PROJECT PROFILE

Title of the Project:	**Genetic Improvement of Eucalyptus through Mapping and Tagging of QTLs/Genes**
Project Components	1. Development of mapping populations in Eucalyptus for identification of QTLs linked with Adventitious rooting and Wood property traits 2. Highthroughput multi environment phenotyping of mapping populations of eucalypts for adventitious rooting and wood property traits 3. Development of Genetic Linkage Maps and QTL analysis in Eucalyptus for Adventitious Rooting and Wood Property traits 4. Candidate Gene Association for identification of pulping trait markers in Eucalyptus tereticornis
Project Partners	• Tamilnadu Newsprints and Papers Limited, Tamil Nadu Tamilnadu Forest Plantation Corporation Ltd., Tiruchy • Andhra Pradesh Forest Development Corporation Limited, Hyderabad • Mysore paper Mills limited, Shimoga
Project Co-ordinator	Director, IFGTB
Technical Co-ordinator	Dr. R. Yasodha, Scientist F
Project Investigators	Dr. R. Yasodha, Scientist F Dr.B. Nagarajan, Scientist F Dr. Modhumita Dasgupta, Scientist E
Project team	Dr. Rekha Warrier Dr. A. Shanthi V.K.W. Bachpai Dr. V. Sivakumar Mr. A. Mayavel Mr. D. Rajasugunasekar
Duration of Project:	2010-2015
Objectives	1. To control pollinate E. tereticornis and *E. camaldulensis*

clones with *E.grandis* selections for developing mapping populations.

2. To raise experimental trials of two mapping populations for multi environmental phenotyping to determine QE effect
3. Phenotyping of mapping populations for adventitious rooting traits
4. Determination of the variation in wood property phenotypes in mapping populations generated from controlled crosses under multiple environmental conditions
5. Generation of genome wide linkage maps for the eucalypts mapping populations
6. Identification of QTLs for wood properties and adventitious rooting traits
7. QTL analysis for marker-trait associations and marker validation
8. Phenotypic characterization of selected populations from *E. tereticornis* provenances for pulping traits
9. SNP discovery in cellulose synthase genes expressed in secondary xylem of *E. tereticornis*
10. SNP genotyping and identification of putative SNPs/haplotypes associated with pulping traits.
11. Validation of candidate SNPs in the mapping population of *E. tereticornis X E. grandis.*

Funding agency: Department of Biotechnology, Govt. of India

Summary:

Under the network program on genetic improvement of *Eucalyptus* for developing markers tagging economically important traits, quantitative traits such as improved pulping, greater rooting, lower lignin and higher salt tolerance were targeted. Pedigreed clones of *E. camaldulensis* (Ec-7, Ec-17 and Ec-111) and *E. tereticornis* (Et 217 and Et 86) and an *E. grandis* (13017 Lorne) were deployed for hybridizing the above mentioned traits. Di-hybrid combinations of *E. camaldulensis* × *E. tereticornis*, *E. tereticornis* × *E. camaldulensis*, *E. camaldulensis* × *E. grandis* and E. tereticornis were developed. Multi-location clonal trials were devloped with commercial clones as benchmark for selecting superior hybrid clones.

Development of genetic linkage maps for the inter-specific cross *E. tereticornis* × *E. camaldulensis* and *E. tereticornis* × *E. grandis* was carried out. The consensus map showed

a map length of 2312.2 cM with 100 SSR loci for *E. camaldulensis* × *E. tereticornis* cross. The cross *E. tereticornis* × *E. grandis* had 130 SSR loci with the map length of 1563.8 cM having average marker distance of 11.8 cM.

High throughput technology of in-solution capture and deep sequencing was employed to identify markers for linkage/ QTL mapping for wood property traits. A total of 763 genes including 692 genes from 156 functional categories and 36 genes expressed during wood formation with unknown functional domains were selected for exome sequencing in two parents (*E. tereticornis* and *E. grandis*) and 30 F1 hybrid progenies. A total of 32,204 polymorphic SNPs were registered across 763 genes, while the number of polymorphic InDels was 2,348. The SNPs and InDels spanned all the 11 chromosomes of the genome. The polymorphic markers are used for construction of linkage/ QTL map in bi-parental population of *E. tereticornis* × *E. grandis.*

The genome –wide transcript expression pattern in *E. grandis* subjected to PEG induced water stress condition was documented using a customized array representing 3359 water responsive genes. The number of differentially expressed genes across control and treated samples were 1014 and the fold expression ranged from -3.09 to 5.10. A Co-expression network was constructed with 932 nodes and 60,309 edges and the top hub transcripts were disease resistance protein, alpha hydrolases-like superfamily protein, photolyase/blue-light receptor, raffinose synthase family protein and osmotin. The study can be used to identify candidate genes involved water stress response and develop functional markers tagging water stress tolerance in Eucalyptus species.