Title:	Mapping Gene Regulatory Network of Shoot Enriched Transcription Factors in Arabidopsis Thaliana
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Abstract:	Cell and tissue specific expression of critical genes is a key hallmark of development in multicellular organisms. How spatially and temporally such gene's expression orchestrated is still not understood fully. Gene expression is driven by transcription factors (TFs). Often TFs involved in specification of cell fate are regulated tightly in a cell and tissue specific manner to exert their influence to few cells. In addition to transcriptional cascades signalling pathways also influences the decision of cell fate by post-translation modification of TFs. The cell types of the Arabidopsis shoot apex are organized in to differentiating progenitors that surrounds the central zone stem cells, which when differentiates in periphery adopt the fate of organ primordia cell types, while underneath the stem cells they differentiates in to rib-meristem, and that then give rise the stem and vasculature cell types. On this, one can impose a layering organization, where epidermal and subepidermal cell types makes the L1 and L2 cell layer, which divides anticlinally and cover the apex with two consecutive layers of cells, while the L3 makes the inner bulk of the meristem. How do these diverse cell type are specified and how do they maintain their fate throughout the life cycle of plant is not understood yet. By identifying the TFs using gene expression studies and studying their regulatory relationship I am trying to establish a regulatory network that will help in understanding the role of TFs in shoot apex development. This study aims to generate a large-scale interaction network that uncovers biologically relevant gene-regulatory interactions for shoot enriched TFs. To unravel the regulatory interactions, a yeast one-hybrid assay has been used to find out transcription factor protein-DNA interactions. In the present study I investigated the putative transcription factor binding sites for the shoot enriched TFs for which yeast one hybrid interactions data was made available. Promoter reporter studies were carried out to find out the functional role of these TFs along with gene expression studies
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