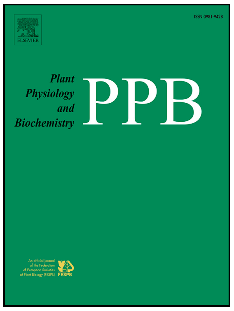

Genome-wide profiling of expression and biochemical functions of the *Medicago* glutathione S-transferase gene family

Xue-Min Han, Zhi-Ling Yang, Yan-Jing Liu, Hai-Ling Yang, Qing-Yin Zeng

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Genome-wide profiling of expression and biochemical functions of the *Medicago* glutathione S-transferase gene family

Xue-Min Han[1,2], Zhi-Ling Yang[3], Yan-Jing Liu[4], Hai-Ling Yang[3] and Qing-Yin Zeng[1,2,4,*]

[1]State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences, Beijing 100093, China.
[2]University of Chinese Academy of Sciences, Beijing 100049, China
[3]College of Biological Sciences and Biotechnology, Beijing Forestry University, Beijing, 100083, China
[4]State Key Laboratory of Tree Genetics and Breeding, Chinese Academy of Forestry, Beijing, 100091, China

[*]Corresponding to Dr. Qing-Yin Zeng, E-mail: qingyin.zeng@ibcas.ac.cn
Phone: +86-10-62836440; Fax: +86-10-62590843

Abstract

Glutathione *S*-transferases are ubiquitous enzyme in plants, playing vital roles in several physiological and developmental processes. In this study we identified 73 GST genes from the genome of *Medicago truncatula*. The *Medicago* GSTs were divided to eight classes with tau and phi being the most numerous. Six clusters were found on four *Medicago* chromosomes. The local gene duplication mainly contributed to the expansion of this large gene family. Functional divergence was found in their gene structures, gene expression patterns, and enzyme properties. A genomic comparative analysis revealed lineage-specific loss/gain events between *Medicago* and *Glycine*. This study offered new insights into the evolution of gene family between closely related species.

Key words: Enzyme activity; glutathione S-transferases; gene expression; functional divergence; *Medicago truncatula*.