PROJECT PROFILE

Title: **Web enabled database and analysis of gene sequences implicated in abiotic stress tolerance for screening gene homologues in salt tolerant tree species.**

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Duration: 3 Years (2012- 2018)

Objectives:

1. Develop a web - enabled database of gene sequences implicated in abiotic stress tolerance.
2. Analyze the gene sequences for designing gene specific primers/ probes for isolation of genes implicated in salt tolerance.
3. Test the gene specific primers for their utility in identification of important gene homologues with particular reference to ion transporters in abiotic stress tolerant tree species of families Casuarinaceae, Myrtaceae and Fabaceae.

Funding Agency: DBT

Total Budget: Rs. 17.99 lakhs

Abstract

Abiotic stress tolerance is governed by polygenic traits. A web enabled database "*In Silico* Gene Bank for Adaptation to Abiotic Stresses" developed and was hosted at http://igbaas-ifgtb.icfre.gov.in

Salt tolerant (TNIPT-4, TNKBM-407,) and salt susceptible (PYN, TNPV2,) clones contrasting for sodium accumulation during salt stress were screened from 85 clones that were tested. In tolerant

clones, roots were shown to be critical in reducing sodium transport to the shoots. Clones showing a shoot to root ratio of sodium greater than 1.6 were generally highly salt sensitive, while those showing values lesser than 0.99 were salt tolerant clones. A progressive increase in proline content with the increasing NaCl concentration upto 450 mM was observed after which there was a decline. Clone TNIPT4 showed the maximum accumulation of proline (25.26 moles/g tissue) at 450 mM salt concentration as compared to clone PYN (17.65 moles/g tissue). These results indicatec that salt tolerance in *C. equisetifolia* could be due to lower shoot to root ratio of sodium and faster and higher accumulation of proline in response to the elevated Na^+ concentration in the cells.

The sodium-hydrogen antiporter genes (NHX) from *Casuarina equisetifolia* (330 bp), *Eucalyptus camaldulensis* (494 bp), *E. tereticornis* (614 bp), *Pongamia pinnata* (385 bp), *Acacia nilotica* (348 bp), *Prosopis juliflora* (371 bp), *Kandelia candel* (725 bp), *Bruguiera gymnorhiza*, (355 bp), *B. cylindrica (*445 bp), *B. sexangula* (351 bp), HKT1 gene from *E.tereticornis* (638 bp), *P. juliflora* (220 bp), AKT1 genes from *C. equisetifolia* (236 bp), *E. camaldulensis* (280 bp), *P. juliflora* (300 bp), *B. sexangula* (325 bp), *B. cylindrica* (230 bp), *K. candel* (310 bp), and *A. nilotica* (361 bp), and the Actin genes from *B. cylindrica* (293 bp), *B. gymnorhiza* (265 bp), *B. sexangula* (255 bp), *K. candel* (234 bp), *A.nilotica* (201 bp), *P. pinnata* (213 bp), *E. camaldulensis* (311 bp) and *C. equisetifolia* (204 bp) were sequenced and published with accession Numbers at the GenBank Database of the National Centre for Biotechnology Information (NCBI), National Library of Medicine, National Institute of Health, USA.