

Genome-Wide Identification & Functional Analysis of the SWEET Gene Family in *Medicago polymorpha*

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Background: The SWEET (Sugars Will Eventually be Exported Transporters) sugar transporter family plays an important regulatory role in plant pollen nutrient transport, nectar secretion, stress tolerance, and plant-pathogen interaction. However, there has been no comprehensive analysis of the SWEET family genes in *Medicago polymorpha* (*MpSWEET*), and phylogenetic relationship, gene characteristics of *MpSWEET* genes, and their expression patterns remain largely unexplored.

Methods: Taking the SWEET protein sequences of *Arabidopsis thaliana*, *Medicago truncatula*, and *Oryza sativa* query objects, the protein and nucleic acid library of *M. polymorpha* were searched by BLASTP. The MEGA7 software was employed to conduct the phylogenetic analysis by the neighbor-joining method. Multiple sequence alignment of *MpSWEET* protein was performed using DANMAN v9 program to analyze the conserved amino acid residues. Interspecific collinearity and duplicated genes were analyzed in SWEET family genes using MCScanX. The expression profiles of *MpSWEET* genes in different developmental stages and different tissues were forecast and examined using microarray data.

Results and Conclusion: A total of 23 *MpSWEET* genes were identified in *M. polymorpha* using whole genome analysis and divided into four clades. Members of the same subclass have similar gene structures and highly conserved motifs. Prediction of transmembrane regions showed that each *MpSWEET* protein contains at least one characteristic MtN3_slv domain. Further analysis of chromosomal location, synteny analysis, and gene duplication suggested that *MpSWEET* genes located on seven chromosomes, the orthologs of *M. polymorpha* and *M. truncatula* showed good collinearity, segmental and tandem duplication events played a crucial role in the expansion of the family in *M. polymorpha*. *MpSWEET* gene of *M. polymorpha* is highly conserved in annual alfalfa. Additionally, the expression pattern of SWEET genes indicated that four *MpSWEET* genes has tissue-specific expression; five *MpSWEET* genes are highly expressed in different tissues; four *MpSWEET* genes from clades III and IV are specifically expressed in disparate developmental stages. Members of *MpSWEET* family participate in a variety of physiological processes of *M. polymorpha*, especially in the regulation of reproductive development, including flower and seed development. This study found that there are complex regulatory networks among *MpSWEET* family members, *MpSWEET02*, *MpSWEET03*, *MpSWEET07*, *MpSWEET12*, and *MpSWEET21* may participate in the growth and development of *M. polymorpha* as core proteins and regulate other proteins in response to stress. These results provide new insights into the complex regulation mechanism of *MpSWEET* genes, and lay the foundation for further analysis of their functions.

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