

CORYMBIA GENETICS AT SOUTHERN CROSS UNIVERSITY

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Research on *Corymbia* spp. genetics at Southern Cross University focuses on molecular tree improvement but also encompasses studies on population structure, comparative mapping and phylogenetics. The Politaria section (Spotted gums) of *Corymbia* contains four taxa including *C. maculata* and *C. citriodora* ssp *variegata* (CCV). The first of these is one of the top ten planted eucalypts worldwide, whilst CCV is a priority plantation species for saw logs in Queensland and NSW. Two projects are underway to support improvement programs for spotted gums and their hybrids. The first project will study the genetics of propagation characteristics in an intersectional *Corymbia* hybrid (*C. torelliana* x CCV, a taxon of emerging importance for forestry in subtropical regions of eastern Australia. The approach taken here is to develop models of genetic architecture from genetic mapping and quantitative trait loci (QTL) analysis in a segregating family. In a second project, association tests will be used to establish genotype-phenotype links between candidate genes for solid wood characters in “natural” populations of CCV. A project examining the population structure of the spotted gum complex is being undertaken to support association studies (this will be reported upon separately by Joel Ochieng).

Cytologically *Corymbia* may be distinguished from *Eucalyptus* by a more symmetrical karyotype and a genome with around ½ the DNA content. We are examining the extent of genome size variation within the *Corymbia*, *Angophora* sp. and hybrids to explore the taxonomic value of this character. We will also use comparative mapping to study whether structural rearrangements (translocations and inversions) or gross genome organisation (the grouping and ordering of genes within its genome) changes have accompanied the change in DNA content during the evolution of the *Corymbia* genome since its divergence with *Eucalyptus*.

Once considered a subgenus of *Eucalyptus*, the relationship of the *Corymbia* genus (bloodwoods and the “ghost gums”) within eucalypts in the broadest sense (*Angophora*, *Corymbia* and *Eucalyptus*) remains controversial. The existence of a dichotomy, the Angophoroid clade (*Angophora* and *Corymbia*) and a non-Angophoroid clade (*Eucalyptus* ss), is widely accepted; however the relationships within the Angophoroid clade remain much less clear, with incongruence between morphological and DNA sequence data. A key issue is whether the *Corymbia* genus is monophyletic. In collaboration with researchers from the University of Tasmania, we propose to extend the intergenic transcribed sequence (ITS) phylogeny within the Angophoroid clade and identify new loci to provide additional characters to increase the confidence of the molecular phylogeny.

COMPARATIVE MAPPING

Orthogonal microsatellite loci are being identified as a foundation for comparative mapping. A set of around 105 polymorphic microsatellite loci have been identified for the development of a framework map in *Corymbia*. These loci were identified from either *Corymbia citriodora* subsp. *variegata* (n=28) or from either *Eucalyptus grandis* or *E. globulus* (n=272). Of these, around 90 are highly conserved and amplify in both *Corymbia* and *Eucalyptus* and will facilitate comparative analysis. A downside to transferring loci from *Eucalyptus* to *Corymbia*

was a reduction in polymorphism (PIC value reduced from 0.8 to 0.6 for transferred loci) but if a locus transferred, it had a low rate of single-allele nulls in a CT x CCV mapping cross.

GENETIC MAPPING OF VEGETATIVE PROPAGATION CHARACTERS IN A *C. TORELLIANA* X *C. CITRIODORA* SUBSP. *VARIEGATA* F₂ HYBRID

Segregation analysis is being conducted in an F₂ population (n=208) generated from parents divergent in propagation characteristics. Genotyping of around 25 microsatellite loci has been completed. Nursery trials to evaluate shoot production, rooting percentages and root quality of stem cuttings are also underway. Seedling germination and rooting of stem cuttings was low in this second generation hybrid compared to F₁, perhaps indicating outbreeding depression. However, while the family average was low (~15% for rooting percentage), variation within the family was extensive and clonal repeatabilities were moderate and highly significant (r=0.48 p-value <0.01). Shoot production also appears to be under strong genetic control (r=0.75; p-value < 0.01).

MOLECULAR PHYLOGENY

We have collected material from an additional 36 species from *Corymbia* and 2 *Angophora* to extend the ITS phylogeny. Sequencing has been completed for 5 species to date but we are encountering difficulties due to fungal contamination and universal ITS primers. We are currently attempting to re-design more specific primers to complete this work.

MOLECULAR VARIATION IN CCR IN THE SPOTTED GUMS: A PRECURSOR FOR ASSOCIATION STUDIES

Cinnamoyl CoA Reductase (CCR) is involved in lignin biosynthesis and has been associated with cell wall stiffness and strength properties in *Arabodopsis* and *Eucalyptus globulus* and therefore is a leading candidate gene for control of solid wood characters in spotted gums. We are currently characterising variation in this 3.2 kb gene in spotted gums.

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