EDEN Undergraduate Internship Report
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The evolution of flowering within the plant kingdom has had a significant impact on reproductive success and diversification of angiosperms. While extensive work has been conducted using model systems such as *Arabidopsis*, *Antirrhinum*, and *Zea mays*, little is known about the function of various regulatory genes in the majority of angiosperms. At the Xiang Molecular Systematics Lab of North Carolina State University, they are working to develop *Cornus canadensis* as a model organism to study the evolutionary development of inflorescence architecture in Cornales, a diverse order of angiosperms. In this study, we addressed the following questions relative to gene function: 1) Is the activity of LFY homologs in dogwoods required for inflorescence development? 2) Do LFY homologs from *C. canadensis* (DW) and *C. florida* (BB) affect the architectural development of inflorescences differently in *Arabidopsis*? 3) Does overexpression of the FT homolog promote early flowering in *C. canadensis*?

In addressing the question of *Cornus* LFY homolog function, we used *Agrobacterium tumafaciens* and *Arabidopsis thaliana* in a transformation experiment. This experiment is currently ongoing. During this exchange, we successfully produced a T1 generation that is currently being evaluated. Additionally, I assisted in the evaluation of other transformed generations of *Arabidopsis* that had been developed prior to my internship.

Relative to the development of *C. canadensis* as a model system, I developed another experiment while working with the Xiang lab in collaboration with the Mountain Crop Improvement Lab at NC State University and the Ornamental Crop Breeding Lab at Oregon State University. While *C. canadensis* has been cited as a diploid species, there is evidence that there are tetraploid individuals as well[1]. In conducting molecular genetic experiments, it is pertinent to know the ploidy of the organisms being studied. I used flow cytometry to determine the ploidy of a random sample of individual plants within the Xiang germplasm collection. I found that there were in fact many tetraploids present. This will be valuable information as their work progresses. In addition, I travelled to the west coast to expand the Xiang germplasm collection of dogwoods for use in future experiments.

I learned other methods of experimentation while at the Xiang lab which include PCR, tissue fixation and embedding, microtome operation, tissue culture, and selection medium preparation. I believe that these are all valuable skills to have as a scientist moving forward through graduate school. Overall, as an undergraduate internship this was a successful experience. While no problem was necessarily solved, there was progress relative to the work being conducted at this lab. The question of evolutionary development of floral architecture will not be answered over the course of three months or even 6 months; however, learning the methods that are applied in answering such questions has been invaluable. There are also greater lessons to be learned here as a scientist. For instance, while conducting one experiment you may find yourself developing another. I look forward to continuing work with Dr. Xiang. Thank you for the opportunity.

[1] Shearer, K. and T.G. Ranney. 2013. Ploidy levels and relative genome sizes of species, hybrids, and cultivars of dogwood (*Cornus* spp.). HortScience 48(7):825-830.