



CALIFORNIA STATE SCIENCE FAIR 2011 PROJECT SUMMARY

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Project Title Screening for Genes Involved in Floral Determinacy	
Objectives/Goals Angiosperms have obtained tightly regulated floral determinacy to ensure proper floral organ development. Within the floral meristem of <i>Arabidopsis thaliana</i> , two genes, AGAMOUS (AG) and WUSCHEL (WUS), have been shown to play a pivotal role in the determination of stem cells after the correct number of floral organs is produced. Additional unidentified genes are likely involved due to the complexity of floral determination. A weak allele of AG was used to screen for mutants that enhance the floral indeterminacy phenotype; two putative mutants were identified, R151 and R24. A genetic analysis of the phenotypes R151 and R24, characterizing their roles in floral determinacy. Both phenotypes exhibit an enhanced indeterminacy phenotype that is indicative of a mis-regulation of meristematic stem cells. Rough mapping and fine genetic mapping was completed and R151 was inconclusive due to phenotypic properties, and R24 encodes a MADS-domain containing protein known as SEPALLATA3 (SEP3). Abstract Angiosperms have obtained tightly regulated floral determinacy to ensure proper floral organ development. Within the floral meristem of <i>Arabidopsis thaliana</i> , two genes, AGAMOUS (AG) and WUSCHEL (WUS), have been shown to play a pivotal role in the determination of stem cells after the correct number of floral organs is produced. Additional unidentified genes are likely involved due to the complexity of floral determination. A weak allele of AG was used to screen for mutants that enhance the floral indeterminacy phenotype; two putative mutants were identified, R151 and R24. A genetic analysis of the phenotypes R151 and R24, characterizing their roles in floral determinacy. Both phenotypes exhibit an enhanced indeterminacy phenotype that is indicative of a mis-regulation of meristematic stem cells. Rough mapping and fine genetic mapping was completed and R151 was inconclusive due to phenotypic properties, and R24 encodes a MADS-domain containing protein known as SEPALLATA3 (SEP3). Methods/Materials DNA extraction, EMS Mutagenesis, PCR, Gel Electrophoresis, Gel Purification, 4Peaks and Arabidopsis.org. Overall materials used were test tubes, gloves, flats of soil, microwave, centrifuge, pipettes, and a PCR machine. Results R151 produced inconclusive results; R24 produced linkage to chromosome one and linked to SEP3. SEP3 is characterized in floral determinacy as it produces heterotetrameric complexes with MADS-box genes (such as Agamous) and binds to CArG boxes. Conclusions/Discussion Plant screening and segregation analysis was obtained, however, when rough mapping began, R151 produced inconclusive results because it is a weak phenotype and could be background phenotype or mutation; due to variability when selecting the plants, an exact locus position could not be found. Rough mapping on R24 found that it was linked to chromosome one; Testing to the left and right of this primer was done. SEP3 was hypothesized to be the gene due to recombination frequency and genes in between primers 1-450 and 1-461. After complementation testing, SEP3 was proven to be the gene with R24. SEPALLATA (SEP) genes are fundamental factors in the ABCE gene model as they help with developmental processes of floral whorls; these genes are also a part of the MADS-box of floral homeotic genes	
Summary Statement In this project, I will study the relationship between R151/R24 and known genes involved in floral determinacy.	
Help Received Used lab equipment at University of California Riverside under the supervision of Theresa Dinh	