

Gene Transcription Profiling of *Medicago truncatula* Due to Changing Nutrient Nitrogen Supply

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Barrel medic (*Medicago truncatula*), is an annual, self fertile, diploid, herbaceous legume cultivated as cover and pasture crop in many parts of the world. Because of the close relationship of *Medicago truncatula* (*Mt*) with the cultivated tetraploid alfalfa (*Medicago sativa*) and its importance as a feed and cover crop, *Mt* is being used as a model plant for legume biology and has been the subject of structural and functional genomics work. The international effort in *Mt* genomics has positioned *Mt* as resource plant for understanding agronomic traits of importance to forage and grain legumes. The mineral nutrient needed in greatest abundance by plants is nitrogen (N) and most plants can utilize nutrient N as nitrate and ammonium forms. But an important aspect of legumes including *Mt* is their unique ability to obtain N via microbial symbiosis with soil bacteria called rhizobia. One such rhizobia is *Sinorhizobium meliloti* strain 1021F that induces nitrogen-fixing nodules (Nod⁺Fix⁺) on both *Mt* and *M. sativa*. This extremely host-specific bacterial symbiosis allows the host plant to acquire biologically fixed nitrogen (BNF) from the atmosphere.

The *Mt* expressed sequence tag (EST) collection at The Institute of Genomic Research contains some 190,000 EST sequences derived from over 40 cDNA libraries representing different plant organs and tissues exposed to several treatments and conditions. Individual overlapping ESTs have been clustered into tentative consensus sequences (TCs) that represent putative genes. There are some 17610 TCs in the release 7.0 of the MtGI, of which 8 cDNA libraries comprising 32135 ESTs were prepared from mRNA extracted from *S. meliloti*-inoculated roots and nodules at different developmental stages. Besides, there are 13513 ESTs prepared from roots of nitrate-starved plants, seedlings that received 5 mM nitrate or uninoculated plants. An *in silico* (electronic northern) analysis was applied to identify those TCs composed of ESTs derived exclusively from symbiotic roots, root nodules, or nitrate starved and/or nitrate limited roots. We identified over 600 TCs containing 2900 ESTs exclusively from *S. meliloti* inoculated root- and nodule-libraries. A further 297 TCs containing 740 ESTs were also found to be specific to nitrate starvation and/or nitrate limitation. About 70% of the symbiotic root- and nodule-specific TCS appear to be novel or showed similarity to proteins of unknown function. The transcription profiles of many of the novel TCs were evaluated in a macroarray analysis to determine if those genes were also expressed in nodules that are not fixing nitrogen (Nod⁺Fix⁻), or in plants that received nitrate and ammonium as fertilizers. Results from the macroarray analysis will be presented. Results obtained from applying genomics tools to identify genes associated with BNF and mineral N nutrition in *Mt* should be transferable to other herbaceous legume species.