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Title:	Understanding the gene expression patterns and regulatory network of epidermal and sub-epidermal cell population enriched transcription factors in Arabidopsis thaliana shoot apical meristem
Authors:	Bhatia, Shivani (/jspui/browse?type=author&value=Bhatia%2C+Shivani)
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Abstract:	<p>Transcriptional control of cell type specific genes is exquisitely regulated process in both animals and plants. Transcription factors (Tfs) and the regulatory networks that drive the expression of epidermal and subepidermal cell layers enriched TF genes in Arabidopsis are largely unknown. Here, we identified 65 TF genes from epidermal and subepidermal cell layers of the shoot apex. To determine how many of them display cell type specific expression patterns in different stages of Arabidopsis development, we made YFP based transcriptional fusions by taking a 3-kb upstream noncoding region. Here, we show that for 50% (22/44) TF genes, we were able to detect transcription. In the early embryo, critical epidermal cell layer enriched TF genes are broadly expressed, but in later stages, their transcription is precisely inhibited in the inner cell layers. TF genes whose expression patterns are associated with subepidermal cell layer identity did not show expression in the embryo. Upstream regulators were identified using enhanced yeast-one-hybrid (eY1H) to decode the regulatory mechanisms behind the expression of promoter reporters. By genetic analysis, we show that the GROWTH REGULATING FACTORS 1, 2, and 3, binds to the HOMEODOMAIN GLABROUS12 (HDG12) promoter and regulates its expression in epidermal cell layer to control the cell differentiation. This study gives us a comprehensive understanding of the expression patterns of epidermal cell layer TFs and how their expression gets modulated in critical developmental stages.</p>
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