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Functional Analysis of Natural Variation in the *CLAVATA2* Gene of
Arabidopsis thaliana

Plants continue to grow throughout their entire lives, forming new organs through the differentiation of undetermined meristematic cells. Vegetative organogenesis is driven by a zone of meristematic cells called the shoot apical meristem (SAM). Complex interactions among many genes in the SAM regulate the division and determination of these meristematic cells. I am investigating protein variation among different alleles of *CLAVATA2*, a gene that codes for a protein which regulates the growth of the SAM. Three wild type alleles of the *CLAVATA2* gene have been identified through DNA sequence analysis. To determine whether these versions of *CLAVATA2* have functionally diverged, these three alleles are being transformed into *Arabidopsis thaliana clavata2* mutants. *A. thaliana clavata2* mutants phenotypically differ from their wild type relatives by having slightly larger SAM's and producing extra floral organs. The flowers of *clavata2* mutants typically have twice as many carpels, extra stamens, and occasionally an extra floral whorl within the carpel. The varying degree of *clavata2* mutant phenotype rescue upon the reintroduction of each of the *CLAVATA2* alleles will then be assessed to gain insight into the functional variation among the different forms of the *CLAVATA2* protein.