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Incharge, Genetic transformation and Functional Genetics Experimental
Facility



Vision:

To reach out to farmers through transgenic trees with enhanced productivity and quality traits for growing in areas affected by biotic and abiotic stresses.

Mission:

To evolve transgenic approaches in Forestry species for genetic modification of desired traits and functional analysis of genes.

Focus species: *Casuarina* sp., *Eucalyptus* sp.,

Other species : *Prosopis juliflora*, *Acacia nilotica*, *Pongamia pinnata*

Traits of interest: *Abiotic and Biotic stress tolerance*

Current activities and Research Interests

Gene prospecting from salt tolerant tree species:

Development of varieties that are able to tolerate salt, and drought stresses would provide an opportunity for increasing the area under tree cover and productivity under these conditions. Salt tolerant trees are unexplored resources of genes conferring salt tolerance. To understand the genetic basis of salt tolerance, **clones of *Casuarina equisetifolia* contrasting for their salt tolerance and sodium accumulation were identified**. Homologues of genes implicated in sodium transport were partially sequenced from salt tolerant tree species and the sequences were deposited in the NCBI database. Sodium hydrogen antiporter (*NHX1*) gene homologues were sequenced from *E. camaldulensis*, *E. tereticornis*, *C. equisetifolia*, *P. pinnata* and *P. juliflora*, while *HKT1* gene homologue was sequenced from *E. tereticornis*. These represent the first sequence information for the respective genes for these tree species.

In order to provide a single point web-resource of such genes, a database "***In silico* Gene Bank for Adaptation to Abiotic Stresses (IGBAAS)**" is in its final stages of development.

Functional analysis of genes via Genetic transformation

The assignment of function to these genes requires functional validation via overexpression or silencing in the trees biological context. However, plant regeneration from transformed tissues is the rate-limiting step for rapid gene function analysis in tree species. Through a collaborative study at the Institut de Recherche pour le Developpement (IRD), France, **composite plant strategy (transgenic hairy roots derived via *Agrobacterium rhizogenes* mediated transformation)** was developed,

and used for functional analysis of the **CgCCaMK** gene involved in nodulation during *Casuarina-Frankia* interaction. Through an ongoing project at IFGTB, composite plant strategy based on GFP screening of transgenic hairy roots was developed for the first time in *Eucalyptus*, and would now be used for the study of sodium transporter genes and promoters. **Methods were also optimized for *in vitro* regeneration and whole plant transformation of *Eucalyptus*.**

Gene silencing for insect resistance

In recent years, *Leptocybe invasa* has emerged as a serious pest in *Eucalyptus*. As the grub feeds within the gall tissue for around 4 months post oviposition, RNAi based silencing of genes vital to the insect's growth and development could be a potent strategy for engineering resistance. In this direction, **first sequence information of the Chitin synthase gene "LiCHS1"** and **LeEF1alpha** were deciphered from *L. invasa*. Similarly, the partial gene sequence of **HpCHS1, HpActin** were deciphered for the teak insect pest *Hyblaea pura* for development of dsRNA based insecticides.

Formal education

Graduated with a Bachelors degree in Agriculture in 1989, Masters Degree in Biotechnology from the Centre for Plant Molecular Biology, Tamil Nadu Agricultural University, Coimbatore, and Doctoral degree in Forest Biotechnology from FRI University, Dehra Dun.

Through a one year post doctoral sabbatical at the Institut de Recherche pour le Développement (IRD), Montpellier, France in 2007-08 made possible through a DBT award, pursued the project "Development of post-transcriptional gene silencing approaches as a tool for the functional analysis of symbiotic genes in the tropical actinorhizal tree *Casuarina glauca*"

Specialization:

Genetic engineering, RNAi, Functional genetics, molecular markers

Experience

Working as Scientist at the Institute of Forest Genetics and Tree Breeding (Indian Council of Forestry Research and Education, DehraDun) since 1998. Started career in the field of Molecular marker applications in tree species, and switched over to harnessing tools of transformation and functional genetics for application in development of transgenics and identification of major genes governing desired traits. Developed a specialized genetic transformation lab with facilities for contained research on development and application of transgenic tools in forestry species, like *Casuarina* and *Eucalyptus*.

