

***KNOX* GENES IN *MEDICAGO TRUNCATULA* VEGETATIVE AND REPRODUCTIVE DEVELOPMENT**

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In plants, the class 1 (*KNOTTED1*-like) *KNOX* family plays an important role in the formation and maintenance of shoot apical meristem. *KNOX* proteins are members of the homeodomain protein family of transcription factors that are found in all eukaryote lineages and are known to function as heterodimers with other homeodomain superclass proteins (BELL).

Four members of class I *KNOX* are present in the *Arabidopsis thaliana* genome. Their expression is first detected as the meristem initiates in the embryo and disappears from the cells that will form leaf primordia. During the transition between vegetative to reproductive stage, the expression pattern of different *KNOX* members diverges. *STM* localises across the apical meristem and in the apex of the developing floral primordium. *KNAT1* transcript is detected in the early floral primordium in what will become the pedicel and, as the pedicel develops, the expression persists in the cortex next to the vascular tissue. *KNAT2* is not active in the inflorescence meristem, it is reactivated subsequently in stage 3 floral meristems and finally becomes restricted to the carpel.

Overexpression of *KNOX* genes in different plant species strongly affects cell fate. The altered cell differentiation produces dramatic changes of the whole plant architecture and alters leaf morphology. Vegetative-to-reproductive transition is also affected by the misexpression of *KNOX* genes, as well as inflorescence meristem formation and flower organ development.

We have isolated *KNOX* genes in *Medicago truncatula*, a model species for legume biology and development, as part of a Post-Genome Initiative – FIRB (Funds for Investing in Fundamental Research) RBN018BHE, funded by the Italian Ministry of University and Research (MIUR).

Here we present the analysis of *MtKNOX* expression during vegetative and reproductive development. Expression profiles of *Arabidopsis* and *M. truncatula* *KNOX* genes will be compared in order to retrieve information and hints on possible molecular and genetic conservation of homeobox transcription factor function during vegetative-to-reproductive transition.