



Comparative sequence and expression analysis of tapetum specific male sterility related genes in *Medicago truncatula*

L.H. Shao, X.W. Zheng, D.X. Yi and C. Li

Institute of Animal Sciences, the Chinese Academy of Agricultural Sciences, Beijing, China

Corresponding author: C. Li
E-mail: licong0520@sina.com

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ABSTRACT. Heterosis, or enhancement through outbreeding, is one of the most promising approaches for increasing crop yield. Male sterility (MS), which promotes heterosis, has been widely applied in hybrid crop production. *Medicago truncatula* is a model legume species and is closely related to *M. sativa*, an important legume forage plant. Although the molecular mechanisms of MS in *M. truncatula* and *M. sativa* remain unclear, several studies of MS have been conducted in *Arabidopsis thaliana*. Previous research has shown that MS is associated with the destruction of tapetal cell layers. Disruption of tapetum developmental processes may result in pollen abortion. In an effort to identify genes useful for breeding in *M. sativa*, we identified MS related genes in *M. truncatula* using BLAST and homology to *A. thaliana* genes. In this study, we identified 63 tapetum specific male sterility (TSMS) related genes. The length of TSMS genes varied from 225 to 3747 bp. We identified 15 conserved domains and 8 *cis*-elements associated with TSMS related genes. Analysis of the phylogenetic relationships among these genes allowed them to be classified into three groups, MtTsms A, MtTsms B, and MtTsms C. Expression analyses revealed that these

genes may be involved in developmental processes and response to abiotic stress.

Key words: *Medicago truncatula*; Male sterility; Genetic analysis; Tapetum