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Title: Mapping Transcription Factor Gene Regulatory Network in the Shoot Apical Meristem Stem Cell

Niche of Arabidopsis thaliana

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Abstract:

Spatiotemporal regulation of gene expression is the key phenomenon in multicellular organisms to specify fate of distinct cell types. Spatial and temporal regulation of gene expression is achieved by the cell signalling and transcription factors (TFs). In both animals and plants several studies have shown role of TF in cell and tissue specialization. Shoot apical meristem of Arabidopsis thaliana harbours a set of stem cells from which the various cell types of plant arise. How stem cells differentiate in to different cell types of the shoot and how organs form from these differentiated cells is still largely unknown. In the present study I investigated the role of broadly expressed TFs in specifying the epidermal and sub epidermal cell type. Epidermal cell types forms an important interface between the outside environment and the inside of plant body and protects the plants from pathogens and drought. Sub epidermal cell types are sandwiched between the epidermal cells and the internal cell layers and play an important role in maintaining the cell-cell communication across the cell layers in shoot apex. In leaves and stem tissue, sub epidermal cells differentiate form the photosynthetic tissue. To uncover the hierarchy of gene regulation among the TFs and to identify the network responsible for cell and tissue specialization, I have mapped the interaction between the TF promoters and their cognate trans-acting factors using yeast-one-hybrid (Y1H). Y1H data was analysed and gene-regulatory network was built. Promoter reporter studies for few selected TFs revealed in planta the importance of trans-acting factors in determining the spatiotemporal expression patterns.

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