

## State Herbarium of South Australia research projects

### Species and populations

**Biogeography and biodiversity conservation** – understanding variances within and between species for conservation

#### **Rates of evolution & extinction in Gondwanan lineages: Biffin E, Heselwood, M, Melick R, Lowe AJ**

Biogeography is the study of species distribution and its biological and environmental drivers. The role of long distance dispersal (LDD) in the evolution of the Australasian and southwest Pacific flora is hotly contended but appropriate tests of alternative hypotheses are still lacking. Using a comparative method combining phylogeny, fossils, mutation-rate estimation, statistical tools and phylogeography, this Australian Research Council funded Discovery project tests central premises of biogeographic theory to examine differences in LDD dynamics, evolutionary potential between groups, and coincidence with major past geological or climatic changes. This project applies biogeographic methods to more accurately estimate lineage divergence and long-distance dispersal. It tests central premises of biogeographic theory by reconstructing the biogeographic history of the Podocarpaceae and Cunoniaceae (and including available Araucariaceae and Elaeocarpaceae data) to reconsider the role of LDD and climate driven diversification.

#### **SE Pacific biogeography: Keppel G, Ottewell K, Biffin E, Costion C, Lowe AJ**

An Australia & Pacific Science Foundation funded project is using genetic markers to investigate the dynamics of diversity and ecology in tropical rainforest trees along the natural biogeographic gradient in the insular southwest Pacific. Many milestone discoveries in evolution and ecology originated from the study of island systems. The SW Pacific Melanesian islands are an ideal natural laboratory for study; they are a mosaic of islands of recent geological origin, and of different sizes and distances from ancient Gondwanan source continents. Many still have extensive and intact stands of tropical rain forest (although many are now severely threatened by logging). Despite their suitability for evolutionary and ecological study, they have received little scientific attention and almost nothing is known about the ecology and population genetics of their species. This project examines genetic dynamics and interactions at three different scales for select taxa:

1. At the Genus level – species and phylogenetic diversity of members of *Myristica* (Myristicaceae) and *Calophyllum* (Clusiaceae) are being examined along the natural east-west gradient of the SW Pacific.
2. At a Species level – three species with broad geographic distribution, from three families, are targeted for phylogeographic and genetic diversity study.
3. At a Population level – the spatial genetic structure of each of these three species is being studied across a series of 1-ha plots that have already been established for ecological study.

#### **Conservation genetics of threatened South Australian plants: Ottewell K, Bickerton D, Lowe AJ**

Rare and threatened plants are typically characterised by small population sizes and population isolation, both of which have consequences for the genetic 'health' of populations and their long-term survival. Small isolated populations are susceptible to the process of genetic drift which depletes genetic diversity over time and leads to increased differentiation between populations. The loss of genetic diversity in small populations can also be exacerbated by inbreeding, from either increased self-fertilisation or mating between a restricted number of individuals. Molecular marker methods can shed light on a range of population processes and dynamics that are important for informing conservation management. For example, assessing genetic differentiation between remnant populations informs decisions on translocation and taxonomic status, and estimation of genetic diversity within and gene flow between remnant populations reveals information on the genetic health of populations, and likely extinction/survival trajectory. Within this framework, this study has been:

1. assessing genetic differentiation between remnant populations of seven species, which will be used for guidelines on translocation potential (Monarto Mintbush, Fat-leaved Wattle, Large Club Spider-Orchid, Beyeria bush-pea, Whibley's Wattle)
2. clarifying the taxonomic status of threatened species or remnant populations (*Cassinia tegulata*, Beyeria bush-pea, *Daviesia sejugata*)
3. assessing the genetic health (from genetic diversity and inter-population gene flow estimations) of endangered remnant populations of six species (Monarto Mintbush, Fat-leaved Wattle, Large Club Spider-Orchid, Beyeria bush-pea, Whibley's Wattle), and likely influence of genetic factors for future population survival
4. assessing whether these species share population genetic characteristics that make them sensitive to extinction and threat.

