ID: P-247

In silico analysis of the WRKY gene family in wheat

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Biotic and abiotic stresses are major limiting factors for crops productivity. WRKY gene family encodes a large group of transcription factors which are involved in the regulation of biotic and abiotic stress responsive genes. Therefore, identification and characterization of this gene family will be valuable in the manipulation of plants in order to improve their stress tolerance. To find WRKY gene family members in wheat, multiple searches were done in the related databases and Rice WRKY conserved sequences were used as the templates for tblastn searches in the nr, EST, HTGS datasets for finding new members in wheat. ESTs partial overlaps were obtained using EST annotator in the database of TIGR. EST and cDNA sequences were translated by the DNAstar software and NCBI ORF finder. Sequence alignment and phylogenetic tree construction of WRKY domains was done by MEGA4 software and the Boot strap neighbor-joining method. Graphical view of the similarities between the subgroups was determined using BioEdit software. In the current study, 95 members of the WRKY family were found in wheat. 76 members of this family had complete WRKY conserved structure (incomplete protein sequences were originated from translation of EST or partial mRNA sequences) containing 16 members in group I, 38 members in group II and 22 members in group III. Conserved region of each group were distinguished in wheat. Based on the phylogenetic relations, subgroups of group II include IIa, IIb, IIc, IId and IIe containing 6, 13, 11, 6 and 2 members in wheat, respectively. Similarly subgroups of group III include IIIa and IIIb containing 10 and 12 members, respectively.

Key Words: *Triticum aestivum*, biotic and abiotic stresses, WRKY gene family, transcription factor