



GENOME-WIDE IDENTIFICATION OF GENES ENCODING DOF TRANSCRIPTION FACTORS IN GRAPEVINE

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Dof (DNA-binding with one finger) proteins are members of a family of plant-specific transcription factors that regulates many cell functions such as response to light, phytohormones and defense, seed development and germination. Recently, many *Dof* genes were identified and characterized in mono- and dicotyledonous plants including *Arabidopsis*, barley, potato, rice, soybean, tobacco and several others. This work aimed to identify and functionally annotate the *Dof* gene family members in grapevine. The consensus amino acid sequence of the Dof domain was used in BLASTP searches for potential *Dof* genes in the grapevine genome (12X, version 1). Twenty-five predicted gene models displaying the characteristic zinc-finger DNA-binding domain were identified. Two phylogenetic trees were inferred using MrBayes (version 3.1.2). The first used only predicted amino acid sequences of grapevine. The second analysis compared grapevine sequences with those of *Arabidopsis* Dof proteins as well as sequences from other characterized members of this family in other plant species. In both studies, predicted protein sequences were aligned using MUSCLE and cured with GBLOCKS to eliminate poor alignment positions and divergent regions. The consensus trees were visualized and edited by the means of the iTOL software. Predicted physical localization of *Dof* genes among the grapevine chromosomes was drawn with MapChart. Family members were named accordingly to their positions in the cladogram constructed with grapevine sequences. The phylogenetic tree generated with Dof protein sequences from grapevine, *Arabidopsis* and with other plant-species allowed us to identify several groups of paralogs and orthologs. Our results suggested that recurrent duplications and diversification of an original *Dof* ancestor seemed to have led to the formation of this complex family of transcription factors in plants. Additionally, our results may guide the interpretation of several transcriptional profiles already available for *Dof* genes in different organs and tissues of grapevine.

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