

A PROTEOMIC APPROACH TO STUDY THE AUTOREGULATION OF NODULATION IN *MEDICAGO TRUNCATULA*

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Plant belonging to *Leguminosae* family can establish a symbiotic relationship with nitrogen-fixing bacteria, termed rhizobia, that lead to the formation of a new organ, the root nodule. This organogenetic pathway starts as a consequence of a molecular cross-talk between plants and bacteria. Plants release flavonoids in the rhizosphere, which induce the rhizobia to produce Nod factors (NFs). NFs perceived by the host plant trigger at least three signalling pathway that control nodule formation and nodule number. Two of these pathways are root-specific whilst the third is systemic. The systemic pathway, also termed Autoregulation Of Nodulation (AON), is a mechanism by which a plant controls the number of nodules inhibiting further nodule formation after the first few nodules have been formed, as a consequence of a molecular communication between root and shoot. Several researches on long-distance signaling in nodulation have identified a number of genes involved in autoregulation; however this process is still under investigation. With the aim of gaining a deeper insight in the signalling cascade of AON, we compared the root and shoot proteomes of *Medicago truncatula* plants inoculated with the symbiotic rhizobium, *Sinorhizobium meliloti*, with those of uninoculated plants. We utilized the technique of two-dimensional polyacrylamide gel electrophoresis for the identification of differentially expressed proteins. Twenty plants per biological sample were used, and 5 technical replicates were performed for each biological sample. We detected 19 differentially expressed spots comparing root samples from rhizobia-infected and uninfected plants and 16 differentially expressed proteins for the aerial parts. The differentially accumulated proteins were isolated and subsequently identified by mass spectrometry.