PROJECT PROFILE

Project Title:	Genetic diversity assessment for management of Eucalyptus seed orchards
Principle Investigators: Project Associates:	Dr. Rekha R. Warrier Dr. R. Yasodha Dr. V. Siyakumar
Start and Completion dates:	April 2012 – March 2019
Objectives	 Estimate genetic diversity in orchards using molecular markers Assessment of quality of seeds from seed orchard Assessment of gene flow over generations
Funding Agency:	Indian Council of Forestry Research and Education (ICFRE)

Summary

A clonal seed orchard of Eucalyptus was evaluated for two seasons for four years for fertility variation and its impact on the seed crop. The frequency of flowering trees was high in the orchard. Flowering varied with seasons and was influenced by climatic variables. Few clones did not produce any flowers during the entire study period.

The sibling coefficient (Ψ) in the orchard varied from 5.21 to 26.01 in February while it was low in November (1.95 to 17.21). The corresponding relative effective population size, (*Nr*) varied from 0.038 to 0.192 in February and was higher in November (0.513) suggesting higher fertility variation during February.

Culling improved seed production in 85 per cent of the clones. The germinability of seeds also recorded greater than 50 per cent increase in 20 per cent of the clones. The progenies from the culled orchard showed uniformity in field performance, as is evident from the low CV values. The percentage polymorphic loci in the progenies was higher (>0.95) when compared to the parents (0.91). High combined non-exclusion probabilities for the first parent, second parent and parent pairs were observed in both the culled and unculled orchard progenies.

Pedigree reconstruction captured progenies for 62 out of 93 candidate mothers present in the unculled orchard. Paternity analysis in the orchard assigned male parent for 122 out of 140 progenies with 95% confidence interval, which equals to 90% of the progenies. In the culled

orchard, 88 candidate mothers were identified in the orchard. 86% of the progenies could be mapped to the pollen parent.

Some of the progenies could not be assigned pollen parents. This could be due to contamination from nearby orchards highlighting the need for adequate isolation distance while planning breeding orchards.