1. Introduction

Globally, species and ecosystems continue to decline, and the impact on threatened species is increasing. The ongoing loss of intraspecific genetic diversity is contributing to the erosion of species’ adaptive potential and can hasten population declines, especially in the face of increasing ecological and anthropogenic disturbance [1]. The field of conservation genetics offers a range of techniques and statistical approaches that enable us to describe and monitor various aspects of genetic diversity and make inferences about the underlying ecological and evolutionary processes driving these patterns, in turn, informing approaches to conservation management [2–4]. In addition, given the strong empirical support for the relationship between small population size, reduced genetic diversity and reduced population fitness [5], it is clear that ongoing monitoring of the genetic diversity in threatened species is going to be crucial for sustaining species’ health into the future. Research in this field has progressed enormously in recent years, alongside growing knowledge on the application of genetics in conservation and interest from managers in incorporating the management of genetic diversity into conservation programs.

There are many areas of conservation where genetic data can provide direct information to guide management actions for threatened species. In this Special Issue, we highlight conservation genetic studies that demonstrate applied outcomes that inform practical threatened species management. These studies present a diversity of research approaches, both in genetic methodology (microsatellites, chloroplast and mitochondrial DNA sequencing, single nucleotide polymorphisms) and in combination with complementary statistical approaches, taken from allied disciplines (e.g., population viability analysis, climate niche modelling), with application to specific questions relating to on-the-ground species management.

1.1. Identification of Conservation Units

Fundamentally, species are the primary units of conservation and delineation of species and subspecies boundaries, and the identification of management units within species, is important to ensure appropriate conservation listings are in place and that conservation actions are properly targeted. This is highlighted in a study of *Banksia nivea*, where Sampson and Byrne [6] found that genetic relationships among subspecies were consistent with the existing taxonomy for two subspecies (one common, one endangered), but not for a third (previously considered rare), indicating further taxonomic assessment is required for *B. nivea* subsp. Morangup. Phylogenetic analyses revealed evidence for a more recent divergence of the localised subspecies, associated with expansion from the dryer sandy soils inhabited by the widespread subspecies into the winter-wet ironstone soils in the southwest of Western Australia, consistent with progressive long-term climatic drying.

Understanding species delimitation is also critical to identifying hybridisation and putative taxa of hybrid origin, with a view to assessing their conservation value. A study by van Dijik et al. [7] investigated the status of a conservation-listed tree that is restricted to the
Fleurieu Peninsula and Kangaroo Island of South Australia and suspected to be of hybrid origin. Genetic analysis of *Eucalyptus paludicola* and its putative parental species identified two genetically distinct clusters, comprising *E. ovata* and *E. cosmophylla*, while *E. paludicola* individuals were admixed between these two species, consistent with a hybrid origin. Given hybrid class assignment tests indicate that the majority of *E. paludicola* individuals are F1 hybrids with a low incidence of backcrossing, these data support the hypothesis that *E. paludicola* is a transient hybrid entity rather than a distinct hybrid species. As such, the authors find little support for the ongoing conservation listing of *E. paludicola* or, indeed, recognition as a distinct species.

1.2. Evaluating Population Structure and Genetic Diversity to Inform Management Approaches

Dispersal is important for maintaining genetic connectivity amongst populations and, consequently, understanding patterns of gene flow and genetic differentiation is critical if managers are to use admixture to maximise diversity and adaptive potential in reintroductions and restoration projects. This is explored by Amor et al. [8], who used a genetic analysis to investigate the genetic relationship among disjunct groups of remnant populations of *Sclerolaena napiformis*, a perennial chenopod endemic to southeast Australia. They found genetic differentiation among the three regions, with low genetic diversity within populations and high levels of inbreeding. A decline in abundance through habitat fragmentation is compounded by climate modelling that predicts a reduction in suitable habitat for the species, under even the most conservative climate change scenario. The study shows the benefits of applying the knowledge of genetic diversity in restoration and recommended an admixed provenance approach to souring of seed for restoration, both within and across regions, to maximise genetic diversity and maintain dynamic evolutionary processes driven by individual plant fitness in response to the novel environmental conditions.

Assessment of gene flow and genetic diversity amongst remnant populations can assist in focusing conservation attention to those most in need. Thavornkanlapachai et al. [9] provided an example of this in an investigation into the genetic relationships amongst a complex of closely related bandicoot species (genus *Isoodon*), which are variously threatened by ongoing habitat loss and predation by introduced predators. Analysis of mtDNA identified three major clades that largely resolved existing taxa, although, with a pattern of ‘intermediate polyphyly’ [10] observed between South Australian (SA) and Western Australian (WA) populations. This highlighted ancestral connections between these groups that were resolved as distinct entities in analyses with nuclear markers. SA and Victorian populations of *Isoodon* bandicoots were identified as suffering genetic erosion, emphasising the prioritisation of these populations for specific conservation efforts to reduce further loss of genetic diversity.

