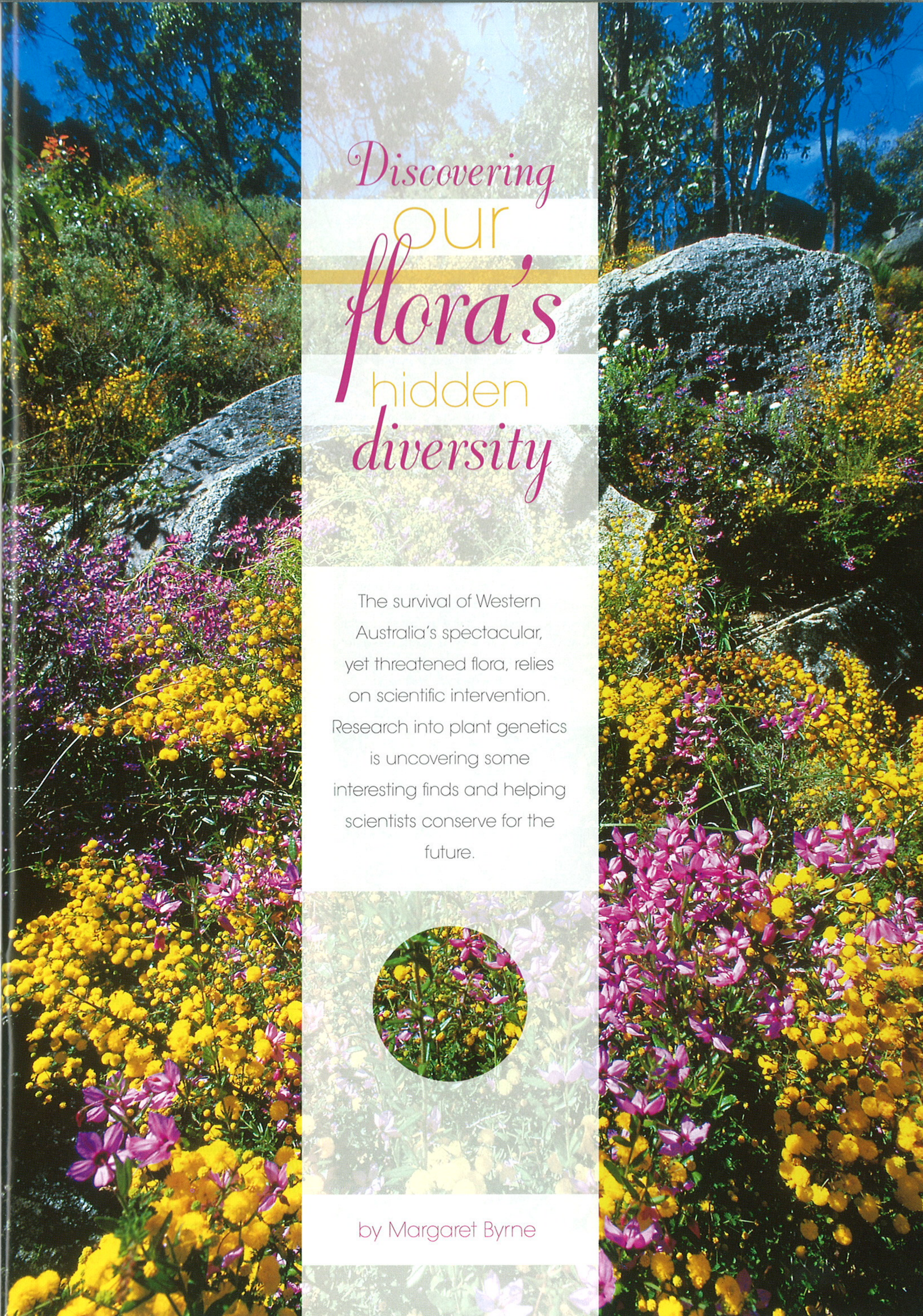
Discovering our flora's hidden diversity

