

## **ROLE OF *KNOX1* TRANSCRIPTION FACTORS OF *MEDICAGO TRUNCATULA* IN ROOT NODULE FORMATION AND HORMONE SIGNAL TRANSDUCTION**

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Legumes represent the second family of crops after cereals in terms of cultivated surface and constitute a crucial source of proteins for food and feed to use in sustainable agriculture. Plant root architecture is determined by the number and distribution of lateral roots, which is adapted to the soil environment. Legumes, additionally, are able to develop symbiotic interactions with bacteria of the Rhizobia family to form another secondary root organ, the nitrogen-fixing nodule. Recently, a crucial role of cytokinin signalling mediated by the MtCRE1 receptor was revealed in *M. truncatula* nodule and lateral root formation. Indeed, the MtCRE1/LHK1 cytokinin receptor is crucial for the initiation of symbiotic nodule organogenesis in *L. japonicus* and *M. truncatula* models.

In seed plants, members of the KNOX1 homeodomain transcription factor family control multiple hormonal pathways involved in the determination of cell fate and organ formation, including cytokinin biosynthesis. In the *M. truncatula* model legume, we identified eight novel KNOX genes (*MtKNOXs*). Gene expression studies revealed organ-specificity, possible cytokinin-dependent transcriptional activation of two *MtKNOXs* and expression of seven *MtKNOXs* in roots. Moreover, three KNOX genes have been found to be modulated in response to *Rhizobium* infection in transcriptomic studies.

Within the framework of the bilateral Scientific Cooperation between CNR (IT) and CNRS (France), we are investigating the role of KNOX genes in rhizobia-induced nodule organogenesis as well as in the control of hormone homeostasis in *M. truncatula* roots.

Real Time qPCR experiments were carried out to analyze *MtKNOXs* early response to different plant hormones related to root and nodule development such as cytokinins, auxin, ethylene, abscisic acid, gibberellins and brassinosteroids. *In situ* hybridizations have been carried out to localize the message RNAs of the MtKNOXs of interest during nodule formation. Constructs for constitutive (i.e. 35S:CaMV) overexpression as well as for RNAi-mediated silencing of MtKNOXs have been obtained. One *mtknos3* knock-out heterozygous line was isolated in collaboration with The Samuel Roberts Noble Foundation (US) and its characterization is in progress to assess the role of this gene in nodulation processes.