

ABSTRACT

The present project is focused on *in-silico* structure and function analysis of uncharacterized genes from the whole transcriptome of *Brassica napus* under salinity stress. Among the sixteen hundred and eighty two sequences, up-regulated genes were selected from RNA-seq data. Among these, 310 sequences were screened based on size. Several databases including the Database for Annotation, Visualization and Integrated Discovery (DAVID), National Center for Biotechnology Information (NCBI) and Protein Data Bank (PDB) were visited for the collection of data about proteins. Homology analysis was performed using Multiple Sequence Alignment, phylogenetic tree construction and domain analysis. Nine gene sequences (Gene symbol: BNACNNG05440D, LOC106435416, LOC106451182, LOC106451156, LOC106436551, LOC106452548, LOC106335751 and LOC106396312) were selected based on the presence of a functional domain. Similarly, various modeling platforms like I-TASSER, Phyre2, SWISS-MODEL and RaptorX were utilized to predict the 3D structure. The homologues of the structures were searched through PDB and RCSB. Sequences BNACNNG05440D (106454729), LOC106435416 (106435416), LOC106426317 (106426317), LOC106452548 (106452548), LOC106335751 (106335751) and LOC106396312 (106396312) were used for docking analysis due to the possible role of these genes in salinity stress tolerance. LIGPLOT/NUCPLOT files of the receptor-ligand complexes were generated using PDBsum. These files were used for the analysis of the binding site of molecules. 106454729 is a GT1 transcription factor, 106435416 is a cyclohydrolase II enzyme, 106451156 is pseudouridine kinase I, 106426317 belongs to DnaQ exonuclease domaincontaining protein, 106436551 is a Tim15 protein, 106452548 is a SAM50 protein, 106335751 is a protein O-fucosyltransferase 2 while 106396312 is SWIB/MDM2 domaincontaining protein. The role of predicted proteins in various pathways was studied and the possible role of GT1 transcription factor under saline conditions was explored through the literature survey.