

Nodule-specifically Expressed Genes involved in the Carbon allocation and metabolism in the Nodule of *Medicago truncatula*

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Although N₂ is abundant, comprising about 79% of the atmosphere, plants cannot convert it to useful organic forms and mineral nitrogen is limited in soils. Legumes are unique among crop plants in the ability to fix N₂ in symbiotic association with rhizobia. Symbiotic nitrogen fixation (SNF) takes place in legume root nodules, organs of tumor-like structure, and is accomplished by nitrogenase. SNF is an energy demanding process, fueled by plant photosynthate that is transported to the nodules as sucrose. There, sugar transport and glycolysis facilitates the production of dicarboxylic acids, the final compounds supplied to bacterial symbionts performing SNF. We have used the model symbiotic system of *Medicago truncatula* – *Sinorhizobium meliloti* to identify plant genes involved in carbon allocation and metabolism in the nodule. *M. truncatula* is an excellent candidate for such studies, due to the available databases concerning the sequencing of the genome, the expression of genes, the active metabolic pathways, and the existence of established Tnt1-insertion mutant lines. *In silico* analysis was conducted to identify *M. truncatula* genes encoding for sugar transporters and glycolysis enzymes that are nodule-specifically expressed or nodule-highly induced. Few such genes were identified; however the corresponding encoded proteins control significant regulatory steps of carbon allocation and metabolism in the plant cell. To verify the *in silico* analysis, total RNA was extracted from different organs and nodule developmental stages of *M. truncatula*, and the expression of these genes is depicted. We present data concerning the structure of these genes, the amino acid sequence, and the predicted secondary structure along with annotated functions of the encoded proteins. Corresponding cDNAs were generated and the coded sequences of these genes were cloned. Finally, we present data concerning the spatial expression and subcellular localization of the gene products in the nodule of *M. truncatula* and results concerning their physiological role during SNF.

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