IGBAAS- a Web Resource for Bioinformatic Analysis of Genes Conferring Abiotic Stress Tolerance

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Abstract

Casuarinas are the preferred trees for planting along tropical coastlines due to their ability to function as a protective shield against wind and waves. They are also planted for reclamation of waste lands. Abiotic stresses like salt stress limit their growth. Several studies have reported existence of considerable variation in the ability of casuarina to tolerate salt stress. Researchers have therefore, focused on understanding the physiological and molecular basis of salt tolerance in casuarina, so that the trait could be bred into highly productive genotypes. Recent sequencing efforts by the Institut de Recherche pour le Developpement (IRD), France, have led to unraveling of the salt induced transcriptome in *Casuarina glauca*. With drastic drop in sequencing costs, similar efforts are proposed to be undertaken in salt tolerant clones of *C. equisetifolia*. Voluminous gene sequence data in Casuarina are thus being generated. To harness these sequence resources for development of molecular markers for salt tolerance, they need to be analysed and classified according to gene function. The Institute of Forest Genetics and Tree Breeding, Coimbatore, has recently hosted the beta version of the database "*In silico* Gene Bank for Adaptation to Abiotic Stresses - IGBAAS" at http://igbaas-ifgtb.icfre.gov.in . IGBAAS presently comprises around 3000 gene sequences involved in abiotic stresses (salt, drought, freezing and heat) from different species. To facilitate researchers in the development of molecular markers for salt tolerance in casuarina, we intend to incorporate selected transcriptome sequence data pertaining to salt tolerance in Casuarina, based on the user friendly functional classification available at

IGBAAS. This paper describes the IGBAAS website, and the utilities that could be made use of by researchers working on abiotic stresses in casuarina. IGBAAS is accessible through a user friendly functional classification, and is searchable for nucleotide and protein sequences of genes, their degenerate primers, and related information from Wikigenes, and Pubmed. The users can also edit and update sequence information available in the database, and also upload new gene sequence information. The database has direct connectivity to bioinformatic tools that enable users to select sequences from the IGBAAS database, convert them to FASTA format, and perform bioinformatic analysis like getting multiple sequence alignment (ClustalW), BLAST, Primer-BLAST, siRNA design and reverse complement. The site also provides links to research groups working in abiotic stress tolerance. Advanced versions of IGBAAS that facilitate query for species cum biochemical-pathway specific gene information, in addition to updated gene sequence information from NGS data are envisaged.