

1.3

GENETIC DIVERSITY

The page features three overlapping white curved lines that sweep across the lower half of the page. The lines are thin and elegant, creating a sense of movement and depth against the solid green background.

INTRODUCTION

Genetic diversity refers to the variety of genetic information in all the individual organisms in an area. This is quite distinct from species diversity, because it operates at the level of genes. Two populations of the same species can vary in their genetic diversity. One population, for example on an island, may be descended from relatively few individuals. Thus the gene pool of that population may be narrow. The other population may be descended from a large number of individuals. Thus the gene pool of that population would have greater variety.

Genetic diversity helps ensure the survival of species because it is what gives rise to the variation between individuals. This variation may allow a species to change over time and thereby survive changing environmental conditions. In other words, greater genetic diversity can offer greater resilience. In order to maintain the capacity of our forests to adapt to future changes, therefore, genetic diversity must be preserved as much as possible through suitable management practices.

Direct measurements of genetic diversity in forest flora and fauna are being carried out but the task is not easy. Specific research is being conducted on representative species to determine population condition and trend information.

This section also considers the extent of native forest and plantations of indigenous species for which genetic resource conservation plans have been prepared and implemented. The forest management plans and guidelines established in most States and Territories have

recognised the significance of conserving the genetic diversity of our forests. As new and more cost-effective methods of monitoring genetic variation in forests are developed, forest management plans will incorporate this information and management practices are expected to change in accordance with the results.

The international Montreal Process Indicator 1.3b, which examined the population levels of representative species from diverse habitats monitored across their range, has been integrated into the Australian regional indicator 1.2c.



Michael F. Ryan

Smooth barked apple (*Angophora costata*)

Genetic variation in forest-dwelling species



Indicator 1.3a

Amount of genetic variation within and between populations of representative forest-dwelling species

Rationale

Direct measures of genetic variation are possible and are sensitive to the loss of variation that will prevent long term survival and adaptation.

Direct measurements of genetic diversity in forest flora and fauna are being carried out but nationally conclusive results are not available.

Genetic diversity can be measured directly by sampling tissue from individuals within a population and by testing for genetic markers to detect the degree of difference between those individuals. These tests have not been carried out extensively because of high costs.

There are limitations, however, on the availability of information on the former ranges of species. Using historical records, expert opinion and incidental observations, some of this information can be mapped or modelled. Existing models currently exist primarily for vascular plants and ecological communities. The Regional Forest Agreements, in particular, provide pre-1750 and current models of forest ecosystems within the production forest estate.

Studies have shown that species whose range has been reduced or fragmented have a consequent loss of genetic variability. Hence, knowing the number of forest-dependent species whose ranges have shrunk gives an idea of how much genetic diversity may have been lost.

Various research institutions, including State, Territory and Australian Government organisations, are undertaking direct measurements of genetic diversity using DNA techniques and genetic markers. The results may help to develop guidelines to minimise decreases in genetic diversity without the need for sampling. Research on direct genetic variability is occurring on both flora and fauna.

Flora

A study on the genetic composition of two eucalypt species across a coupe following harvesting and regeneration identified the impacts of different management practices on their genetic composition. The practices involved were clear-felling with aerial sowing, seed tree system with burning, and seed tree system with mechanical disturbance. These were compared with unharvested controls. The results of this study have been supported by studies in East Gippsland, Victoria, where sampling has shown that the genetic diversity of dominant *Eucalyptus* species is less affected by harvesting and management techniques than that of minor species. Specific methods to ensure maintenance of the genetic diversity of minor species are yet to be developed.

A study of the three remaining isolated populations of the rare tree species *E. benthamii* (Camden white gum) has shown a high level of genetic differentiation between populations. The conservation of the entire *E. benthamii* gene pool relies on the future availability of genetic material from all three populations. The two smallest populations are in danger of



Tasmanian quoll (*Dasyurus maculatus maculatus*)

extinction. Should this happen, the total genetic diversity of this species would be permanently reduced.

Genetic studies have also been undertaken on the mangrove species *Avicennia marina*. Within some populations there was considerable genetic variation, but in the populations towards the extremes of this species' range, there was relatively little variation.

Fauna

There is a reasonable amount of information available on population and distribution of animal species. This can be used for the broader genetic diversity indicator, which is based on the number of forest-dependent species that occupy only a small portion of their former ranges. The information required for this surrogate on current populations coincides with the information available in Indicator 1.3c.

For example a genetic study of quolls (*Dasyurus species*) suggested that the Tasmanian tiger quoll (*Dasyurus maculatus maculatus*) was sufficiently genetically different from mainland animals that it should be reclassified as a separate subspecies and conserved accordingly.

Further reading

Glaubitz, J.C., Strk, J. and Moran, G.F. (1999). Genetic impacts of different silvicultural practices in native eucalypt forests. In: Matyas, Cs (Ed) *Forest Genetics and Sustainability*. Kluwer Academic Publishers, Dordrecht, the Netherlands, pp 183-195.

Skinner, A. (2002). The effects of tree isolation on the genetic diversity and seed production of Camden White Gum (*Eucalyptus benthamii* Maiden et Cambage). Centre for Plant Biodiversity Research Summer Scholarship Program, Canberra.