The survival of Western Australia's spectacular, yet threatened flora, relies on scientific intervention. Research into plant genetics is uncovering some interesting finds and helping scientists conserve for the future.



by Margaret Byrne

The diversity of Western Australia's wildflowers has been recognised internationally as one of the great wonders of the natural world, a biodiversity 'hotspot' renowned for its diverse, yet threatened, flora. The measure of diversity used to come to this conclusion was based on the appearance of the plants (their morphology). But these plants also have a high degree of hidden diversity in their genetic makeup, which is not seen because it doesn't cause any specific change to how the plants appear. This unseen genetic variation is just as diverse and complex as the morphological diversity we can see. Although the genetic diversity of plants cannot be seen by the human eye, it can be made visible with new genetic techniques.

Why genetics is important to conservation

Genetic diversity is fundamental to the functioning of all plants, animals and ecosystems. It is the means by which species evolve and adapt to new environments and is important in adaptation to climate change. Effective conservation management means conserving both the morphological diversity we can see and the genetic diversity underneath it.

Conservation genetic analyses have not only confirmed the high diversity of our plants but have also revealed some interesting surprises that directly influence conservation management. Knowledge of genetic relationships between species, known as phylogeny, means that our conservation management activity is based on the evolutionary history of our flora—a flora that has persisted for very long periods of time in this ancient landscape.

In WA there are many species that are quite restricted and occur in localised areas that may be large distances apart. These plants may show few morphological differences but that does not necessarily mean that they have no genetic differences. For example, most populations of the round leaf honeysuckle (*Lambertia orbifolia*) occur near Augusta but there are also small populations approximately 200 kilometres away near Narrikup, north of Albany. There are no obvious morphological differences between the plants from the two areas but genetic analysis has shown that the isolated populations near Narrikup are quite distinct from the populations near Augusta. This means that they have been separated for long periods of time and have not been isolated by recent events such as agricultural clearing. The long period of separation for these populations means that they have accumulated lots of differences and have changed over time into different genetic forms that are known as evolutionary lineages. This pattern of restricted distribution is quite common for plant species in WA and is a result of the biogeographical history of the region. As such, the Narrikup populations have now been recognised as distinct and have been described as different subspecies. This means that the Narrikup subspecies has a higher conservation status than previously allocated, and has been targeted for conservation activity through translocation to a secure, disease-free site (see 'Critical Action', *LANDSCOPE*, Spring 2006). This translocated population is now flowering and new seedlings have become established thus reducing the chance that the subspecies may go extinct.

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Masses of wattle and black-eyed Susan on a Perth hillside.
Photo – Bill Belson/Lochman Transparencies

Above left Round-leafed honeysuckle (*Lambertia orbifolia*).
Photo – Andrew Davoll/Lochman Transparencies

Left WA is renowned for its floral diversity.
Photo – Rob Olver

Above Karri (*Eucalyptus diversicolour*) with flowering understorey.
Photo – Len Stewart/Lochman Transparencies

Right Stirling Range National Park located in WA's biodiversity hotspot.
Photo – Rob Olver

Defining a species

The flora in south-west WA contains many species complexes with lots of morphological variation. Narrow leaved mallee (*Eucalyptus angustissima*) is one such species complex where species and subspecies have been defined but there are still some uncertainties about the relationships and whether the species are valid. The complex has a restricted distribution in flat low-lying areas north of Esperance, and contains three species—*E foliosa, E. misella* and *E. angustissima*—with two subspecies in *E. angustissima*. If there are few genetic differences between the species they should not be recognised as separate species and would have a low priority for conservation. A phylogenetic study of the narrow leaved mallee complex showed that the species were all genetically distinct and thus the species are valid. In addition, the two subspecies of *E. angusissima* showed large genetic differences and should therefore be recognised as separate species instead of subspecies. This means that the conservation listing of the rare species in this complex should be retained, although further field survey is required to confirm their geographic distribution and abundance, and hence their conservation status.

