PROJECT PROFILE

Title: **Documentation of population demography and genetic structure of teak for developing sustainable conservation strategies and resource management**

Principle Investigators: Dr. R. Yasodha, Scientist – G
Institute of Forest Genetics and Tree Breeding, Coimbatore
Dr. Suma Arun Dev, Scientist E
Kerala Forest Research Institute, Peechi, Kerala
Dr. R. Vasudeva, Professor
College of Forestry (Sirsi, Karnataka), University of Agricultural Sciences, Dharwad, Karnataka

Co Investigators: Dr. V.K. W. Bachpai
Dr. A. Nicodemus
Dr A.Rajasekaran
Dr. P. K. Chandrasekhara Pillai

Duration: 2015-2020

Objectives:

- Documentation of demography and population genetic structure of teak
- Decipher the spatial genetic structure of teak using genetically divergent populations of teak.
- Develop strategies for the execution of teak genetic conservation and management plan by the State Forest Departments

Funding Agency: Department of Biotechnology, Govt of India

SUMMARY

A total of 18 natural teak populations covering the areas in Kerala, Karnataka, Tamil Nadu Gujarat and Madhya Pradesh were selected for the study. Highest amount of genetic diversity was observed in the very moist populations of Kerala (Na 9.106; Ho 0.664; He 0.710) followed by moist/ dry Tamil Nadu (7.53, 0.571, 0.669) and Karnataka (5.935, 0.554, 0.662) populations. Dry populations of Gujarat (6.17, 0.572, 0.599) and Madhya Pradesh (4.09, 0.581, 0.543) were observed to have almost similar genetic diversity measures. Inbreeding coefficient (*Fis*) within population ranged from -0.079 (H) to 0.151 (ATR). Mean genetic

differentiation coefficient for overall population (F_{st}) was 0.202. Thus, ~80 per cent of the genetic diversity was distributed within populations and 20 per cent across populations.

The peak of ΔK value was highest when K=8 ($\Delta K=18.5401$), indicating the presence of a minimum of 8 distinct clusters (ancestral populations) and 425 genotypes were inferred and assigned into clusters. Maximum genetic admixture was observed in nine Kerala populations which differed from the admixture pattern of Tamil Nadu, Karnataka, Gujarat, and Madhya Pradesh populations. Identical population structure was shared between few populations namely, Thenmala, Achenkovil and Konni populations of Kerala, between Tamil Nadu (ATR, STR, KMTR) and Karnataka (TTM and TEL) populations, between two Karnataka populations (HAL and SHI) and between Gujarat (CU) and Madhya Pradesh (H) populations. The genotypes of Ariyenkavu, Wayanad and Idamalayar populations (Kerala) clearly differed from the other populations in their genetic admixture pattern. Population structure analysis of all populations excluding Kerala showed 5 subpopulations wherein ATR, KMTR populations had minimum admixture and TTM and TEL had maximum admixture pattern. PCoA grouped 18 populations into three distinct clusters comprising genotypes of Kerala, Madhya Pradesh-Gujarat-Karnataka , and Tamil Nadu-Karnataka populations.

Hands on training and recommendations on seed zonation provided to Tamil Nadu Forest Department. The main objective of the training was introduction on the importance of teak genetic resources, conservation, management, seed collection and storage methods, seed germination, nursery raising and modern silviculture methods. Detailed project report was sent to the forest department.