Title of the project: Improvement and popularization of *Swietenia mahogani* for rural livelihood promotion in Tree–Outside-Forests (TOFs) – A potential timber yielding tree species of Meliaceae. (TNFD VII)

- 1	
Theme/Area:	Forest Genetic Resource Management and Tree Improvement
Year:	2015 – 2018
Project duration:	3 years
Sanctioned budget:	Rs. 13.95 lakhs
Funding Agency:	Tamil Nadu Forest Department
Principal Investigator: Dr. S.P. Subramani, CTO	
Co-Investigators:	Dr. M V Durai, Dr. R.Anandalakshmi and Dr. A. Shanthi Scientists
Project findings:	

Extensive survey was made in different parts of Tamil Nadu and Karnataka and selected 29 CPTs of Swietenia mahagoni (19 from Tamil Nadu and 10 from Karnataka) which showed distinct and desirable characteristics. The morphological characteristics and variations of S. mahagoni fruits and seed like weight, size, shape etc were studied using image analyzer. The fruit and seed showed significant variation among the selected trees which will be useful for genetic improvement of the species. Seed germination was standardized. Studied the flowering phenology and reproductive biology and pollinator interaction based on regular observation. Bees are the major pollinator in S. mahagoni. Wood core samples were collected from selected CPTs and studied the wood moisture content and wood density. Wood moisture varied from 21.678 and 101.149 and wood density recorded from 0.383 to 0.695. Vegetative propagation was standardized for the species S. mahagoni through stem cuttings using terminal juvenile shoots collected from selected CPTs in different concentrations of IBA using different potting media i.e. sand, sand+coir-pith, sand+coir-pith+vermiculate. For genomic study, DNA were extracted from fresh leaves using Dneasy mini kit (Quiagen). The purity and quantity were measured using nanodrop and also running 0.8% agarose gel electrophoresis. Fifteen RAPD primers were optimized and PCR analysis was done for the forty samples. A progeny trial of S. mahagoni was established at Neyveli, by randomized block design (RBD) method in the espacement of 3m x 3m in five replications and the data were analyzed for best performing seed sources for further studies.