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Genome-wide identification of Hsp70 protein family members in European ash trees

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Abstract: Molecular control mechanisms for plant stress tolerance are regulated by specific stress genes. Members of Heat Shock Protein 70 family (*Hsp70*) are one of them and act as molecular chaperones. They are known as regulatory proteins which promote protein folding and prevent misfolding and aggregation of protein structure. Ash trees are the largest native deciduous trees throughout the Northern Hemisphere. The genome of a low-heterozygosity *Fraxinus excelsior* tree was sequenced in 2017. About 39.000 protein-coding genes were determined in ash tree genome. Compared to genomes of other plant species, 25% of these genes appear ash specific. Although some of these genes have been characterized in ash genome, genome-wide analysis of these chaperon proteins has not been studied yet. In this study, we reported identification, molecular and functional characterizations of *Hsp70* family members in ash tree genome. A total of 43 *FexHsp70* genes were detected in genome based on their PFAM search. PFAM accession number of *Hsp70* is PF00012.15 which reveals *Hsp70* family domain. Gene structure and motif analysis of *FexHsp70* genes were performed using Gene Structure Display Server and MEME Suite Server, respectively. Phylogenetic tree was constructed using MEGA 7 program. Exon-intron organization of 43 *FexHsp70* genes were examined. In addition, fifteen conserved motifs were found in *FexHsp70* protein sequences. FexHsp70 proteins were phylogenetically classified as six main clusters. Gene structure analysis and motif compositions were correlated with phylogenetic tree in which *FexHsp70* genes with similar exon-intron structure were found in same clusters. For prediction of Gene Ontology terms of the *FexHsp70* genes, Blast2GO package was used. As a prediction of molecular function of FexHsp70 proteins, binding activity to organic cyclic compounds, ions, proteins and carbohydrates was mainly observed. Besides, oxidoreductase activity was another molecular function of these family members. They were chiefly located in intracellular regions and membrane of the cell. The psRNA Target server was used for *in silico* identification of miRNAs which targeted to *FexHsp70* transcripts. A total of 13 different *FexHsp70* genes were targeted by 11 different plant miRNAs. Among them, the most observed one was miR414. Our results can provide valuable information for further exploration into the functions of this significant gene family members. Additionally, understanding of the evolution and function of these important family members will be useful for comparative and functional genomics studies.

Keywords: Genome-wide identification, Bioinformatics analysis, Hsp70, F. *excelsior* L.