

The Application of Genetics in Balancing the Conservation and Utilisation of Biodiversity in Multi-Use Environments

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Biodiversity conservation and in changing environments

Environmental change is a significant challenge worldwide for biodiversity conservation and poses serious consequences for the management of plant communities. At the same time, our well-being depends on making use of diverse ecosystems and the plants within them so management plans must recognise the pressures imposed by multiple users and promote sustainable use of natural resources.

Habitat fragmentation and climate change are the two global drivers of current biodiversity loss and ecosystem change (Breed et al. 2013). To ensure that plant communities and species have the ability to respond to change, it is essential to maintain a balance between the ecological and genetic requirements of species and the modification of natural systems due to human use. We aim to mitigate the detrimental effects of human activity on natural ecosystems while acknowledging that environmental change has been a constant evolutionary force (Moritz 2002). Understanding the patterns of genetic diversity within species and across landscapes can assist in establishing conservation policy (Laity et al. 2015), prioritising conservation targets (Moritz & Potter 2013) and developing practices for sustainable use (Dickson & Cooney 2005).

Most plant species are unlikely to have the capacity to track climate changes by adjusting their geographic range because of dispersal limitations (Cunze et al. 2013). A mismatch between the rate of contemporary climate change and habitat loss, and the capacity of species to respond (Cunze et al. 2013; Jump & Peñuelas 2005), may precipitate a loss of biodiversity and a demise in ecosystem properties and processes (Malcolm et al. 2002). Human-assisted migration (Ste-Marie et al. 2011) and restoration based on matching genetics to predicted climates (Weeks et al. 2011) have been suggested as potential tools to maintain population and species viability.

The Australian flora

The Australian flora, estimated at more than 20,000 angiosperm species, is large, diverse and highly endemic. It is also considered very vulnerable to climate change (Preston & Jones 2006). A dramatic increase in environmental stressors is anticipated in coming decades (Dunlop et al. 2012). It is predicted that a majority of the Australian land mass, including south-eastern Australia, will experience climatic changes that result in significant environmental stress for organisms that are adapted to current conditions (Dunlop et al. 2012). Annual mean temperature anomalies in Australia since 1910 show a change from colder to warmer anomalies with the moving ten year average becoming positive from 1980 (Fig. 1). Based on the projections of the Australian Bureau of Meteorology, using data from 1970 onwards, most regions are expected to receive less rainfall (Fig. 2) and experience higher temperatures (Fig. 3).

Worldwide, there is an increased likelihood of extinction for many taxa (Groom et al. 2006). In Australia, 1265 plant species are considered to be critically endangered, endangered or vulnerable and 39 species have become extinct in recent decades (<http://www.environment.gov.au/>, accessed 14-9-2015). Many extant Australian plant species are likely to have experienced and responded to past climate change. However, the timescale has changed and the majority of Australian landscapes in which they exist have undergone the most dramatic changes in the last 200 years (Nix 1981). Farming, forestry and urbanisation have caused rapid and extensive human-mediated modification to vegetation systems and loss of habitat for many species. The disjunct distributions of many species most likely indicate that previously suitable habitat has been lost rather than long-distance dispersal and exploitation of new habitat. As many Australian species are restricted in distribution, regional extinction is likely to mean global extinc-

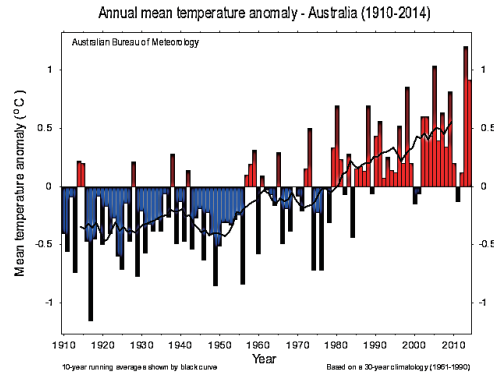


Fig. 1 Temperature anomalies across Australia based on 10 year moving average from 1910 (image from www.bom.gov.au).

