

RESEARCH

THE diversity of Western Australia's wildflowers has been recognised internationally as one of the great wonders of the natural world, a biodiversity "hotspot". The measure of diversity used to come to this conclusion was based on what the plants look like (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 in what the plants look like. This array of genetic variation is just as diverse and complex as the morphological diversity we can see. Although the genetic diversity of plants can not be seen by the human eye it can be made visible with new genetic techniques. Not only has this genetic information confirmed the high diversity of our flora but it has also revealed some interesting surprises that will influence conservation efforts. Just as morphology can tell us a lot about plants and how they function, the patterns of genetic diversity can also teach us much about the evolutionary history of our flora.

In Western Australia there are many species that are quite restricted and occur in localised areas which 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 200km 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

DISCOVERING OUR FLORA'S HIDDEN DIVERSITY.

Margaret Byrne



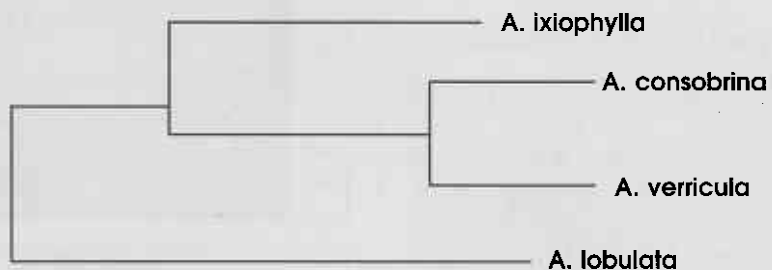
populations means that they have accumulated lots of differences and have changed over time into different genetic forms which are known as evolutionary lineages.

This pattern of restricted distribution is quite common for plant species in Western Australia and is a result of the biogeographical history of the region. The south-west is an ancient flat landscape with no mountain ranges which has been very stable with no major

glaciation events. However there has been some instability resulting in changes in climatic conditions in the semi arid region between the relatively high rainfall zone in the extreme south west and the arid zone in the north and east. This climatic instability has occurred over the last 2 million years during the Pleistocene time era, and has led to a complex mosaic of different soil types and a flora that has a high degree of natural fragmentation. So perhaps it is not so unexpected to find that populations that are isolated from each other are genetically different. But these differences have also been found in studies of widespread species and is not what we would have expected.

Genetic studies on York Gum (*Eucalyptus loxophleba*), Sandalwood (*Santalum spicatum*) and Jam (*Acacia acuminata*) have identified two different genetic lineages in each of these species. The level of genetic differences between these lineages suggest that they became isolated from each other around 800,000 to 1,000,000 years ago. This is during the middle of the Pleistocene time period when the significant changes in climatic conditions would have caused isolation and fragmentation of the flora in the region. These studies show that even species that have widespread, more-or-less continuous distributions now, have been affected by isolation and fragmentation in the past.

The ancient landscape of Western Australia means that the

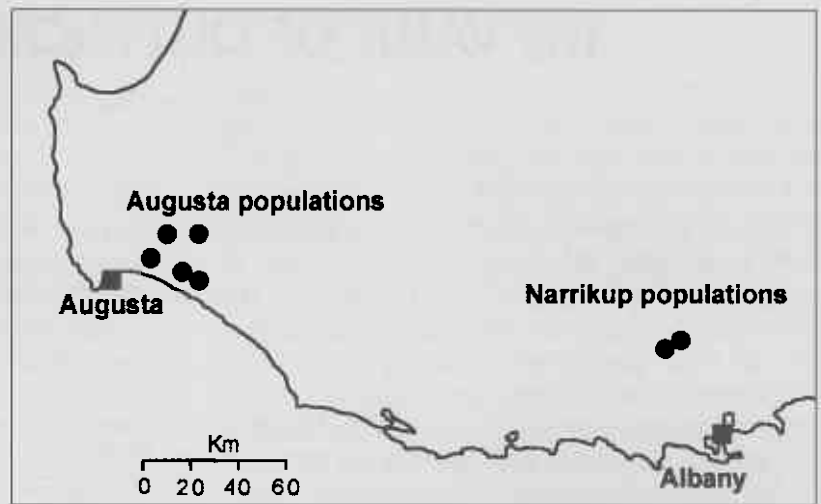


A genetic tree showing Acacia lobulata on a different branch to A. verruculata. Note that two other acacia species are more closely related to A. verruculata than A. lobulata is.

RESEARCH

flora is a combination of ancient relict species that have persisted for a long period of 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 close 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 morphological characters.

For example, the wattle *Acacia 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 acacias). But a genetic study has shown that they are very distinct and have probably been separated for over 3 million years. Also 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 3 million years. Chiddarcooping Wattle and Oldfield's Wattle have very restricted distributions and are most likely ancient relict species that have persisted in suitable habitat (such as south side of granite rocks or mild coastal areas) through the climatic changes that occurred during the Pleistocene era. In contrast other restricted species are not ancient. For example, Wundowling Wattle (*A. sciophanes*) is a rare species that shares a similar wispy growth habit with *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.



Distribution of *Lambertia orbifolia* in two areas near Augusta and near Narrikup.

This knowledge of genetic relationships is interesting and provides background on the evolutionary history of the region but how does it help us with conservation? These studies enable us to identify genetic lineages that represent distinct conservation units. For example the Narrikup populations of the round leaf honeysuckle have now been recognised as distinct and are being targeted for conservation activity through translocation to a secure, disease-free site. In a region like Western Australia where there are a large number of species identified as rare and threatened, we don't have enough resources to do all the things we would like, and some assessment of priority has to be made. Most often priorities are assigned based on the degree of threat that 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 lot more 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. 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 we are more likely to identify the particular aspects of a species biology that is contributing to its rarity. We can then target our conservation action much more precisely and achieve better results.

So you can see that the study of genetic relationships between populations and species (phylogenetics) is particularly valuable in areas such as south-west Western Australia where the historical influences on an ancient landscape has led to complex genetic patterns in a highly diverse flora. Next time you wander through the bush think of the hidden diversity that's present as well as the wonderful morphological diversity on display.

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