Genetic resource conservation



Indicator 1.3c

Extent of native forest and plantations of indigenous species which have genetic resource conservation plans prepared and implemented

Rationale

Genetic resource management plans aim to maintain the range of genetic diversity of commercially utilised indigenous species, and to avoid the introgression of genetic resources from native forest plantations.

The importance of maintaining genetic diversity in native forests and plantations is acknowledged by various forest management organisations in management plans and guidelines.

Genetic variation within native plantation and native forest species makes individuals in each species physically different from one another and gives each species the chance to adapt to environmental change over time. Genetic diversity is therefore important for long-term survival. Genetic resource conservation plans enable us to maintain genetic diversity within and between species in our native plantations and native forests.

The forest management plans and guidelines established in most States and Territories recognise the significance of conserving the genetic diversity of our forests. As new and more cost-effective methods of monitoring genetic variation in forests are developed, forest management plans should incorporate this information and management practices will change in accordance with the results.

In most States and Territories, forest management plans stipulate that regeneration and rehabilitation strategies are to be conducted using species and provenances native to the area or the general locality. This is undertaken with the aim of maintaining the local gene pools and the approximate composition and spatial distribution of species that were present before harvesting. These plans include guidelines for seed collection and the selection of seed trees of good form and health.

The Australian Tree Seed Centre maintains a national collection of seeds of more than 30 000 genetically distinct seed acquisitions from 1 300 species, providing a high quality, representative sample of genetic diversity. Other seed collections are maintained by various communities, forest and research agencies. For example, in Western Australia the Department of Conservation and Land Management and The Botanic Gardens and Parks Authority are partners in the Millennium Seed Bank Project designed to conserve and maintain Western Australia's biodiversity at the levels of ecosystem, species and gene. By 2010, the seeds of 2 340 taxa listed as rare, threatened or poorly known for Western Australia will be collected and held within germplasm facilities both in Western Australia and in the United Kingdom (although not all these plants are forest species.) This seed will be used to implement the species recovery plans for the restoration of threatened species and ecological communities.

Also important is monitoring and controlling genetic flow from native plantations into native populations, where such flows could result in a diminution of the full range of

variation within the population. This could occur when pollen from the native plantation fertilises the adjacent native forest. Limiting such flow would help preserve the diversity and integrity of the genetic resources in the native forest. On the other hand, genetic resource management plans aim to maintain the range of genetic diversity of commercially utilised indigenous species, and to avoid genetic flow that is identified as potentially damaging to the whole genetic resource.

Conservation of genetic diversity can be achieved through the preservation of native populations and habitats or through storing genetic resources in special plantations, seed collections and breeding programs.

Tree-breeding programs are an integral aspect of maintaining genetic diversity in plantation species. A diverse genetic resource base decreases the risk of pest or disease epidemics. It provides sufficient genetic variation for continued genetic gains over multiple generations and a source for new traits to be incorporated into future breeding programs. Tree breeding programs exist for many native and exotic hardwood and softwood species (Table 43).

Table 43: Conservation plans for some widely planted forest species in Australia

Organisation	Species
CSIRO – Australian Tree Seed Centre	<i>Acacia</i> species, <i>Casuarina</i> species, <i>Eucalyptus</i> species
Southern Tree Breeding Association	Blue gum (<i>Eucalyptus globulus</i>)
Cooperative Research Centre for Sustainable Production Forestry	Blue gum (<i>E. globulus</i>), shining gum (<i>E. nitens</i>)
Queensland Forestry Research Institute	Blackbutt (<i>E. pilularis</i>), broad leaved red mahogany (<i>E. pellita</i>), flooded gum (<i>E. grandis</i>), Gympie messmate (<i>E. cloeziana</i>), Dunn's white gum (<i>E. dunnii</i>), Chinchilla white gum (<i>E. argophloia</i>), mangium (<i>Acacia mangium</i>), red cedar (<i>Toona ciliata</i>), silky oak (<i>Grevillea robusta</i>), spotted gum (<i>Corymbia variegata</i> , <i>C. henryi</i>), hoop pine (<i>Araucaria cunninghamii</i>), Wollemi pine (<i>Wollemia nobilis</i>)
Australian Low Rainfall Tree Improvement Group	Blue-leaved mallee (<i>E. polybractea</i>), mulga (<i>E. sideroxyton</i>), red ironbark (<i>E. tricarpa</i>), river red gum (<i>E. camaldulensis</i>), spotted gum (<i>Corymbia maculata</i> , <i>C. variegata</i>), sugargum (<i>E. cladocalyx</i>), swamp yate (<i>E. occidentalis</i>), Western Australian oil mallees (<i>E. kochii</i> and <i>E. horistes</i>)

Source: National Forest Inventory (2003)

Minimising genetic pollution

The national Joint Venture Agroforestry Program is conducting research and providing strategic recommendations to limit the flow of genetic pollution from Farm Forestry initiatives into native forest. Its recommendations include:

- selection of species/provenance;
- genetic manipulation of flowering times and abundance; and
- silvicultural practices such as isolation distances, buffer zones and reduced spacing.