### **Designing seed sourcing, forest restoration and landscape configuration to maximise diversity: Gardner M, Scoble J, Pavlacky D, Wells J, Lowe AJ**

Supply of appropriate germplasm is a critical factor in reforestation programs. Use of inappropriately sourced material (due to lack of knowledge or availability) can prompt ecological and/or commercial failures, as trees die or fail to meet the particular objectives of the restoration project. With recent interest in the conservation and restoration of native habitat, there is a growing trend towards planting trees for wider objectives than simply maximising production. The contrasting interests of production and ecological restoration mirror underlying scientific issues. The source of planting stock needs to be considered at both the population level and the individual level, i.e. which populations and which trees within that population? The key scientific question is how gene flow and selection interact to influence population delimitation and reproductive fitness. The overall objective of the EU-funded SEEDSOURCE project is to apply appropriate molecular and quantitative genetic tools to study both aspects of scale (populations and trees within them) in the sourcing of germplasm for varied use of widespread tree species of high socioeconomic importance in the neotropics. This information will be disseminated in a practical and relevant format to forestry and agroforestry stakeholders across tropical Latin America (e.g. policy makers, seed banks, forest management certifiers and educators).

Other projects are examining the scale and dynamics of gene flow across different forest contexts, testing permeability of landscape contexts (native vegetation mixed with other socioeconomic uses) to improve biodiversity corridor design and using the range wide distribution of gene diversity within species as a tracer for identifying illegally harvested timber.

### **Climate change**

#### **Phenological shifts due to climate change: MacGillivray F, Lowe AJ**

Shifts in phenology provide a reliable signal for the early detection of change in biological systems. However, long-term datasets for determining the nature and magnitude of climatic impacts are very limited in Australia. Current research incorporates an interrogation of archival records to redress this important issue. Herbarium collections, with their broad temporal, geographic and phylogenetic representation, are a unique and readily accessible source of data, independent of season. Photographic collections, including time series obtained by repeat or time-lapse photography, could also contribute. Both sources have been found to provide robust estimates broadly in keeping with those published in the literature. However, such records are often variable, discontinuous and incomplete, and research so far has generally been restricted to dates of full flowering of species represented in arboretum plantations. The impact of rising temperatures is highly significant in the northern hemisphere but the non-uniform periods of warming throughout the 20th century pose a particular challenge when linear regression analysis is used to reconstruct trends. In Australia, other climatic factors such as rainfall and periods of drought take on greater relative importance, and natural variation across sites, including local microclimatic conditions, genetic differences and other non-climatic factors contribute to the uncertainty. This project is investigating possible non-linearities between herbarium records and climate.

## Environmental weeds

### Weed evolution, adaptation and invasiveness: Prentis P, Dormontt E, Lowe AJ

Invasive weeds affect both agricultural and native ecosystems equally but the mechanisms of weed invasion are not well understood. Only a small proportion of introduced plants become significant weeds and why this should be is unclear. Using the important east-coast weed, *Senecio madagascariensis* (fireweed), as our model, we are testing different demographic and genetic hypotheses as to why some plants become weeds. The project combines leading-edge genomic techniques with demographic modelling to identify specific genes responsible for weediness in fireweed. This project specifically tests four alternative hypotheses about how weeds have become invasive:

- (i) The influence of admixture of source ranges on invasion potential is being tested by ascertaining the geographic and temporal introduction sequence of South African source(s) of fireweed into Australia. Microsatellites are being used to compare genetic diversity in source and invasive range populations and herbarium specimens.
- (ii) The potential influence of hybridisation (possibly through introgression) with Australian native species as an evolutionary fast-track mechanism to introduce adaptive variation in the invasive species is being investigated by using microsatellite variation to assess the landscape and temporal (using herbarium specimens) incidence of hybridisation between fireweed and Australian native species.
- (iii) The potential for regulatory and rapid genomic adaptation and selective changes between invasive and native range material is being assessed using screens of genomic expression change and direct tests of selective sweeps for genes that show significant regulation changes.
- (iv) The potential for a demographic expansion only scenario and the potential for recent bioclimatic adaptive shift are being tested using a combination of GIS bioclimatic modelling for source and invasive ranges and direct superimposition of environmental variables and allelic variation at genes under selection at a landscape scale.

Another project is investigating the source introduction dynamics of *Acacia* species into South Africa and non-native range introduction around the south coast of Australia.

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