
CSIRO PUBLISHING



Australian Journal of Botany

Volume 48, 2000
© CSIRO 2000

An international journal for the publication of
original research in plant science

www.publish.csiro.au/journals/ajb

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Australian Journal of Botany

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Australia has a species-rich and highly diverse flora of some 25 000 species, combining ancient relictual species that can be traced to Gondwanic origins, a vast array of Australian-derived species and an invasive element of about 3000 naturalised species. About 85% of the native species are endemic. The evolution and origins of this flora are associated with a unique series of geohistorical and climatic processes that have characterised the Australian landmass over the last 100 million years. These include the geographical isolation of the temperate floras of eastern and western Australia and significant climatic changes, particularly in the Quaternary, that have dramatically affected biogeographical patterns.

Although the biodiversity represented by this vascular flora is immense and largely unique, the survival of many plant communities and species is problematic. Over the last 200 years since European settlement, 48% of the Australian land cover has been subject to significant disturbance, with nearly 20% of all native vegetation now cleared. At a global scale, some 17.6% of all threatened, rare and poorly known plant species are recorded from Australia as are nearly a quarter of the world's presumed extinct vascular flora. These alarming figures highlight the significant loss of genetic diversity and genetic resources that has already taken place in the Australian flora and, with ongoing land degradation and land clearing, indicate that these losses are likely to continue well into the 21st century.

Over the last 50 years, Australian geneticists have made significant contributions to our understanding of variation and evolution in the flora. More recently, with the emergence of conservation biology as a discipline in its own right, genetic studies have expanded to address the many issues associated with the conservation of this unique and diverse flora.

Genetic diversity is a key level of biological diversity embraced in the concept of biodiversity conservation. Genetics has a multifaceted role in conservation not only in the direct assessment, monitoring and management of genetic diversity but also because of the valuable contributions it can make to other fields of conservation biology such as ecology, systematics, demography and biogeography. This role may cover the analysis of population genetic structure, mating systems, phylogenetics and phylogeography, hybridisation and patterns of gene flow. Yet it is important to stress that genetics alone is unlikely to provide the definitive basis for the development of successful conservation outcomes. There needs to be a broad integrative scientific approach by biologists to the conservation and management of biodiversity with genetic data contributing along with many other scientific disciplines.

This issue of *Australian Journal of Botany* follows a symposium on 'Genetics and Conservation of the Australian Flora' held at the Society for Conservation Biology Conference, Macquarie University, Sydney, on 13–16 July 1998. It incorporates a selection of papers presented at that symposium and other invited papers. These papers include a range of approaches and

methods used in plant conservation genetic studies and cover both rare and threatened species, and more widespread taxa, from many different Australian plant groups. The species and genera studied occur in a diversity of ecosystems from the rainforests of northern Australia, lowland native grasslands in south-eastern Australia and temperate shrublands, mallee woodlands and forests in southern Australia.

Some of the first conservation genetic studies on the Australian flora targeted the genetic resources of species related to a number of the world's important crops and commercially valuable hardwoods. Not only did these studies focus on defining genetic resources and their *in-situ* conservation, as discussed by Moran, Butcher and Glaubitz, but they also looked at *ex-situ* conservation issues associated with germplasm sampling strategies. Brown and Brubaker revisit some of these important theoretical issues that are not only critical for the use and management of genetic resources in wild relatives of crops but also rare and threatened species and native species utilised in revegetation programs and agroforestry.

With the diverse array of evolutionary patterns evident in the Australian flora, studies of phylogenetics and population genetic structure play a significant role in informing conservation of populations and species, and developing conservation priorities and strategies. Brown and Brubaker demonstrate the importance of these studies in *Glycine* and *Gossypium*. They also indicate the value of using different molecular markers in resolving phylogenetic relationships. For example, there is only limited congruence between cpDNA-based phylogenetic relationships with the taxonomy of *Glycine* but much closer congruence following the analysis of sequence variation at the histone H3 gene. However, Byrne shows that phylogeographic analysis of cpDNA variation in the *Eucalyptus kochii* complex reveals little congruence with the taxonomy—a finding confirmed by her previous work by nuclear RFLPs. Both studies emphasise the additional and sometimes contrasting resolving power provided by different molecular markers in phylogenetic analyses of the same material.

More recently, the application of phylogenetic analysis and population genetic structure to conservation has expanded to include links to historical biogeography encompassed in the relatively new discipline of phylogeography. Hopper points out that this linkage has considerable potential in informing conservation of the Australian flora at ecosystem and landscape levels. He suggests that the scaling up of phylogenetic knowledge of genetic resources for all taxa at the local landscape level can make a significant contribution to the conservation of Australian plants. This approach is also emphasised by Coates in relation to defining conservation units on the basis of phylogenetic and phylogeographic studies in the species-rich flora of south-west Australia. Coates indicates that determining conservation units in this way not only delimits suitable units for conservation but also the appropriate geographical scale for management.

Understanding patterns of genetic differentiation and phylogenetic relationships among populations and species provides one level for prioritising and managing genetic resources. Equally important is our understanding of those processes that structure and maintain genetic diversity within and among populations. Building upon close to four decades of research on the genetics of small populations of Australian plants, James highlights the significance of genetic-system studies on our native flora. He stresses the insight these studies can provide in relation to our interpretation of genetic diversity and the development of conservation strategies. This genetic-systems approach includes the assessment of the mating system, population genetic structure and the analysis of chromosome structure and behaviour, particularly recombinational patterns determined from chromosome behaviour at meiosis. He emphasises the point that lack of understanding of the genetic system and mechanisms that reduce recombination may lead to quite erroneous interpretations of the significance of observed genetic diversity patterns.

