

Genetic and genomic studies of shoot and flower growth in *Arabidopsis*

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in memory of my grandfather, Edwin Pratt Jordan

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Abstract

This thesis is organized around the theme of modulation of transcriptional states in *Arabidopsis thaliana*. The two particular mechanisms on which this work focuses are (1) microRNA-mediated negative regulation of protein levels (either by mRNA cleavage or by repression of translation) and (2) transduction of extracellular signals into the cell to affect the transcription program.

Chapter 2 characterizes the role of the *EARLY EXTRA PETALS (EEP1)* microRNA in the regulation of organ formation in the flower and shoot. The *eep1* loss-of-function mutant has extra petals, and it enhances the shoot phenotype of the *pinoid* mutant, which has defects in auxin signaling and organ formation. *EEP1* is nearly identical to a pair of published miRNAs (*MIR164a* and *b*); all three are predicted to target the mRNAs of six genes in the NAC family of transcription factors. Two of these genes, *CUPSHAPED COTYLEDONS1* and 2 (*CUC1* and 2), are redundantly required in flower development. Phenotypic and molecular analysis of lines overexpressing *EEP1* are consistent with (1) negative regulation of *CUC1* and *CUC2* by *EEP1* and (2) cleavage of the *CUC2* mRNA promoted by *EEP1*.

Chapter 3 describes the investigation, by reverse genetics, of five proteins encoded by genes in the *CLV3/ERS (CLE)* family. Due to the similarity of these proteins to *CLAVATA3 (CLV3)*, the likely secreted ligand for the *CLAVATA1* receptor-like kinase, functional analyses were performed in order to determine whether these proteins might also function as ligands for *CLV1* or other receptor-like kinases. The results presented here derive from experiments using overexpression, double-stranded RNA interference (dsRNAi), and promoter-glucuronidase (GUS) reporter expression.

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