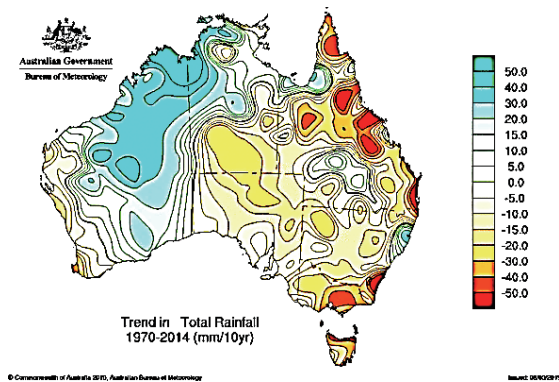


Fig. 2 Reduced rainfall over most of Australia since 1970 (image from www.bom.gov.au).

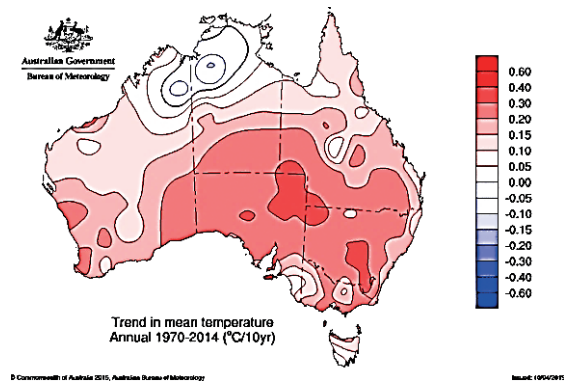


Fig. 3 Increased temperatures over most of Australia since 1970 (image from www.bom.gov.au).

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Using genetic information for conservation

Conservation genetics uses the principles of population genetics and conservation biology to enhance the long-term viability of species and ecological systems. Conservation strategies must offset threats to species persistence to maintain species diversity and genetic diversity (Thuiller et al. 2008). There is a difference between the use of genetics for conservation (Broadhurst & Young 2007) and its application, for example, to the development of commercial crop lineages that are often limited in genetic diversity (Mohammadi & Prasanna 2003). Biodiversity conservation is reliant on dynamic evolutionary processes that enable adaptation in response to change (Sgrò et al. 2011) whether natural or human-mediated whereas vegetative propagation of a single genotype may be required to ensure a genetically uniform lineage that displays particular desirable traits.

Habitat fragmentation contributes to species decline and extinction because it can lead to small, isolated

populations that are ultimately more susceptible to demographic fluctuations and the loss of genetic variation (Frankham 2005; Lienert 2004; Young & Augsberger 1991). The effects are not restricted to rare species; common plants may be equally or even more susceptible to the population genetic consequences of fragmentation depending on previous history of inbreeding and outcrossing (Honnay & Jacquemyn 2007).

The maintenance of evolutionary processes remains one of the major goals for the management of genetic resources (Sgrò et al. 2011). It is dependent on understanding the genetic consequences of habitat fragmentation and changing climate on populations (Hoffmann & Sgrò 2011; Young et al. 1996) because the capacity of ecosystems to respond to environmental changes is dictated by the ecological and genetic constraints on evolutionary processes (Stein et al. 2013). Genetic decline and demographic factors may affect the adaptive capacity of populations (Willi & Hoffmann 2009; Willi et al. 2006) but manipulating genetic diversity has the potential to enhance resis-

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tance to stress (Pauls et al. 2013).