There has also been a shift from the planting of any provenance in Landcare ventures to the use of more local provenances.

Rare species

Rare and threatened plant species are the targets of specific genetic resource conservation plans in most states and Territories. A good example is the Wollemi Pine Recovery Plan in New South Wales.



Jaime Plaza

Nets catch seeds of the Wollemi pine (*Wollemia nobilis*) as part of the Wollemi Pine Recovery Program

Case Study: Wollemi Pine Recovery Plan

The Wollemi pine was discovered in 1994 in the Wollemi National Park, 150 km from Sydney. This endangered species has only 43 known adult trees in the wild and is from an evolutionary line once thought to be extinct. A thorough management strategy has been implemented to protect the existing wild specimens. This includes protection of the species under the New South Wales *Threatened Species Conservation Act 1995* and Commonwealth *Environmental Protection and Biodiversity Conservation Act 1999*. A Memorandum of Understanding exists between New South Wales National Parks and Wildlife Service and the Royal Botanic Gardens Sydney for the management of the wild populations and development of a cultivation and propagation program.

The site of the wild stand is carefully protected. The exact location of the known stands is not revealed, other than to scientific research teams; the sites are monitored, minimising the number and duration of visits; and permitted visitors must adhere to strict procedures to avoid trampling seedbeds and seedlings, compacting the soil or introducing disease.

Research and development programs designed to protect the species include ecological studies, botanical research and horticultural development. As part of the protection strategy, commercial propagation is being developed and licensed to make the plant widely available.

Further reading

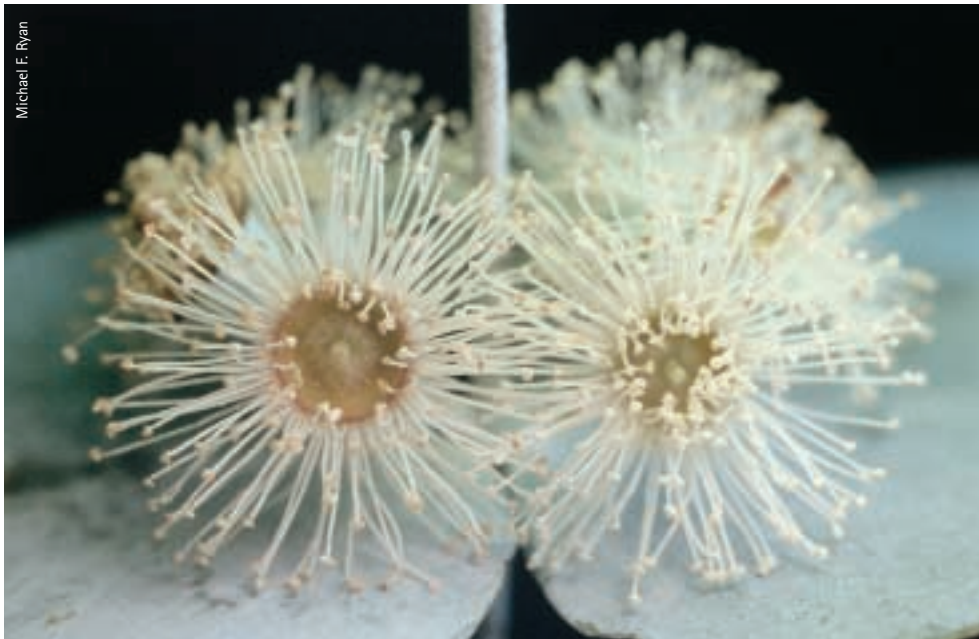
Barbour, R., Potts, B.M., Vaillancourt, R.E., Tibbits, W.N. and Wiltshire, R.J.E. (2001). Gene flow between introduced and native *Eucalyptus* species. *New Forests* 23: 177–191.

Barbour, R.C., Potts, B.M. and Vaillancourt, R.E. (2003). Gene flow between introduced and native *Eucalyptus* species: Exotic hybrids are establishing in the wild. *Australian Journal of Botany* 51 (in press).

Harwood, C., Bulman, P., Bush, D., Mazanec, R. and Stackpole, D. (2001). Australian Low Rainfall Tree Improvement Group Compendium of Hardwood Breeding Strategies. Report to RIRDC/ LWA/ FWPRDC Joint Venture Agroforestry Program. RIRDC Publication No 01/100 RIRDC Project No CSF-58A, Canberra.

Potts, B.M., Barbour, R.C. and Hingston, A.B. (2001). Genetic Pollution from Farm Forestry using *Eucalypt* Species and Hybrids. Report to RIRDC/ LWA/ FWPRDC Joint Venture Agroforestry Program. RIRDC Publication No 01/114 RIRDC Project No CPF-3A.

Victorian Government Policy Statement on Forests (2002). *Our Forests Our Future – Balancing Communities, Jobs and the Environment*. A government statement by the Premier of Victoria, The Hon Steve Bracks MP and Minister for Environment and Conservation, The Hon Sherryl Garbutt MP, February 2002, Melbourne.



Argyle apple (*Eucalyptus cinerea*) blossom