

Research Experience

My summer internship with the Dr. Jenny Xiang lab at North Carolina State University focused on the FLOWERING LOCUS T (FT) gene and on the dwarf dogwood *Cornus canadensis*. The Xiang lab studies the genetic controls of flower development and morphology in the angiosperm order Cornales, especially the dogwood genus *Cornus*. The Cornales is the basal-most order of the Asterid clade, and so an understanding of the genetic mechanisms at work in this order has the potential to be highly informative about the evolutionary trends shaping this important and diverse group, as well as those shaping the evolution of flowering plants in general.

Cornus canadensis is a perennial herbaceous dogwood being developed by the Xiang lab as a model organism to study flowering genetics in the Cornales. One barrier to this development is the generation time of the plant. The FT gene is a controller of flowering phenology in plants, and FT transgenes have been shown to promote early flowering in several model species. Therefore, reducing the generation time of *Cornus canadensis* by *Agrobacterium*-mediated genetic transformation using a *Nicotiana* FT gene was one primary objective of this research. While results are heartening, the ultimate success of this effort remains to be confirmed, as several control calli are still alive and the surviving experimental calli must regenerate further before performing PCR confirmation. To test the link between transgene and flowering phenology, transformed plants must be grown to maturity. These temporal limitations are inherent in *Agrobacterium*-mediated transformation systems, but there is a procedural modification which could help to confirm transformation more quickly, thereby streamlining the transformation protocol and experiments using it: construct a vector which contains both an FT transgene and a marker transgene, such as GFP, for quicker visualization of transgenic calli.

A related contribution I made to the Xiang lab's research effort was the acquisition of live specimens of *Cornus canadensis* and its sister species, *C. suecica*, from several sites along the coast of Nova Scotia, Canada. The transformation system optimized for *C. canadensis*, as well as other study systems optimized for this plant, should be adaptable with little or no change to *C. suecica*, potentially making the entire study system more robust. I also collected *C. canadensis* DNA samples from sites from Maine to northern Nova Scotia to examine any latitudinal or other geographic variation in the FT gene.

A second primary objective was to understand the phylogenetic history of the FT gene and the PEBP gene family of which it is a part. I mined GenBank for FT orthologs and performed a number of phylogenetic analyses of this gene subfamily, identifying a large number of putative gene duplications and branch-specific positive selection. Using this alignment I designed primers for the isolation of the FT gene. Bayesian inference consistently returned tree topologies of a higher resolution and with more statistical support than maximum likelihood methods. I developed simple Perl scripts to parse sequence data from hundreds of accessions, which worked far better than processing these records manually.