

A Family of Peroxidase Genes from the Model Legume
Medicago truncatula

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Medicago truncatula is an annual, self-fertile plant suitable for molecular genetic studies. Its characteristics such as small diploid genome (~400 Mb/1C), short life cycle and a capacity for rapid transformation and regeneration have placed this species as a model legume for genomic research. *M. truncatula* serves as a host for symbiotic nitrogen fixation with the soil bacterium *Rhizobium meliloti*. Of numerous *Rhizobium*-induced changes that take place during nodulation, a gene encoding a peroxidase is induced strongly in 3 h post-infection. As peroxidases are involved in many important aspects of plant-microbe interactions, we initiated to study differential expression of peroxidase genes in *M. truncatula*. To identify members of the gene family, nucleotide databases were searched for putative sequences that exhibit similarities with known genes from other organisms. Over seventy peroxidase-like sequences were collected and compared to construct a phylogenetic tree. Similarly to the results obtained from the alignment of various peroxidases of *Arabidopsis*, peroxidases of *M. truncatula* were apparently divided into 7 groups. Two or three representative members of each phylogenetic branch were chosen to design oligonucleotide primers that permit amplification of corresponding genomic regions. PCR fragments amplified from each gene are presently used for developing intron-targeted markers. Additionally, a multiplex DNA pool of a BAC library is screened to obtain full genomic sequences. Specific probes devised with the BAC clones will be helpful for investigating differential expression patterns of peroxidase genes.

Keywords: *Medicago truncatula*, model legume, peroxidase, gene family