

Northeastern Illinois University (NEIU), my undergraduate institution, did not offer many research opportunities in Botany, but that did not stop me from participation in research. With help from my advisor, Dr. Joel Olfelt, I obtained a small grant to investigate germination in two locally native prairie species. Our goals were to increase the use of locally native species in landscaping by optimizing the propagation of these two species. I investigated the germination responses of the two species to gibberellic acid and cold stratification, with and without light for 0 to 6 weeks. I significantly increased germination frequencies for these species. This was a perfect introduction to research because I largely worked independently to develop questions, design experiments, interpret results, and present my research to the public. The experience was extremely gratifying and made me eager to pursue more opportunities in further research.

Ultimately, it was the development of plant architecture that drew me to botanical research and I was eager to gain experience in this area. I won a spot in an REU program in Dr. Pamela Diggle's Lab at the University of Colorado in Boulder. My main project in Dr. Diggle's lab was examining the effects of *fw2.2* on sex expression in *Solanum lycopersicon* (domestic tomato). *Fw2.2* is a quantitative trait locus that explains significant differences in fruit size between wild and domesticated tomato. The purpose of the study was to determine 1) if fruit set affects flower form and function and 2) if fruit set differs with fruit size. I looked at two nearly identical lines of *S. lycopersicon*; one had an allele from a small-fruited relative, *Solanum pennelli*, introgressed at the *fw2.2* locus; the other was *S. lycopersicon* carrying the domesticated *fw2.2* allele. I collected data on flowering, fruiting, and floral organ size from each line. I found a significant difference in ovary size between the two lines, suggesting evolutionary significance of the *fw2.2* allele in establishing sex expression characteristics in *Solanum*. I presented my work at the REU symposium, and my experiences in Dr. Diggle's lab gave me extensive knowledge of flower anatomy, which became one of my interests: the evolution of flower development.

My work in Dr. Diggle's Lab, led me to understand that the questions that were most interesting to me were of a molecular nature, so I returned to Chicago, looking for research experience that would incorporate flowering plants and molecular genetics. I began working as a research technician in Dr. Rick Ree's Lab at the Field Museum of Natural History, determining phylogenetic relationships in the family *Corydalis*. *Corydalis* is of particular importance because it is a signature clade in the biodiversity hotspot of Southwest China. Understanding the phylogeny of *Corydalis* can help explain the role biodiversity hotspots have in global speciation and radiation. I sequenced two non-coding mitochondrial DNA fragments from 200 species of *Corydalis*. I then aligned the regions for further phylogenetic analysis. Using maximum likelihood criteria to estimate phylogenetic relationship, I created a phylogenetic tree of 200 species of *Corydalis*. It was through my work in Dr. Ree's lab, that I learned about the theories and principles of phylogenetics and gained an understanding of measurement of the strength of my data. An interesting aspect of this experience is that my work was part of a larger exhibit at the Museum, The DNA Discovery Center, where I would work in front of museum visitors. At certain times of the day visitors could ask questions about the work we were performing. I was surprised and delighted at the interest and positive response from so many people. It was so rewarding to help a general audience understand the excitement of lab work. That experience is one of the many reasons I remain motivated to make science approachable to a broader audience.

I graduated from NEIU with a major in Biology and a minor in Chemistry and took advantage of an amazing opportunity to gain experience in molecular developmental research by working in Dr. Lena Hilman's Lab at University of Kansas studying the evolution of flower symmetry. Flower symmetry was a major innovation in the history of flowering plants because

it allowed plants to interact with pollinators in innovative ways. This research was aimed at understanding how symmetry genes *CYCLODIA* (*CYC*) and *DICHOTOMA* (*DICH*) function in *Plantago major*. *CYC* and *DICH* establish bilateral symmetry in the flowers of the closely related species, *Antirrhinum majus* (snapdragon), but *P. major* flowers are radially symmetrical. My work will help determine how *CYC*-like genes are employed in the development of different flower morphologies. I isolated *CYC*-like genes from *P. major* made probes for *in-situ* hybridization. In bilateral flowers the *CYC*-like genes are expressed in specific regions of early flower tissue to set up bilateral symmetry. Interestingly our *in-situ* results suggested that the *CYC*-like genes in *P. major* indeed show *CYC*-like expression but employed these genes in all areas of the developing flower. I also learned and solidified my techniques in molecular biology, including cloning, mRNA extraction, cDNA synthesis, and degenerate primer design and optimization. This work has contributed to a paper, which has been submitted to PNAS (1).

I was accepted in the PhD program at University of California in Davis, which is the perfect place for me to make important scientific contributions using my interests and skills. In the first year my knowledge of plant systems grew immensely and I was extremely productive. I spent most of my first year rotating, with five weeks learning histology in Dr. Andrew Groover's lab. I worked on woody tissue, and my histological sections that presented an example of successive cambium were used in a paper that was published this year (2). I also began work on a project combining my background in phylogenetics and my interest in genes that regulate development, which carried over into my rotation in Dr. Daniel Potter's lab. In order to determine the evolutionary context of the gene POPCORONA and its relationship to other related genes, I made a comprehensive phylogenetic tree of the plant developmental genes Class III HD ZIPs. This work was included in a paper that was recently submitted to PLoS ONE (3). I am currently in Dr. Neelima Sinha's lab, where I have become fascinated with the phytohormone auxin and how it affects leaf complexity, which is the motivation behind my proposed research project.

For me one of the most exciting aspects of scientific inquiry is that my intellectual interests drive the research, and the results from this research further drive the curiosity to ask more questions. My research has only accelerated my interests and I am excited to continue working on unraveling the story of evolutionary development in plants through my doctoral studies. The NSF pre-doctoral fellowship would be vital in supporting my drive to incorporate all my past experiences into my current goals, while also supporting my desire to mentor, teach, and communicate these findings to a wide variety of audiences.

References:

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2. Preston, J, Martinez, C, Hileman, L. Gradual disintegration of the floral symmetry gene network is implicated in the evolution of a wind-pollination syndrome. PNAS, in revision.
3. Du, J, Miura, E, Robischon M, Martinez, C, Groover A, The Populus class III HD ZIP transcription factor POPCORONA affects cell differentiation during secondary growth of woody stems. PLoS, in revision.