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Poster Abstract - B.07

FUNCTIONAL GENOMICS OF KNOX TRANSCRIPTION FACTORS IN *MEDICAGO TRUNCATULA*

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Class I *knotted-like* (*KNOX*) homeobox genes are known to play a key role in the acquisition and maintenance of meristem identity, vascular development and leaf morphology. Their function in development is likely to be exerted through the regulation of multiple hormones pathways in a complex network of protein-protein interaction.

In *Arabidopsis thaliana KNOX 1* genes expression is first detected as the shoot meristem initiates in the embryo, disappears from the cells that destined to form leaf primordia and in some cases it extends to the vascular tissues underneath the vegetative shoot meristem (Hake et al. 2004). Currently there are very few reports of roles for *KNOX* genes in root development.

Five *KNOX* genes have been identified in *M. truncatula*, a model species for legume genetics, as a part of the project FIRB-MIUR on Post-Genomics of Forage Legumes.

All the five *MtKNOX* genes (two belonging to class I and three belonging to class II) have been shown to be expressed in roots, suggesting a possible role in root development and/or establishment of root symbioses.

In order to investigate the involvement of this class of transcription factors in root biology, we are setting up *Agrobacterium rhizogenes*-mediated iRNA root transformation assays for a functional genomics approach (Limpens et al. 2004). Moreover, this fast and effective tool will be used to test whether glucocorticoid-inducible systems, such as XVE (Zuo et al. 2000), can be utilized for studying gene function in legumes.

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