A significant component of the genetic-system approach is the assessment of the mating system. Levels of outcrossing, incompatibility systems, analysis of paternity and the significance of structure within populations all provide vital clues to a population's viability and how it should be managed. Krauss demonstrates the resolving power provided by new molecular markers, in this case AFLPs, in analysing mating system changes in *Persoonia mollis*. He examines the sensitivity of this approach in unambiguously assigning paternity within a population and how it may be used in monitoring mating system changes within populations in relation to differences between populations following habitat disturbance and degradation. Richardson, Ayre and Whelan offer another approach in studying mating systems by combining investigations of pollinator behaviour (potential mating system), crossing experiments (preferred mating system) and genotype analysis of progeny arrays using allozyme markers (realised mating system). They emphasise the importance of understanding the pollination and reproductive biology of the plant when analysing and interpreting estimates of mating system parameters.

Throughout this issue of *Australian Journal of Botany*, a broad range of molecular genetic markers and approaches have been used for assessing population genetic structure, mating systems, and phylogenetic relationships in relation to plant conservation. Although isozymes are still the most widely used genetic marker, many others, particularly PCR-based DNA markers, are being increasingly used in plant conservation genetic studies. For example, the AFLP technique described by Krauss has considerable application in mating system and subpopulation structure analysis. Another group of extremely useful molecular markers are microsatellites or simple sequence repeats (SSRs). Microsatellites are highly polymorphic and codominant, and show tremendous potential in population genetic structure and mating system

studies, particularly in species where other markers such as isozymes have low levels of polymorphism. Rossetto, Harriss, McLauchlan, Henry, Baverstock and Lee overview the value of these markers with particular reference to their development in *Melaleuca alternifolia* and their potential use in other genera in the family Myrtaceae.

A focus on rare and threatened native species by Australian geneticists first developed at a landmark conference in Canberra in 1981 at a symposium on the 'Biology of Rare and Threatened Species'. Today the conservation of rare and threatened species continues to attract the interest of population geneticists where factors associated with reduction in population size and habitat fragmentation such as inbreeding, loss of genetic diversity and reduced gene flow may be critical in managing populations to prevent extinction. Yet it is also clear that not all rare and threatened plants can be considered for conservation genetic studies. Indeed, in some cases such studies would provide little additional relevant information for the conservation and recovery of those species. Hogbin, Peakall and Sydes stress this point in their overview of achieving practical outcomes from genetic studies of rare plants. They indicate that genetic studies on rare plants need to be focussed on clear outcomes and ideally should progress in two separate ways. The first involves a model-system approach integrating relatively long-term ecological and genetic work. In the second approach, a genetic study would provide specific management outcomes highlighted as issues at the commencement of the recovery process for the target species.

One of the difficulties in assessing the significance of genetic diversity and inbreeding levels in rare and threatened plants are the differences in evolutionary histories and life-history traits that may characterise different species. Different types of rarity will have different types of genetic implications. A useful approach to this problem is to carry out comparative genetic studies of rare and widespread species which have similar life histories and ecology. Both James and Brown, and Shapcott use this approach to investigate patterns of genetic variation and population divergence in rare species. Shapcott found that the rare rainforest palm, *Ptychosperma bleeseri*, shows extremely low levels of isozyme variation compared with a related co-occurring species, *Carpentaria acuminata*. She also showed that genetic diversity levels within *C. acuminata* are associated with the geographical isolation of rainforest patches but not patch size. James and Brown showed markedly lower levels of genetic diversity and higher genetic differentiation among populations of two rare *Agrostis* species, particularly the endangered *A. adamsonii*, when compared to the common species *A. avenacea*. In contrast, other similar comparative studies of Australian eucalypts and triggerplants (*Stylidium*) have documented equivalent levels of genetic diversity in rare and common species. Such idiosyncratic patterns in rare species suggest the need for careful experimentation to establish whether

genetic diversity is a problem needing management intervention. The present focus on recovery programmes for rare and threatened species presents an excellent opportunity for such experimentation to proceed.

The ultimate goal in the recovery of a threatened species is the successful re-establishment of viable populations. Apart from actually achieving this goal, the major difficulty for any conservation biologist involved in the recovery process is determining how to evaluate success and how long the evaluation should take. As pointed out by Young and Murray, there are very few empirical data on the genetic effects of re-establishment and the implications for the long-term viability of new populations. They compared allozyme and chromosome variation between five small re-established populations and two large parental populations, of the endangered grassland daisy *Rutidosia leptorrhynchoidea*. Young and Murray observed both chromosomal and allozyme changes that may adversely affect the viability of the new populations. Re-establishment is associated with increased chromosome abnormalities and also appears to be associated with a significant genetic bottleneck resulting in loss in allozyme diversity. This study highlights the importance of sampling sufficient genetic variation for effective recovery programs (see Brown and Brubaker) and the need to fully understand critical components of the genetic system (see James), such as chromosome architecture of the populations before commencing translocation programmes.

This issue reflects the broad range of roles genetics has to play in the conservation of a flora that appears to be characterised by certain ecosystem and evolutionary processes quite different to many other parts of the world. Given the ongoing loss of populations, species and ecological communities, there is a significant challenge for conservation biologists, geneticists and botanists to provide a sound scientific basis for the conservation of this diverse and highly endemic flora. We hope that this issue not only highlights the contribution genetics can make to flora conservation in Australia but will also encourage others to pursue research that will help conserve a unique genetic resource.

This volume is respectfully dedicated to Associate Professor Sid James, who was an active contributor at the 1998 Symposium, and whose influence on Australian plant conservation genetics was evident by the number of his students who also participated. Sid died suddenly at home in Perth in 1998. Hopper and Barlow provide an overview of his many contributions over a rich and productive career.

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