Sometimes the large amount of morphological variation in our widespread species means that closely related species are not recognised as clearly different. The rare splendid wattle (*Acacia splendens*) was recently recognised as a distinct species separate from the very widespread manna wattle (*A. microbotrya*), based on a genetic study of the group. Splendid wattle is restricted to a ridge outside Dandaragan on the western edge of the range of the manna wattle. It has been listed as a threatened species that is critically endangered. However, there was some uncertainty about its taxonomic status in relation to the common manna wattle. Genetic analysis showed that splendid wattle is distinct from manna wattle and confirmed that it should be recognised as separate species. The identity and conservation status of rare species may be masked by unresolved variation present in species complexes such as manna wattle, and phylogenetic studies provide assistance in resolving these ambiguities so that the conservation status of species is appropriately recognised.

An ancient flora

The ancient landscape of WA means the flora is a combination of ancient relictual species that have persisted for a long time, along with newly derived species that have recently diverged

from their common ancestors. But morphological similarity between species is not always a reliable way of knowing which species are closely related. In the same way that family trees can show the pattern of relationships through many generations in human families, genetic trees can show whether plant species are closely or distantly related. Several studies using genetic trees have identified species that are quite genetically different from what has been presumed to be their closest relatives based on similarities in appearance. For example, dragnet wattle (*A. verricula*) and Chiddarcooping wattle (*A. lobulata*) were thought to be related since they both have a network pattern in the veins on the 'leaves' (technically known as phyllodes in wattles). But a genetic study has shown that they are very distinct and have probably been separated for more than three million years.

In another example, Oldfield's wattle (*A. oldfieldii*), which was thought to be closely related to jam (*A. acuminata*), is quite distinct and has also probably been isolated from jam for nearly three million years. Chiddarcooping wattle and Oldfield's wattle have very restricted distributions and are most likely ancient relictual species that have persisted in suitable habitat (such as near granite rocks or mild coastal areas) through the dramatic climatic changes that have occurred during the Pleistocene era over the past two million years. In contrast, other restricted species are not ancient. For example, Wundowlin wattle (*A. sciophanes*) is a rare species that shares a similar wispy growth habit with Yilgarn broken wattle (*A. anfractuosa*). These species have few genetic differences and can be considered sister species that have arisen through recent separation. In this case similarity in physical characters does indicate a close relationship between the species.

Top left Coastal heath in the south-west's Ravensthorpe Range.

Centre left Coastal dune with wattle, Shark Bay rose and poverty bush in flower.

Left Carpet of everlastings in the Midwest Region.
Photos – Jiri Lochman

Right Karri dampiera (*Dampiera hederacea*) and holly flame pea (*Chorizema ilicifolia*).
Photo – Jiri Lochman

Right box insets (left) DEC staff at work in the DNA laboratory; (right) liquid handling robot.
Photos – Shelly McAuthur

Below Raspberry jam (*Acacia acuminata*).
Photo – Marie Lochman

Defining flora conservation priorities

In a region like WA there are a large number of species identified as rare and threatened. Unfortunately, conservationists don't have enough resources to do all the things they would like, and some assessment of priority has to be made. Most often priorities are assigned based on the degree of threat the species is under. But some would argue that ancient species have greater priority for conservation than more recently derived species. This is because ancient species carry a greater level of different genetic history than more recent species. Therefore, if we conserve the ancient species we will be conserving more genetic variation than if we conserve recently derived species. Hence genetic studies can identify the relationships between species and this can be taken into account when making decisions about priorities for conservation efforts. For example, the ancient species Chiddarcooping wattle would have a higher priority for conservation than the more recently derived species Wundowlin wattle which has a widespread common relative.

Knowledge of genetic relationships between species also allows appropriate comparisons between rare species and their common relatives, rather than between rare species and other unrelated species that have no common history. This means that scientists are more likely to identify the particular aspects of a species biology that is contributing to its rarity. They can then target conservation action much more precisely and achieve better results.

