

Genome-Wide Analysis & Expression Profiling Reveals the Functional Diversity of *Dof* Gene Family in *Medicago polymorpha*

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The *Dof* transcription factor is a plant-specific transcription factor gene family that plays various biological functions in plant development and stress response. However, no relevant research has been conducted on *Medicago polymorpha*. In this study, thirty-six *Dof* genes were identified from the genome of *M. polymorpha* showed that each *MpDof* gene has a highly conserved C2-C2 zinc-finger structure. The *Dof* genes from *M. polymorpha*, *Medicago truncatula*, *Oryza sativa*, and *Arabidopsis thaliana* were divided into 10 groups (A, B1, B2, C1, C2.1, C2.2, C3, D1, D2, and E) based on the comparative phylogenetic analysis, group D1 contains the maximum number of *MpDof* members, with 11 *MpDofs*. Group E is monocot-specific. *MpDof* genes are unevenly distributed on the seven chromosomes. The whole-genome duplication (WGD) event of *MpDof* genes occurred, and two tandem duplications and 13 segmental duplications were identified. The ratio of $Ka/Ks \leq 0.617927$, revealing that the *MpDof* genes evolved under purifying selection. The synteny analysis among different species showed that there is a complex syntenic relationship between *M. polymorpha* and *M. truncatula*. Exon-intron structure and conserved motif analysis showed that the structures and motif components of the *MpDof* genes in the same subgroup are similar, but significant differences among subgroups reflect the functional diversity of *Dof* genes. All 36 *MpDof* genes are predicted to contain cis-acting elements related to hormone response, development, and abiotic stress response. The protein-protein interaction network analysis also reveals that some *MpDof* genes such as *MpDof11*, *MpDof25*, and *MpDof26* may be involved in the photoperiod blooms process. The *MpDof* genes showed diverse expression patterns in different tissues and development stages, indicating that these genes played an important role in the growth and development of *M. polymorpha*. Notably, *MpDof26* is highly expressed at the early flowering stage. Furthermore, *MpDof29* and *MpDof31* are specifically expressed in large pod and root, respectively, revealing their key role in the pod and root development. The results of genome-wide analysis for the *Dof* gene family in *M. polymorpha* will provide new information to further understand and utilize the function of these *Dof* genes.

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