

INDO GLOBAL JOURNAL OF PHARMACEUTICAL SCIENCES ISSN 2249- 1023

Cloning and Comparative Modelling with Phylogenetic Analysis of SOD-2 in Drought Tolerant Maize Inbred Line HKI-335

Anuradha Gautam *, Surbhi Priya, Ishwar Singh, Pranjal Yadava

ICAR- Indian Institute of Maize Research, PUSA Campus, New Delhi 110012, India

 $\label{eq:com:main:address} \textbf{Address for Correspondance}: Anuradha Gautam, \underbrace{anu.gautam10@gmail.com}_{\text{granjal.yadava@icar.gov.in}}; \underbrace{surbhipriya.ssm@gmail.com}_{\text{granjal.yadava@icar.gov.in}}; \underbrace{surbhipriya.ssm@gmail.com}_{\text{granjal.yadava.gov.in}}; \underbrace{surbhipriya.ssm@gmail.com}_{\text{granjal.yadava.gov.in}$

Keywords Maize; Abiotic Stress; SOD; Cloning; Bioinformatics. ABSTRACT: Maize is one of the most versatile emerging crops having wider adaptability under varied climatic conditions. However, abiotic stresses trigger the production of Reactive Oxygen Species (ROS) as well as the enzymes that can scavenge the reactive oxygen radicals such as Superoxide dismutase (SOD). The present study aims at cloning and bioinformatic analysis of Sod-2 from a drought tolerant maize inbred line HKI-335. The Sod-2 was amplified using gene specific primers and cloned. The recombinant plasmid was sent for sequencing and the sequences were submitted in National Centre for Biotechnology Information (NCBI) database. The FASTA sequences were retrieved and used for homology modelling and secondary structure prediction using PSIPHRED software. Comparative modeling revealed 151 amino acid residues present in SOD-2 of HKI-335. The homology search revealed 83% sequence identity with Potentilla atrosanguinea SOD-2 (PDB ID: 2Q2L A) with an e-value of 4e-86. The model was evaluated on the basis of geometrical and stereo-chemical constraints using PDBsum and ProSA-Web. Ramachandran plot revealed (~98.0% expected); 193(84.6%) residues falling in most favoured region, (~2.0% expected); 34(14.9%) residues in additionally allowed region, and 0.4% residues in generously allowed region with no residues in the disallowed region. In PROSA-Web plots displaying Z-scores, value (-6.51) of the target model was determined by X-ray crystallography and Nuclear Magnetic Resonance (NMR). This value was extremely close to the value of template 2Q2L (-6.44). Root Mean Squared Deviation (RMSD) was used to see three dimensional structural similarities between the target and template. The phylogenetic relationship analysis showed a clear demarcation of the plant SOD-2 into two prominent clusters; cluster A and B. The Cluster A comprised of sequences from monocots (10), whereas cluster B included sequences from dicots (8).© 2016 iGlobal Research and Publishing Foundation. All rights reserved.

Conference Proceedings: International Conference on Advances in Plant and Microbial Biotechnology (PMB-2017); JIIT, Noida: February 02-04, 2017

Indo Global Journal of Pharmaceutical Sciences (ISSN 2249 1023; CODEN- IGJPAI; NLM ID: 101610675) indexed and abstracted in EMBASE (Elsevier), SCIRUS (Elsevier), CABI, CAB Abstracts, Chemical Abstract Services (CAS), American Chemical Society (ACS), Index Copernicus, EBSCO, DOAJ, Google Scholar and many more. For further details, visit http://iglobaljournal.com