Title:	Determining the protein-DNA interactions for transcription factors specific to L1-L2 layer of shoot apical meristem in Arabidopsis thaliana
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Keywords:	Arabidopsis thaliana protein-DNA interactions for transcription factors specific to L1-L2 layer DNA Baits: Cell Type-Specific TFs Molecular Biology Techniques
Issue Date:	Jun-2020
Publisher:	IISER Mohali
Abstract:	Several complex processes characterize development in Arabidopsis thaliana and one of them is the establishment of meristems during embryogenesis. Meristems are formed at the two opposite ends of the embryo and thus are called the root apical meristem (RAM) and the shoot apical meristem (SAM). SAM can be further divided into three zones, namely central zone (CZ), peripheral zone (PZ), and rib meristem (RM). The plant SAMs comprise of well-defined cell layers as well (Ottoline Leyser & Furner, 1992). A number of genetic studies have been done in the past to comprehend the formation of organs and stem cell specification in SAM. But None of them were focused precisely on unraveling the regulatory mechanisms underlying this sophisticated arrangement of SAM (S. M. Brady et al., 2007; Jiao et al., 2009). Several network studies are coming into picture nowadays that turn out to help handle large data sets and thereby elucidating the physical interaction between sequence-specific regulatory transcription factor proteins and their respective target sites (Alexander M. Jones et al., 2014; Mukhtar et al., 2011). In the Y1H screen, 37 DNA baits were successfully screened against a library of 321 TF prey proteins at 220C, which is known to be the ideal temperature for Arabidopsis to grow. A total of 78 interactions could be made out using the Y1H screen among 22 DNA baits, and 54 TF protein preys. The network consists of 69 nodes connected through edges. The edges signify the physical interaction among the nodes.
URI:	http://hdl.handle.net/123456789/1414
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