

MtKNOX TRANSCRIPTION FACTORS: FROM THE SHOOT BACK TO THE ROOTS

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In seed plants, the class I KNOX (KNOTTED1-like) homeodomain transcription factor family plays a key role in the formation and maintenance of the shoot apical meristem (SAM). We isolated three class I and three class II *KNOX* genes in *Medicago truncatula* that are putative orthologs of the Arabidopsis homeodomain proteins STM, KNAT1/BP, KNAT3 and KNAT7. Interestingly, mRNA localization studies carried out on class I *MtKNOX* genes revealed important differences with previously characterised legume *KNOXs* as *M. truncatula* transcripts were not down-regulated in leaf primordia and early stages of leaf development. Gene expression studies revealed organ-specificity, cytokinin-dependent transcriptional activation of two *MtKNOXs* and expression of five *MtKNOXs* in roots. So far *KNOX* genes have been solely associated to aerial development and few data are available on Arabidopsis *KNOX* expression in roots. In *M. truncatula* three *KNOX* genes have been found to be modulated in response to *Rhizobium* infection in transcriptomic studies carried out in Pascal Gamas institute (CNRS-INRA, France). Therefore, we decided to explore a possible role for MtKNOXs in root development and/or establishment of root symbioses. Real-time quantitative PCR analyses, whole mount *in situ* hybridisation (WISH) and *Agrobacterium rhizogenes*-mediated root transformation with overexpression and RNAi constructs were carried out on *M. truncatula* seedlings grown in pouches and inoculated with *Sinorhizobium meliloti*.