1.3. Managing Genetic Diversity in Translocations

Genetic analysis provides a basis to guide translocations and inform options for undertaking genetic rescue. White et al. [11] demonstrated how genetic data can be used in an investigation into the genetic effects of past translocations in a once widespread mammal species that is now restricted to islands and fenced enclosures in Australia, to inform future translocations of the species. Genetic analysis of the banded hare-wallaby (*Lagostrophus fasciatus*) showed serial translocation from a single source population has led to a loss of genetic diversity in a translocated fenced reserve, whilst inbreeding is of concern in the translocated island population. Population viability analysis and gene retention modelling indicated founder population sizes of ~100 individuals and mixing of two source populations were optimal to maximise demographic resilience and genetic richness in a planned translocation to facilitate persistence in the face of various stochastic environmental events.
1.4. Implementing Genetic Rescue to Manage Inbreeding

The introduction of new genetic diversity into an inbred population to assist in genetic rescue must be balanced against the risk of ‘genetic swamping’, leading to the loss or disruption of local adaptive genotypes. Zilko et al. [12] combined genetic data with population viability analysis to guide genetic rescue in the inbred lowland population of Leadbeater’s possum (*Gymnobelideus leadbeateri*), a threatened species in the forest of south-eastern Australia, whilst balancing the maintenance of local adaptation. Translocated animals were sourced from the outbred and genetically diverse highland population and this resulted in higher retention of local alleles in the supplemented lowland population due to the reduction in genetic drift. Nevertheless, carrying capacity in the lowland population is currently insufficient to enable population recovery. Consequently, the authors recommended the establishment of a new population of lowland possums, in a high-quality habitat, and gene exchange with highland populations, to alleviate inbreeding depression and maximise the retention of locally unique neutral genetic variation.

1.5. Managing Genetic Diversity in Captive Breeding Populations

Captive breeding populations can be important sources of diversity to support reintroduction efforts for threatened animals, although ongoing assessment is required to ensure diversity is captured in the founding populations and breeding is managed to maximise retention of diversity. In a study of the captive Mesoamerican scarlet macaw (*Ara macao cyanoptera*) population at Xcaret Park, Escalante-Pliego et al. [13] revealed that founding and current breeders showed high retention of genetic diversity, low inbreeding and low relatedness, and that the captive population has a similar level of genetic diversity to the wild population in the Mayan Forest. As a consequence, the captive breeding population at Xcaret is an important source of birds for the reintroduction program of this subspecies.

1.6. Genetic Approaches to Managing Wildlife Disease

Managing in-situ populations exposed to disease threats, based on genetic principles, is an integral component of recovery programs for highly vulnerable species. Glassock et al. [14] reviewed the underlying principles of genetic management and highlighted how managing gene flow, diversity and inbreeding assists in reducing the extinction risk of Tasmanian devil (*Sarcophilus harrisii*) populations, threatened by the deadly devil facial tumour disease. This disease poses a significant risk to the persistence of the species. The supplementation of populations establishes gene flow and genetic analysis and can inform how best to increase adaptive potential, whilst minimising any potential for outbreeding depression or loss of local adaptation. This review provides timely discussion on the issues faced by conservation managers for managing emerging diseases in threatened species, where disease eradication is not possible.

Similarly, Palmas et al. [15] used genetic analyses to investigate whether there was an underlying genetic cause of a reported record of pug-headedness in a critically endangered population of native Mediterranean trout (*Salmo trutta*) from Sardinia, Italy. The genetic analysis suggested that inbreeding or outbreeding depression are not contributing factors in the instance of the deformity in this population, and variation in environmental factors during larval development seemed the most likely factors influencing the deformity.

2. Conclusions

These studies are just a few examples of the ways in which genetic analysis can inform effective conservation actions for the management of threatened species. Importantly, in these exemplar papers, authors provide explicit recommendations to enable positive impact on the management of their species of interest. We hope that conservation managers not so familiar with genetic tools and techniques find value in the studies provided here, in demonstrating the link between the conservation questions of interest, analytical approaches and the ensuing conservation management outcomes. Further information and
exploration of the application of genetics and genomics for the conservation of threatened species is available in the book Conservation and the Genomics of Populations [16].

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