Title:	Characterization of Gene Regulatory Networks in Shoot apex of Arabidopsis thaliana
Authors:	Sundaram, Jayesh Kumar (/jspui/browse?type=author&value=Sundaram%2C+Jayesh+Kumar)
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Abstract:	Cell types specific gene expression plays an important role in cell and tissue specialization in various developmental process. Specifically, TFs contribute a lot for the differential gene expression profiles observed among the cell types. The gene regulatory networks involved in the specification and maintenance of tissue layers in Arabidopsis thaliana SAM are not understood fully. Cell type specific gene expression profiling techniques have identified the genes that are differentially expressed or enriched including the TFs that regulate target genes. In this study, we have constructed PPI and PDI networks using yeast-two-hybrid (Y2H) and enhanced yeast-one-hybrid assays (eY1H), respectively, to understand how cell layer specific gene regulation is achieved in Arabidopsis SAM. Some of the interactions were validated by other experiments. The constructed PPI and PDI networks were characterized in the study by in-silico approaches. As the interactions were tested in the yeast model, the significance of the constructed network in- planta was analyzed using co-expression and co-occurrence properties of the interacting pairs. The nature of the transcription regulation in the PDI network were also predicted by co- expression of the TFs with its target genes and protein-protein interactions of the TFs with cofactors. The expression patterns of the interacting gene pairs were analyzed and the over- represented interaction types in the networks were identified. The eY1H assay was compared with other experimental methods available in the field, and we found that interactions captured by eY1H assay are both novel and reproducible in nature. The plant gene regulatory network is very complex and has many genetic redundancies. In order to identify redundant pairs, various association networks were created among TFs based on PPI similarity, target gene similarity, upstream regulator similarity and transcription factor binding site (TFBS) co-occurrence. SAM cell type specific PPI and PDI networks were constructed by in-silico approaches to understand the formation of different cell layers and stem cells maintenance in the shoot apex. Finally, we also identified cell type specific annotated transcripts / isoforms in the SAM of Arabidopsis thaliana by RNA-sequencing.
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