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Genetics and biosystematics for the conservation, circumscription and management of the Western Australian flora

Plant Science and Herbarium

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Context

The flora of Western Australia is complex due to the antiquity of the landscape, and this can lead to obscurity in taxonomic identity, which impacts on conservation status of rare and threatened taxa. Genetic analysis can inform the conservation and biosystematics of these taxa.

Aims

- Provide genetic information for the conservation and management of Western Australian flora, especially rare flora.
- Determine the phylogenetic and population genetic relationships among the disjunct populations of *Eucalyptus virginea* and related species, including the potential hybrid status of *E. x phylacis*.
- Determine the phylogenetic relationships among Western Australia *Leptospermum* species and examine the genetic boundaries among several species complexes.
- Determine the potential for hybridisation and genetic differentiation among *Seringia exastia*, *S. katatona*, *S. elliptica* and *S. nephrosperma*.
- Determine the geographic range of two identified genetic lineages within *Eucalyptus salubris* and investigate genomic relationships among nine species within the gimlet complex.
- Investigate potential hybrid origins and parental sources of several *Eucalyptus* entities within the Stirling Ranges.
- Determine the genetic relationship between *Verticordia spicata* subsp. *spicata* and the critically threatened *V. spicata* subsp. *squamosa*
- Determine the genetic relationship between populations of *Davesia obovata* in the Stirling Ranges and the Fitzgerald River National Park
- Determine the genetic relationships among several subspecies and unnamed entities within *Conospermum* caeruleum.
- Determine the genetic relationships among Australian *Arivela* species and the genetic relationships in two species complexes.
- Determine the genetic relationship among disjunct populations of *Banksia mimica* and the degree of clonal reproduction in different populations.
- Investigate the role of lignotuber loss or gain in the evolution and conservation of eucalypt diversity, through deriving phylogentic relationships and quantifying genetic differentiation among a clade of eucalypts with obligate-seeder and lignotuber-resprouter taxa, using high density, genome-wide markers.
- Determine the genetic diversity and differentiation among sub populations of *Marianthius aquilonaris* in the Bremer Range.

Progress

- A paper detailing genomic assessment of the relationships among *E. virginea*, *E. relicta*, *E. lane-poolei*, and *E. x phylacis* has been written and will soon be submitted to *Biodiversity and Conservation*.
- Phylogenomic analysis of eastern Australian Leptospermum taxa is ongoing. A paper detailing phylogenomic relationships in the Leptospermum genus, with a focus on Western Australian taxa, is in preparation.
- Field collections, sequencing and genomic analysis for the *L. erubescens* species complex has been completed. These data showed clear separation of *L. maxwellii* and a clinal relationship between *L. erubescens* and *L. oligandrum*.
- A paper combining the genomic analysis of the *S. exastia* species complex with subsequent taxonomic revisions has been published in *Taxon*.



- A paper detailing the genomic, morphological and ecological divergence of cryptic lineages in *E. salubris* is currently under review in *Molecular Ecology*.
- Genomic analysis of the nine species of the gimlet complex is near completion.
- Genomic analysis is complete for the putative Eucalyptus hybrid entities in the Stirling Ranges. This
 study confirmed eight suspected hybrid combinations and identified the parental taxa involved. A paper is
 currently under review in Annals of Botany.
- Genomic analysis and morphological assessment of *V. spicata* has shown that there is a lack of evidence
 to support the continued recognition of *V. spicata* subsp. squamosa as a subspecies distinct from *V. spicata* subsp. spicata. A paper to publish these data and revise the taxonomy will be prepared.
- Genomic analysis of *D. obovata* is underway. Early analysis indicates strong differentiation between the disjunct Stirling Range and Fitzgerald River NP populations.
- Field collections, sequencing and preliminary genomic analysis of the *C. caeruleum* species complex has been completed and a report has been written. Genomic data warrant the recognition of at least three distinct species, and three independent Management Units within the southwest species.
- Relationships among *Arivela* spp. have been determined using cpDNA and ITS sequencing and a manuscript is in revision for resubmission in *Molecular Phylogenetics and Evolution*. Genomic sequencing of *A. viscosa* and *A. tetandra* has been carried out and analysis is being undertaken.
- Relationships among populations of *B. mimica* and the degree of clonal diversity within different populations has been determined using nuclear microsatellite markers. A paper detailing the strong differentiation and variable clonality has been accepted for publication in *Conservation Genetics*.
- A review of genetics and ecology of species that occur on Banded Iron Formations of the mid-west has been published in *Biological Reviews*. A special issue of *Australian Journal of Botany* was published on genetics and ecology of plant species on banded iron formations.
- Taxonomic revision of Eucalyptus subseries Levispermae has been completed and published in Nuytsia.
- The second component of the *Marianthus* project has been completed, results showed high levels of self-pollination and the majority of pollination is by fathers within the sub-population, however there is a small amount of pollen coming from other sub-populations.

Management implications

- Population genetic analysis of relationships among disjunct populations of *E. virginea* will inform management of the populations, and will inform on the potential hybrid status, putative parental species and conservation status of *E. x phylacis*.
- Assessment of the genetic relationships among *Leptospermum* species will inform taxonomic revision of the group, and define taxonomic entities to inform use of natural resources for honey production.
- Recognition of *S. xkatatona* as a hybrid and synonymisation of *S. exastia* and *S. elliptica* mean that neither taxon meets the criteria for needing protection and conservation listing of both can be reconsidered.
- Resolution of lineages in *E. salubris* and genetic relationships among all nine species in the gimlet complex will provide a basis for potential taxonomic revision.
- Analysis shows lignotuber state is an important taxonomic character in eucalypts, supporting recognition as separate taxa for populations that differ in this trait.
- Identifying putative hybridisation within several *Eucalyptus* entities, including *E. erectifolia*, within the Stirling Ranges will allow for potential taxonomic revision and reconsideration of conservation listings.
- Resolution of the taxonomic status of *V. spicata* subspecies will allow re-assessment of the need for conservation listing of *V. spicata* subsp. *squamosa* and ongoing management of this subspecies.
- Population genetic analysis of *D. obovata* will inform the management of these highly disjunct populations.
- Genomic analysis of the *C. caeruleum* subspecies will provide a basis for taxonomic revision of this highly morphologically variable group, particularly in regard to potential new taxa that may be threatened and require conservation listing and management.
- Identifying genetic entities in *A. viscosa* and *A. tetandra* will provide a basis for taxonomic resolution of these species complexes.
- Strong genetic differentiation and variable degrees of clonal diversity among populations of *B. mimica* indicate taxonomic revision is required and informs on management of different populations.
- High genetic differentiation over very short distances in *M. aquilonaris* provides information for management of the species.



Future directions

- A paper detailing genomic analysis of *E. virginea* and related species will be submitted for publication.
- Phylogenomic analysis of *Leptospermum* will be progressed and 1-2 papers written.
- Fieldwork and population genomic analysis of a final *Leptospermum* species complex will be undertaken and a paper to delineate the major Western Australian taxa will be written.
- Nominations for the delisting of *S. exastia* and *S. xkatatona* as species of conservation concern will be submitted.
- Genomic analysis of the gimlet complex will be completed and a paper written.
- A paper regarding the *V. spicata* subspecies will be written and the taxonomy revised.
- Further genomic analysis of *D. obovata* will be undertaken.
- Additional genomic analyses to further clarify relationships among southwest populations of *C. caeruleum* will be conducted, a paper will be written and the taxonomy revised.
- Analysis of genetic relationships in A. viscosa and A. tetandra will be completed.