PROJECT PROFILE

Title:	**Generation of genomic resources and mapping of genetic diversity of sandalwood populations for conservation and improvement (AICRP-3; Activity 1.2)**
Principle Investigators:	Dr. Modhumita Dasgupta, Scientist G, ICFRE-IFGTB, Coimbatore Dr. Suma Arun Dev, Principal Scientist, KFRI, Peechi Dr. K. Ulaganathan, Professor, CPMB-OU, Hyderabad
Co Investigators:	Dr. A. Balasubramanian, ICFRE-IFGTB Dr. R. Jayaraj, KFRI
Duration:	2020 - 2025
Objectives:	1. Integrated RNA, small RNA and long non-coding RNA sequencing and analysis in different tissues and genotypes. 2. Analysis of RNA editing in organellar genes and its implications in regulating the sesquiterpene pathway. 3. Genetic diversity and population structure analysis of seed sources and selected populations using SSR/SNP markers. 4. Development of web-based genomic portal of sandalwood
Funding Agency:	Ministry of Environment, Forest and Climate Change, GoI under the CAMPA scheme 'Scheme Strengthening forestry research fpr ecological sustainability and productivity enhancement (SFRESPE

SUMMARY

- Voluminous genomic datasets were generated and the first insight into the post-transcriptional regulation of sesquiterpene pathway and climate adaptation in sandalwood was deciphered. Construction of single-base resolution methylome maps, competing endogenous RNA (ceRNA) networks and identification of RNA edited sites in organellar genes are landmark genomic knowledge in the genus *Santalum*.

- An online interactive portal was developed in collaboration with CSIR-Indian Institute of Chemical Biology, Kolkata. The portal was hosted at http://sandalgdb.org:3000/ under 'National Network Project' (NNP) program of Biotechnology Information Network for Biological Scientific Community (BTISNet) implemented at CSIR-IICB, Kolkata.

- Genome-wide SSR markers were used to assess the genetic diversity in selected CPTs, bulked seedlots and base population. Populations from Rajasthan exhibited low genetic diversity. Diversity in the progenies was low, indicating mild inbreeding or genetic drift within the base population. Chikkanahalli Sandal Reserve in Karnataka and Marayoor Sandal Reserve in Kerala exhibited the highest number of unique and private alleles in both standing tree and base population genetic diversity analysis, indicating the presence of rare gene pool within these populations.

- Base populations in the Dindigul-Mudumalai and Nilgiri belts of Tamil Nadu showed higher genetic diversity than standing trees, suggesting higher outcrossing rates that may restore heterozygosity, improve demographic variability, and enhance evolutionary potential.