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

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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*.

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