Projects:

Intramural Projects

- Development of methods for functional analysis of genes involved in salt tolerance in *Eucalyptus tereticornis*. ICFRE: 30.93 lakhs (2009-14)
- Determination of target genes in *Leptocybe invasa* for engineering resistance in Eucalyptus through gene silencing approaches. ICFRE: 23.50 lakhs (2010-2014)

Extramural Projects

- Web enabled database and analysis of gene sequences implicated in abiotic stress tolerance for screening gene homologues in salt tolerant tree species . DBT: 20.096 lakhs (2009-2012)

CSIR Student Project Supervisor

- Identification and functional analysis of genes of the teak insect pest *Hyblaea pura* Cramer (Hyblaedae: Lepidoptera) for the development of gene silencing based pest control. CSIR student project (2009-2014)
- Genetic transformation of Casuarina for functional analysis of genes conferring salt tolerance. CSIR student project (2010-2015)

International partnership

- One of the four international partners for "Transcriptome analysis of salt tolerance in Casuarina trees" by the Joint Genome Institute, US along with the principal collaborator from Research Institute for Development, France, and other partners including Université Chiekh Anta Diop, Dakar (UCAD), Senegal and University of New Hampshire, US.

Journal Publications

Mathish, N.V., Sangeetha, M., Sowmiya Rani, K. S., Aravinthakumar, V., Selvakesavan R. K., Balasubramanian, A., Venkatachalam, R., Abraham, S. M., Jacob, J. P. and Krishna Kumar, N. 2011. Identification of insect-specific target genes for development of RNAi based control of the Eucalyptus gall pest *Leptocybe invasa* Fisher & La Salle (Hymenoptera: Eulophidae). BMC Proceedings, 5 (Suppl 7):P98

Balasubramanian, A., Venkatachalam, R., Selvakesavan R K., Abraham, S. M., Gherbi, H., Svistoonoff, S., Franche, C., Bogusz, D., Krishna Kumar, N. and **Mathish, N.V.**

- 2011.Optimisation of methods for *Agrobacterium rhizogenes* mediated generation of composite plants in *Eucalyptus camaldulensis*. BMC Proceedings 5(Suppl 7):O45.
- Perrine-Walker, F., Gherbi, H., Imanishi, L., Hocher, V., Ghodhbane-Gtari, F., Lavenus, J, Benabdoun, F. M, **Mathish, N.V.**, Svistoonoff S., Laplaze L. 2011. Symbiotic signaling in actinorhizal symbioses. Current Protein and Peptide Science. 12: 156-164. **JIF:** 3.854, Citation: 2
- Svistoonoff, S., Gherbi, H., **Mathish, N. V.**, Zhong, C., Michalak, Z., Laplaze, L., Vayssaire, V., Auguy, F., Hocher, V., Dumas, P., Bonneau, J., Bogusz, D., and Franche, C. 2010. Contribution of transgenic *Casuarinaceae* to knowledge of the actinorhizal symbiosis. Symbiosis. 50: 3-11. **JIF:** 0.611, Citation: 2
- Gherbi, H., **Mathish, N.V.**, Zhong,C., Félix, J., Autran, D., Girardin, R., Vaissayre, V., Auguy, F., Bogusz, D and Franche, C. 2008. Post- transcriptional gene silencing in the root system of the actinorhizal tree *Allocasuarina verticillata*. Molecular Plant Microbe Interactions. 21: 518–524. **JIF:** 4.275, Citation: 14
- Tripathi, S.B., **Mathish, N.V.**, Gurusurthi, K. 2006. Use of genetic markers in the management of micropropagated *Eucalyptus* germplasm. New Forests. 31:361-372. **JIF:** 0.915, Citation 8