

## In silico identification and bioinformatics analysis of Hsp90 (Heat shock protein 90) gene family in *Fraxinus excelsior* L.

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**Abstract:** *Fraxinus excelsior* L. is a common tree in Europe and also considered native in Asia from northern Turkey east to the Caucasus and Alborz mountains. As this aspect, it has great ecological and economic value as a key forest species. “The British Ash Tree Genome Project” results have been published in January 2017. Genomes of 37 *F. excelsior* trees from Europe were re-sequenced to indicate long-term decline in population size. As known, the fungus *Hymenoscyphus fraxineus* causes ash dieback. Biomarkers for ash dieback have been also improved based on genome analysis results. So, genome study of ash tree provides a basis for tree breeders for selection of functional genes and proteins. Specific stress proteins activate chaperones which bind to network sequences. Members of the Heat Shock Protein 90 (*Hsp90*) gene family have been conserved thorough evolution. However, no systematic analysis of gene characterization of *Hsp90* proteins has been performed in *F. excelsior* L. *Hsp90* protein domain (PF00183.13) was searched against to ash genome. Then, we have identified 14 *FexHsp90* genes in *F. excelsior* genome. We firstly generated a maximum likelihood phylogenetic tree to examine the phylogenetic clusters among the *FexHsp90* proteins. They were phylogenetically clustered into three major groups. Exon/intron organization of *FexHsp90* genes were also investigated. All genes were composed of exons. The structural diversity of *FexHsp90* genes were relatively conserved motif composition. Fifteen distinct motifs were identified among *FexHsp90* proteins. There was a positive correlation between gene structure, motifs and phylogenetic tree. *FexHsp90* genes with similar exon-intron structure and motif composition were found in same branch of phylogenetic tree. For 3D protein homology prediction, Protein Homology/analogY Recognition Engine (Phyre2) was used. A total of twelve *FexHsp90* proteins were modeled at >90% confidence and the percentage residues were varied from 80 to 100. The secondary structure was predominantly constituted of  $\alpha$ -helix with having rare incidence of  $\beta$ -sheets. The amino acid sequences of *FexHsp90* proteins were imported into Blast2GO program and were obtained for GO classification. Binding activity, protein folding and response to stress were main biological processes for *FexHsp90* proteins. Besides, they were mainly located in cytoplasm and organelles. This genome analyses will enable researcher to open new perspectives for further functional investigations of these genes. Additionally, these results will be useful for comparative genomics analysis of forest trees whose genome analyses have been completed.

**Keywords:** Gene characterization, *Fraxinus excelsior* L., *Hsp90* gene family, Bioinformatics analysis