



Genome-wide identification and characterization of the Dof gene family in *Medicago truncatula*

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ABSTRACT. The DNA-binding one zinc finger (Dof) family is a classic plant-specific zinc-finger transcription factor family, which is involved in many important processes, including seed maturation and germination, plant growth and development, and light responses. Investigation of the *Medicago truncatula* genome revealed 42 putative Dof genes, each of which holds one Dof domain. These genes were classified into four groups based on phylogenetic analysis, which are similar to the groups reported for *Arabidopsis* and rice. Based on genome duplication analysis, it was found that the MtDof genes were distributed on all chromosomes and had expanded through tandem gene duplication and segmental duplication events. Two main duplication regions were identified, one from tandem duplication and another from segmental duplication. By analyzing high-throughput sequencing data from *M. truncatula*, we found that most of the MtDof genes showed specific expression patterns in different tissues. According to cis-regulatory element analysis, these MtDof genes are

regulated by different cis-acting motifs, which are important for the functional divergence of the MtDof genes in different processes. Thus, using genome-wide identification, evolution, and expression pattern analysis of the Dof genes in *M. truncatula*, our study provides valuable information for understanding the potential function of the Dof genes in regulating the growth and development of *M. truncatula*.

Key words: Dof transcription factor; *Medicago truncatula*; Phylogenetic analysis; Genomic duplication; Expression patterns; Cis-acting element