CROSS-TALK BETWEEN HORMONES AND TRANSCRIPTION FACTORS IN PLANTS

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Plant development depends on the activity of meristems. During shoot growth, lateral organ primordia differentiate at the periphery of the shoot apical meristem, while a population of totipotent cells is maintained at the centre of the meristem to ensure continuous growth. For many years, plant hormones have been known to play a major role in developmental processes: gibberellins (GA) are involved in cell expansion, stem elongation and flowering, ethylene in senescence, cytokinins (CK) in promoting cell division, auxin in cell expansion and phyllotaxis. Developmental processes follow precise genetic programmes controlled by regulatory genes. In this respect, a central role has been attributed to transcription factors (TFs) whose spatial/temporal expression patterns contribute to define developmental domains and cell fates. In this context, KNotted1-like homeobOX (KNOX) genes are specifically expressed in the meristem and their repression is a key event in the differentiation of leaf primordia. Recently, work on Arabidopsis has in part elucidated the mechanisms by which genetic developmental programmes and hormonal signals interact to shape the plant body. KNOX genes, in particular, have been demonstrated to act closely with hormones in determining SAM maintenance, leaf initiation and morphogenesis. Cytokinins have been shown to facilitate SAM maintenance through the activation of KNOX genes; these in turn mediate the exclusion of gibberellins from the meristem, both through repression of GA bioynthesis and activation of GA catabolism. Auxin accumulation in peripheral areas of the SAM has been associated with repression of KNOX genes and determination of the position of incipient leaf primordia.

Despite the utility of manipulating hormone pathways and developmental genes in breeding for flowering time, plant height and plant architecture, little is known on the cross-talk between circuits involving hormones and genes in cereal species.

In our group, characterisation of the barley Hooded (K) mutant has provided new insight into mechanisms of KNOX gene regulation: the dominant K phenotype is associated with the duplication of a 305 bp element in intron IV of the Barley knox3 (Bkn3) gene. This regulatory element acts as an enhancer and causes ectopic expression of Bkn3 in the lemma-awn transition zone, leading to the formation of a new meristem that develops into an epiphyllic flower. A one hybrid screen aimed at isolating putative regulators of the BKn3 gene uncovered four proteins capable of interacting with the 305 bp element (K Intron Binding Proteins, KIBPs). In vitro binding of KIBPs to the 305 bp enhancer has been confirmed and binding sites identified. Based on homology with transcription factors previously associated with hormone pathways, we have investigated the involvement of
KIBP proteins in ethylene and gibberellin responses. A model summarizing interactions between plant hormones and the KNOX pathway will be discussed.