HORMONAL REGULATION OF MT\textsc{knox} TRANSCRIPTION FACTORS

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Homeobox genes are known to play a role in developmental regulation. The \textit{knotted-like} homeobox (\textit{KNOX}) genes fall into two classes. The class I \textit{KNOX} genes like \textit{KN1}, \textit{STM}, and \textit{KNAT1} are expressed in shoot meristems and loss of function mutations in different species revealed that \textit{KNOX} genes are involved in the acquisition and maintenance of meristem identity. The function of class II \textit{KNOX} genes is still undetermined.

Recent evidence suggests that \textit{KNOX} transcription factors may control meristem development by regulating the balance of activities of multiple hormones. However, little is known about a possible feed-back regulation of \textit{KNOX} gene expression by hormones.

We identified five \textit{KNOX} genes in \textit{M. truncatula}, a model species for legume genetics, which belong either to class I (\textit{MtKNOX1} and \textit{MtKNOX2}) or to class II (\textit{MtKNOX3}, \textit{MtKNOX4}, \textit{MtKNOX5}).

The expression of \textit{MtKNOX} genes was investigated by RT-PCR, Northern blotting analysis and \textit{in situ} hybridisation. All \textit{MtKNOX} transcripts were found in leaves, stems, shoot apex and roots although class I \textit{MtKNOX} expression was very poor in leaves.

In order to investigate a possible regulation of \textit{MtKNOX} by different hormones, we analysed gene expression in response to auxin, cytokinins, gibberellins, ethylene, abscisic acid and jasmonate.