Genetic studies are particularly useful for managing species that reproduce vegetatively, where taxonomic uncertainty may affect the recognition of conservation targets, where divergent genetic lineages may represent different evolutionarily significant units (Moritz 1994) or management units (Palsboll et al. 2007) and for the management of genetic resources under predicted environmental change (Pressey et al. 2007; Thuiller et al. 2008; Weeks et al. 2011). The complexity of factors that affect ecological and evolutionary processes limits the applicability of generalisations to specific cases yet it is not possible to assess the conservation requirements of all species (Frankham 2010). Thus we must rely on more generally applicable guidelines such as the strategies detailed by Sgrò et al. (2011) designed to build evolutionary resilience into biodiversity conservation.

Species' persistence may be facilitated by managing for predicted ecological changes rather than existing or historical conditions (Seastedt et al. 2008; Weeks et al. 2011). This idea has led to recommendations for seed sourcing and composite provenancing (Broadhurst et al. 2008), where seed from a range of environments is combined for habitat restoration, to take into account the need to mitigate the effects of changing climate (Breed et al. 2013; Prober et al. 2015).

The use of a range of genetic techniques such as DNA sequence variation and the genotyping of individuals enables us to identify maternal lineages, to differentiate between individuals and clone mates and to accurately measure differences in genetic varia-

tion between individuals, populations and species. In conjunction with field-based information, better understanding of the patterns of diversity is leading to integrated management plans that try to balance the multiple pressures imposed by our use of resources with the essential requirements for biodiversity conservation.

Case studies

The following examples from south-eastern Australia show the application of genetic techniques to three different conservation issues:

1. Conserving clonal species

Population genetic analysis of two *Grevillea* species (Proteaceae) from the same informal taxonomic group of holly-leaved grevilleas has shown that both species are extensively clonal and sterile. Despite thousands of stems, *G. renwickiana* occurs in only a few populations in New South Wales and consists of eight clonal lineages (James & McDougall 2014) and *G. infecunda* (Fig. 4) occurs in only a few populations on the southern coast of Victoria and consists of 38 clonal lineages ((Kimpton et al. 2002), James, unpublished data).

Another rare plant, *Olearia passerinoides* subsp. *glutescens* (Asteraceae), was recently discovered in Victoria, hundreds of kilometres from known locations in South Australia. Genetic analysis has revealed that the five Victorian populations, all found within 10 km of each other, contain only 8 clones (Fig. 5) but South Australian populations have higher levels of genotypic diversity suggesting that they reproduce mainly from seed (Suyama et al, unpublished



Fig. 4 Holly-leaved *Grevillea infecunda*. This sterile species contains fewer than 50 clonal lineages despite the presence of several thousand stems. Image: E.James



Fig. 5 A population of *Olearia passerinoides* subsp. *passerinoides* (individuals marked with pink flags). Genetic analysis showed that the plants here belong to a single clone and there are only 8 clones in Victoria. (image: Karly Learmonth)

data).

Knowledge of the spatial distribution, fecundity and extent of clonality in these species allows them to be managed to ensure continued vegetative reproduction.

2. Threatened plants species of the Victorian Volcanic Plain

Native temperate grasslands are the most threatened ecosystems in Australia (Williams et al. 2015). The Victorian Volcanic Plain in south-eastern Australia has been converted to a highly productive agricultural region at the expense of native grassland communities. As a result, naturally occurring habitat is highly fragmented and occupies less than 1% of the 2.3 million hectares comprising the VVP (Williams et al. 2015) and the once extensive grasslands exist mostly as small, isolated remnants.

Patterns of genetic variation have been collected for 5 species, *Pimelea spinescens* (Thymeleaceae) (James & Jordan 2014) (Fig. 6), *Diuris basaltica* and relatives (Orchidaceae) (Ahrens et al. unpublished data), *Comesperma polygaloides* (Polygalaceae) (Ahrens & James 2016), *Senecio macrocarpus* (Asteraceae) (Ahrens & James 2015) and *Ptilotus microcephalus* (Amaranthaceae) (Ahrens & James 2016). All species showed a much lower level of population genetic structure than expected despite significant habitat destruction and small population size.

