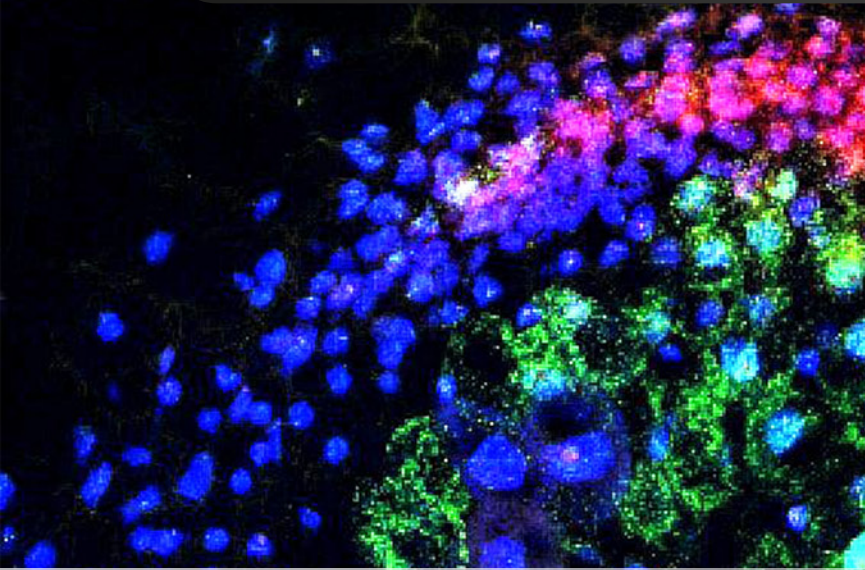
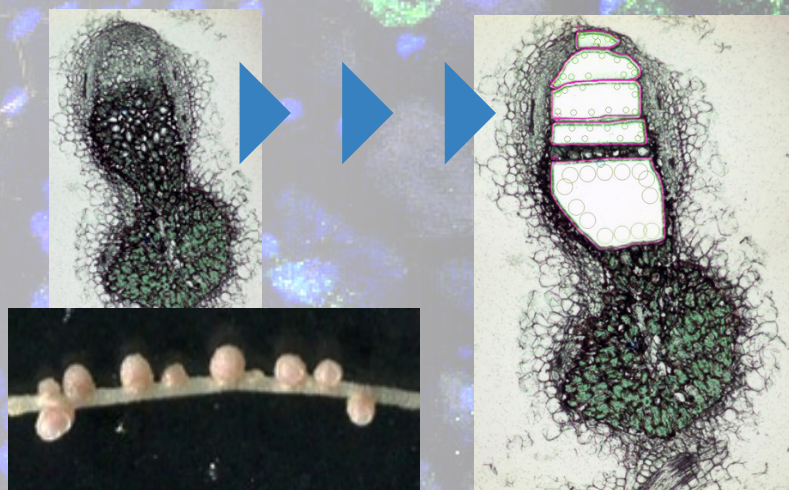


An integrated analysis of plant and bacterial gene expression in symbiotic root nodules using laser-capture microdissection coupled to RNA sequencing



Rhizobium-induced root nodules are specialized organs for symbiotic nitrogen fixation. Indeterminate-type nodules are formed from an apical meristem and exhibit a spatial zonation which corresponds to successive developmental stages. To get a dynamic and integrated view of plant and bacterial gene expression associated with nodule development, we used a sensitive and comprehensive approach based upon oriented high-depth RNA sequencing coupled to laser microdissection of nodule regions.

This study, focused on the association between the model legume *Medicago truncatula* and its symbiont *Sinorhizobium meliloti*, led to the production of 942 million sequencing read pairs that were unambiguously mapped on plant and bacterial genomes. Bioinformatic and statistical analyses enabled in-depth comparison, at a whole-genome level, of gene expression in specific nodule zones. Previously characterized symbiotic genes displayed the expected spatial pattern of expression, thus validating the robustness of our approach. We illustrate the use of this resource by examining gene expression associated with three essential elements of nodule development, namely meristem activity, cell differentiation and selected signaling processes related to bacterial Nod factors and redox status. We found that transcription factor genes essential for the control of the root apical meristem were also expressed in the nodule meristem, while the plant mRNAs most enriched in nodules compared with roots were mostly associated with zones comprising both plant and bacterial partners. The data, accessible on a [dedicated website >>>](#), represent a rich resource for microbiologists and plant biologists to address a variety of questions of both fundamental and applied interest.



Top: nodules of *Medicago truncatula*, before and after laser dissection. Right picture shows 5 different regions where different genes are expressed. **Down:** nodules on a *M. truncatula* root. **Background:** in situ mRNA hybridization on a nodule section showing transcript accumulation of two *M. truncatula* genes (pink and green signals respectively) specifically expressed in the apical zone of the nodule.

