PROJECT PROFILE

Title: Development of methods for functional analysis of genes

involved in salt tolerance in Eucalyptus

Principal Investigator: Dr. Mathish Nambiar-Veetil, Sci- E

Co Investigators: Dr. B. Nagarajan, Sci- E

Dr. V. Sivakumar, Sci- D

Dr. Modhumita Dasgupta, Sci- E Dr. V.K.W. Bachpai, Sci- C

Associates: Mr. A. Balasubramanian, R.A. I

Mr. R. Venkatachalam, JRF

Smt. S. Sudha, TA I (2011 onwards)

Ms. Dhanya Nair, Skilled Assistant (2009-2010)

Ms. Sanu Abraham, Skilled Assistant

Start and Completion dates: 5 Years (2009- 2014)

Objectives:

1. Develop methods for generating composite *E. tereticornis* plants cotransformed with GFP based vector.

- 2. Develop in vitro system for phenotyping of salt tolerance in composite plants.
- 3. Clone, sequence and quantify expression of the Eucalyptus HKT1 orthologue.
- 4. Develop EtHKT1-silencing constructs, and generate composite *E. tereticornis* plants cotransformed with the construct.
- 5. Optimise biolistic/ *Agrobacterium tumefaciens* mediated transformation for heterologous expression of AtNHX gene in *E. tereticornis*.

Funding Agency: Indian Council of Forestry Research and Education

(ICFRE)

Total Budget: Rs. 30.93 lakhs

Summary

Eucalyptus is among the most widely planted tree species in India, because of its utility in pulp and paper industries and their ability to grow in wastelands. Engineering for enhanced salt tolerance in Eucalyptus would, therefore, contribute to enhanced productivity in stressed sites. Understanding major genes contributing to its salt tolerance is important for targeted engineering for desired traits. However, the bottle neck is the low efficiency of transformation in Eucalyptus. Key achievements in the project include development of a method for rapid generation of composite Eucalyptus transgenic plants derived from *Agrobacterium rhizogenes* mediated transformation. The strategy developed was used for evaluating the role of *EcHKT1:1* in salt tolerance in Eucalyptus. Further, methods were refined for gene transfer using *Agrobacterium* and biolistics.