

Nodule-specific and Nodule-induced Monosaccharide Transporters (MSTs) in *Medicago truncatula*.

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Legumes are cornerstones of sustainable agriculture, as the symbiotic relation they form with soil bacteria, called rhizobia, results in nitrogen fixation (symbiotic nitrogen fixation – SNF). SNF takes place inside new plant organs that develop for this reason, the legume root nodules. Plant cell membrane transporters are essential for nutrient exchange between legumes and rhizobia, facilitating the appropriate conditions for nodule metabolism and for being potential sites of SNF regulation. We have used the model symbiotic system of *Medicago truncatula*–*Sinorhizobium meliloti* to identify plant genes involved in carbon transport in the nodule. *M. truncatula* is an excellent candidate for such studies, due to the available databases regarding the sequencing of the genome (<http://mtgea.noble.org/v2>, <http://www.medicago.org/genome>, NCBI), the expression of genes (<http://mtgea.noble.org/v2>) and the active metabolic pathways (<http://www.genome.jp/kegg/pathway.html>). *In silico* analysis was conducted to identify *M. truncatula* Monosaccharide Transporters (MSTs) that are nodule-induced or nodule-specifically expressed. Here, we present data concerning the phylogenetic taxonomy of these transporters, their gene structure, their amino acid sequence and a prediction of the topology/secondary structure for the corresponding encoded protein. Furthermore, total RNA was extracted from different organs and nodule developmental stages of *M. truncatula*, and the expression of these genes, analysed by RT-qPCR, is depicted. This work represents the starting point for the elucidation of the identified MSTs exact physiological and biochemical role during SNF using the available reverse genetic resources for *M. truncatula*.

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