The conclusion reached from these studies is that, historically, the open plains of the VVP facilitated gene flow within the VVP and there has not been a



Fig. 6 Protecting *Pimelea spinescens*, a threatened species of the grasslands of the Victorian Volcanic Plain, grows in remnant vegetation in a mosaic of agricultural land. Signs remind landowners and the general public that we value this plant. (Image: courtesy of the Spiny Riceflower Recovery Team)

significant decline in genetic diversity, in part because many of the plants are long-lived. The general lack of population structure does not reflect the recent habitat fragmentation of the VVP but instead reflects historical levels of diversity and gene flow and suggests a common factor that has influenced patterns of genetic diversity more generally across the VVP. The importance of these findings is that germplasm from throughout the VVP can be used for restoration purposes. The information will assist in managing the genetic diversity of each species to facilitate adaptive responses to environmental change.

3. Wetlands of the Gippsland Lakes

The Gippsland Lakes in south-eastern Australia is an extensive Ramsar-listed wetland system of > 60,000 ha. It supports commercial fishing, hunting, tourism and agricultural pursuits. It has experienced chronic salinisation since the late 19th century following the construction of a permanent channel to the sea (Fig. 7) to improve boat access (Boon et al. 2015). The effects were exacerbated in the mid-late 20th century when fresh water from inflowing rivers was increasingly regulated and extracted.

Changes to hydrology and the competing demands from users of the land and wetlands have led to substantial ecological impacts on the Lakes' ecosystem including changes in the distribution of *Melaleuca ericifolia* (Myrtaceae) and *Phragmites australis* (Poaceae) (Fig. 8). Both species establish from seed but clonal growth can be substantial. Lowered water levels allowed the establishment of *M. ericifolia* which became dominant with extensive clonality and replaced much of the *P. australis* (Fig. 9). Little genetic structure was observed in *P. australis* and was not correlated with salinity (Hurry et al. 2013; James et al. 2013). A recent transcriptome study of *P. australis* has identified differences in gene expression between plants sourced from high and low salinity sites when exposed to fresh water and high salt levels (Holmes et al. 2016). Evidence of adaptation to salinity may provide a basis for selecting germplasm for restoration.

Conclusions

Genetic studies have enabled significant advances in our understanding of populations, species, habitats and their conservation requirements. Studies ranging from rare species to widespread species and across

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Fig. 7 A permanent opening of the Gippsland Lakes to the ocean was constructed in 1889. Salinity levels have risen since then and lakes have become increasingly salinised. Image: E. James



Fig. 8 A wetland in the Gippsland Lakes dominated by Common Reed, *Phragmites australis*. An individual plant of *Melaleuca ericifolia* is visible in the centre of the image. Image: E. James

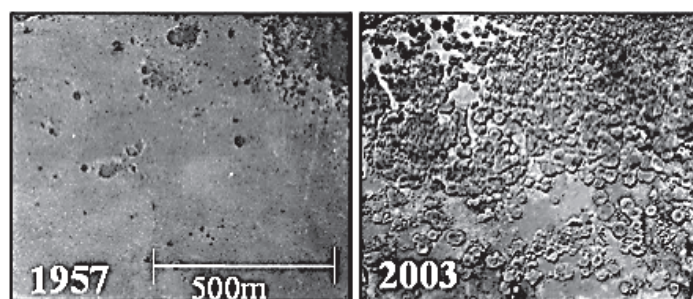


Fig. 9 The relative abundance of *Melaleuca ericifolia* and *Phragmites australis* changes with management. In 1957, *M. ericifolia*, visible as small dark areas, was uncommon and *P. australis* occupied most of the area. By 2003, large clones of *M. ericifolia* dominate. (Image modified from Robinson et al. (2012)).

different ecological niches are helping to build up a picture of the variability in patterns of genetic diversity and an understanding of the processes that have led to them. This will assist us balance our use of natural resources with the need to retain the evolutionary processes necessary for adaptation to the pressures of environmental change at all levels of biodiversity.

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