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Title:	Investigating the Mechanism of Repression of DEWAX in Stem Cells of Arabidopsis thaliana
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Abstract:	DEWAX (DECREASE WAX BIOSYNTHESIS) locus encodes an AP2/ERF-type transcription factor that is preferentially expressed in the epidermal layer. It was demonstrated that DEWAX is a diurnally regulated transcription factor and is involved in the repression of cuticular wax biosynthesis genes under dark conditions in Arabidopsis thaliana. Based on the transcriptional reporter, I observed the expression pattern of DEWAX. Interestingly, it is repressed in the central zone (CZ) of shoot apical meristem (SAM) of Arabidopsis thaliana. WUSCHEL (WUS) is a homeodomain transcription factor produced by cells of the organizing center (OC). It moves towards the L1 and L2 layer of CZ, where it activates CLV3 and represses differentiation promoting genes in the stem cells. I analyzed the WUS microarray data and found DEWAX is a direct target of WUS and further validated by qRT PCR after WUS induction using the 35S::WUS-GR line. To investigate WUS binding on the promoter of DEWAX, I did Y1H assay using a 3 kb promoter of DEWAX and WUS as prey. The TAAT element is well characterized binding element for WUS, and I found several putative binding sites on DEWAX promoter.
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