

PROJECT PROFILE

Title: Identification of conserved motifs in genes conferring salt tolerance to develop strategies for gene isolation

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Co Investigators: Mr. R. Vivekanandan, Scientist E

Start and Completion dates: 3 Years (2005- 2008)

Objectives:

1. Data mine for DNA and protein sequence information of salt tolerance conferring genes
2. Identify conserved motifs in the genes conferring salt tolerance
3. Arrive at gene isolation approaches for salt tolerant tree species based on the identified conserved sequence motifs.

Funding Agency: Indian Council of Forestry Research and Education (ICFRE)

Total Budget: Rs. 0.57 lakhs

Summary

The nucleotide and protein sequences of genes conferring abiotic stress tolerance including transcription factors, transporters, Cellular signaling components, those involved in Protein and Membrane protection were downloaded from NCBI website. They were analyzed for conserved regions using the multiple sequence alignment programme viz ClustalW. The phylogenetic tree produced using the alignment showed the evolutionary relationship between the species selected based on the nucleotide sequences. Of the downloaded nucleotide sequences, the sequences from different species which are found to be phylogenetically related were selected for identifying the conserved regions. The primer designing software (PriFi) was used to design PCR primers for the phylogenetically related species based on the results of multiple sequence alignments. In cases where conserved regions were not found, primer pairs were obtained for individual gene

sequences. The primers designed for HKT1 were used to specifically amplify *HKT1* gene sequences from *Eucalyptus tereticornis*, *E. camaldulensis* and *E. alba*. The tables for information on abiotic stress tolerance conferring genes were created in Excel Sheets. The gene information for transcription factors and transporters in Excel Sheets were imported to Microsoft Access by import spreadsheet wizard. WAMP environment was installed and explained. phpMyAdmin was installed to create the database and relational tables in MySQL database. MS-Access to MySQL converter was used to transfer the sodium Antiporters genes information to the MySQL database. The Home, Glossary, Links, About Us, Updates, Submit Info, Sitemap, Search Classification and Advanced Search pages were designed for the TIGBAST "The *In Silico* Gene Bank for Abiotic Stress Tolerance" using the Dreamweaver software. The Advanced Search option in TIGBAST was able to retrieve information for sodium antiporter genes.