PROJECT PROFILE

Title of the project: **Identification and Tagging of QTLs/Candidate genes for wood property and adventitious rooting traits in Eucalyptus and establishment of phenomics facility for water stress tolerance studies**

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Duration: 2016-2021

Objectives:

1. Documentation of variation in wood property traits across multiple environmental conditions and estimation of heritability values for selected wood property traits.
2. Identification of high throughput markers by targeted exome sequencing in inter-specific hybrids of Eucalyptus.
3. Generation of high density genetic linkage maps and localization of QTLs for wood properties and adventitious rooting traits.
4. Validation of marker-trait associations for wood property traits across different bi-parental families.
5. Screening of Eucalyptus clones for water stress tolerance and development of water stress tolerance indices for selection of tolerant clones in nursery.
6. Cataloging of undistorted SNPs and InDels for linkage/ QTL map construction and marker validation in inter-specific hybrids with different genetic backgrounds.

Summary

- Phenotyping for multiple wood property traits was completed in three mapping populations established across six locations and clones were ranked based on their superior wood properties.

- Broad sense heritability (H^2), inter-trait correlation and predicted genetic advance in absolute (GA) and percent mean (GAM) was evaluated for wood property traits in *E. camaldulensis* (Ec111) X *E. tereticornis* (Et86).

- In-solution target capture and exome deep sequencing of 763 genes involved in secondary development was conducted in parents and hybrids and 32,204 polymorphic SNPs and 2,348 polymorphic InDels were predicted. SNP datasets were used for linkage map construction, QTL localization and genome –wide association analysis.

- GWAS analysis was conducted using 13,610 SNPs using 23 wood property traits assessed in 102 genotypes across 3 locations. All markers were associated with fibre traits with 9 markers in Hosakoppa, 4 in Chennagiri and 8 in Nellore. Three markers were found common across Nellore and Chennagiri.

- Refined linkage maps were generated for two crosses targeted for adventitious rooting traits and wood property traits. Genome wide SNP markers (5278) and candidate gene specific SNP markers (3103) were mapped in the inter-specific crosses *E. tereticornis* (clone 217) x *E. camaldulensis* (clone 17) and *E. tereticornis* (clone 86) x *E. grandis* (clone 9) respectively.

- QTL analysis for adventitious rooting traits such as rooting percent and root volume indicated the presence three QTLs for rooting percent explaining 19.3 to 58.7% phenotypic variation, while two QTLs identified for root volume explained phenotypic variation of 10.2 and 12.3%. Further, nine and three QTLs were detected for cellulose and lignin content.

- Screening of 160 *Eucalyptus* clones was conducted under progressive water retrieval condition and morphometric and physiological parameters were documented. Six top performing clones were re-screened for stress tolerance. Further, intra-specific and inter-specific variations in morphometric, physiological, biochemical, metabolites and molecular profiles were documented.

- Screening of clones under controlled environmental and nursery conditions revealed that leaf surface temperature and RWC can be used as screening indices for water stress response under nursery conditions.

- The bacterial endophyte diversity in leaf tissues between susceptible and tolerant clones belonging to *E. camaldulensis* and *E. tereticornis* was documented. Several taxonomic biomarkers were identified which could differentiate the species and the water stress tolerant groups.