Reading DNA

Analysing a plant's genetic diversity involves examination of its DNA. One method of doing this is through a process known as 'Polymerase Chain Reaction' (PCR). This method uses just a small amount of DNA and is therefore useful on small herbarium specimens or on plants that only have a few small leaves. So how does it work?

PCR produces many copies of a piece of DNA. DNA is made of two strands which are held together by bonds. However, these bonds can be broken and the strands multiplied by a series of heating and cooling cycles. A single piece of DNA would not be visible, but after 30 or 40 heating cycles the many copies of the piece of DNA are clearly seen when run on a gel and stained—a process which reveals a plant's DNA and therefore highlights differences between plant species.

Technology

In this modern age we rely more and more on technological innovations. These technological innovations are also relevant to conservation biology. The Department of Environment and Conservation (DEC) established a DNA laboratory 11 years ago so the genetic diversity of flora could be determined with modern molecular techniques (see 'More than meets the eye', *LANDSCOPE*, Spring 1997). Through the *Saving our Species* program, the department is continuing to implement such vision (see 'Saving our Species, Saving our State', *LANDSCOPE*, Winter 2007). It recently purchased an advanced liquid handling robotic system to improve the speed and accuracy with which scientists can use DNA techniques to assess phylogenetic relationships in our plants. This robotic system processes 96 samples at a time to extract DNA, determine DNA concentration and set up analysis reactions, all with high accuracy.

This means that the conservation management of our rich and diverse flora will continue to be based on the best scientific knowledge we can get. The flora we have is rich and diverse but faces many threats, and there is much that we still have to learn about the diversity hidden in its genetic makeup so that we can conserve and manage the rich inheritance of a long period of evolutionary history.

Dr Margaret Byrne is a DEC Principal Research Scientist. She specialises in genetics for conservation and uses of native flora. She can be contacted on (08) 9334 0503 or by email (margaret.byrne@dec.wa.gov.au).

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Executive Editor Kaye Verboon.

Editors Samille Mitchell, Rhianna King, Carolyn Thomson-Dans.

Scientific/technical advice Kevin Kenneally, Paul Jones, Keith Morris.

Design and production Maria Duthie, Tiffany Taylor, Gooitzen van der Meer.

Illustration Gooitzen van der Meer.

Cartography Promaco Geodraft.

Marketing Cathy Birch
Phone (08) 9334 0296 *Fax* (08) 9334 0432.

Subscription enquiries
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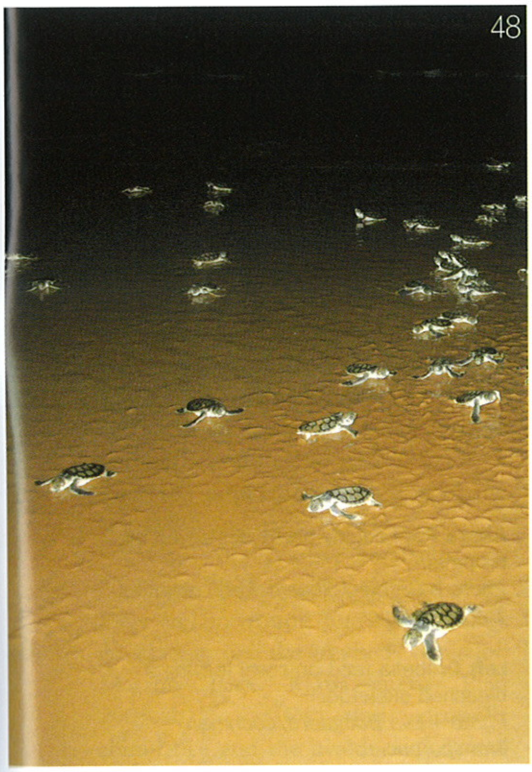
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