Title:	A cellular expression map of epidermal and subepidermal cell layer-enriched transcription factor genes integrated with the regulatory network in Arabidopsis shoot apical meristem
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Abstract:	Transcriptional control of gene expression is an exquisitely regulated process in both animals and plants. Transcription factors (TFs) and the regulatory networks that drive the expression of TF genes in epidermal and subepidermal cell layers in Arabidopsis are unexplored. Here, we identified 65 TF genes enriched in the epidermal and subepidermal cell layers of the shoot apical meristem (SAM). To determine the cell type specificity in different stages of Arabidopsis development, we made YFP based transcriptional fusion constructs by taking a 3-kb upstream noncoding region above the translation start site. Here, we report that for ~52% (22/42) TF genes, we detected transcription activity. TF genes derived from epidermis show uniform expression in early embryo development; however, in the late globular stage, their transcription activity is suppressed in the inner cell layers. Expression patterns linked to subepidermal cell layer identity were apparent in the postembryonic development. Potential upstream regulators that could modulate the activity of epidermal and subepidermal cell layer-enriched TF genes were identified using enhanced yeast-one-hybrid (eY1H) assay and validated. This study describes the activation of TF genes in epidermal and subepidermal cell layers in embryonic and postembryonic development of Arabidopsis shoot apex.
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