Title:	Developing Gene Regulatory Network of Differentially Expressed Transcription Factors in Shoot Apical Meristem of Arabidopsis thaliana
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Abstract:	Shoot apical meristem (SAM) of dicot plants consists of multiple cell types. Conveniently, it can be divided into zones, such as central zone, peripheral zone, rib meristem zone. Likewise, it can also be classified into cell layers such as L1 layer / epidermis, L2 layer / sub epidermis and L3 / corpus. Stem cells reside in the central zone of SAM and are surrounded by differentiating cells, which are the part of peripheral zone. Rib meristem zone is located just beneath the central zone and it provides positional cues to the central zone for maintaining stem cells. How cells acquire their identity in various zones of SAM is still not understood at molecular level. We developed a gene regulatory network for epidermal and subepidermal cell types enriched transcription factors using yeast one-hybrid (Y1H) approach to develop a better understanding of the cell fate specification and maintenance. In total, we have set up 3026 interactions and found 886 positive. We have studied the network of two genes in detail, namely, ARABIDOPSIS thaliana MERISTEM LAYER1 (AtML1) and PROTODERMAL FACTOR2 (PDF2). Several downstream and upstream regulators of these transcription factors (TFs) were involved in providing resistance against biotic and abiotic stresses. Further, to confirm the interactions of AtML1, PDF2 and PHABULOSA (PHB), we multimerized the motif cassette three times recognized by these TFs and again carried out Y1H assay. We expected to get more yeast growth as compared to the baits carrying the natural promoter, having only one motif cassette. But to our surprise that wasn't the case and therefore, the experiment need to be repeated atleast three times
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