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IDENTIFICATION OF GENES MODULATED BY NITRIC OXIDE IN *MEDICAGO TRUNCATULA* DURING SYMBIOSIS AND/OR PATHOGENESIS

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There is increasing evidence that nitric oxide (NO), which was first identified as a unique diffusible molecular messenger in animals, plays important roles in diverse (patho)physiological processes in plants. Recent studies highlights its involvement during leaf expansion, root growth, senescence, iron homeostasis and abiotic stress.

Although its role in symbiosis has not been unrevealed, a few data suggest that NO could play a role in the establishment of symbiotic associations. The symbiotic interaction between legumes and rhizobia leads to the formation of roots nodules, which are the sites of atmospheric nitrogen fixation and transformation into ammonium. The infection and the establishment of symbiosis are controlled through a complex signalling network that involve reactive oxygen species (ROS) and NO. These reactive molecules are also involved in gene regulation during the hypersensitive response (HR) to pathogens. Therefore, plant pathogenesis and symbiosis may be considered as variations of a common theme.

Although *Arabidopsis* serves as the model system for most plant processes, it suffers from two major weakness in consideration to plant-microbe interaction: the lack of mycorrhizal and rhizobia symbiontic associations. To reveal the mechanisms regulated by NO in pathogenesis and symbiosis, we started a transcriptional analysis of genes modulated by this molecule in *Medicago truncatula*, the model system for legume biology. In this work we performed a study using a cDNA-amplified fragment lenght polymorphims (AFLP) transcript profiling approach. cDNA-AFLP is a gel based technique that allows comparison of gene expression profiles and can identify novel genes without previous sequence information. In this work *M. truncatula* roots from 4 week-old aeroponic-grown plants were treated with the NO donors sodium nitroprussiate (SNP) and nitrosoglutatione (GSNO). Using 32 primer combinations we isolated 1800 cDNA fragments which present an expression pattern altered between the control and at least one of the treatments. Differentially expressed cDNA fragments were eluted from gel, reamplified and cloned in pGEM-T vector. A prior sequence analysis of 600 cDNA fragments revealed that about 13% are not represented by any known expressed sequence tag (EST) databases. A microarray containing 1500 cDNA fragments will be used to perform a broader monitoring of transcriptome changes in *M. truncatula* upon different physiological condition such as incompatible plant-pathogen interaction and symbiontic associations with mycorrizhal fungi and with rhizobia. This extensive analysis of the transcriptome map in response to NO would allow identifying of the interaction between NO and other pathways beside the identification of novel genes involved in NO signalling.