found that body condition plays an integral part in the reproductive success of female lizards which highlights the importance of supplementary feeding to support population establishment and growth.

The results of this study aimed to inform a broader question of whether mixed-lineage source populations would fare better at a new site in terms of population growth although it yet needs to be established whether mixed lineage individuals can reproduce successfully. Establishment of new populations, and successful reproduction at a new site, without detrimentally affecting co-occurring species are both fundamental to the success of a translocation and the present study provides empirical data on both areas. The results of this study will be integral to conservation of species existing in small isolated populations and increase the success rate of subsequent movements.