

Project Summary

Overview

How does historical selection in natural populations lead to contemporary constraints on growth under novel environments? Even if standing genetic variation is large, negative correlations among functional traits may constrain evolutionary responses. However, the **genetic basis of some adaptive traits appears more complex because the genotype to phenotype map shifts alongside environmental gradients**. This suggests that even the same trait (growth) has a dynamic genetic and genomic architecture when genotypes are exposed to different environments, yet we understand very little about this process. Thus, non-linear phenotypic responses due to significant gene by environment interaction leads to difficulty in predicting genotype growth to new environments.

I propose to decompose the complexity of genotype by environment interactions that produce non-linear phenotypic expressions in a Department of Energy flagship genus, *Populus*, known for their economical and ecological significance. In a close relative to the model *P. trichocarpa*, *P. basamifera* is a powerful system to understand the impact of historical selection and gene by environment interactions on productivity. This species shows genetically based clines in phenology with signatures of positive selection and gene-environment associations in regions related to phenology and growth under common garden experiments. However, growing season length (GSL) cues driven by photoperiod vs temperature are typically confounded in these analyses because these environmental parameters covary. Clonal propagation in *Populus* is ideal for assessing the phenotypic expressions of genotypes across environmental gradients, and clonal selection is the principal mode used by plant breeders. Therefore, I aim to achieve two research aims: **1) identify genetic constraints on growth across an environmental gradient of GSL and two levels of soil moisture while controlling for photoperiod and 2) uncover the genomic landscape of trade-offs associated with variable GSL that may be modulated by soil moisture.**

Intellectual Merit

This work will contribute to understanding the limits of adaptation and productivity to novel environments generated by climate change, particularly when the genetic architecture of adaptation involves trade-offs of the same trait measured among different environments. Quantitative genetic theory and genomic analyses will uncover the nature of trade-offs of an ecological and economically important trait: woody biomass production. Therefore, proper identification of trade-offs not only aids in predicting resiliency or susceptibility to climate change, but it also has an applied value. No single genotype is best suited for all environments and this work will inform optimal selection of cultivars for plant breeders and growers.

Broader Impact

The proposed work will simultaneously advance discovery while promoting teaching, learning, and training. I will work closely with my post-doctoral mentor, Dr. Stephen Keller, to develop foundations in population genomics to create new knowledge which will be disseminated in peer-reviewed journals. Through active engagement I will facilitate others in the creation process, including those from under-represented groups such as myself. Specifically, I will involve undergraduates in the plant biology department at the University of Vermont in this research with the goal of leading them to co-authored publications. At Burlington High school, which harbors many refugee students because Burlington is a major resettlement site, I will leverage their **2 week-long Year End Studies (YES) program** to provide real life experiences of how science works and foster appreciation for sustaining plant productivity under climate change. I will further disseminate the outcomes of the proposed work to scientists at conferences and poplar breeders. All data generated

will be stored and shared on open data repositories such as *NCBI SRA*, *iPlant*, and *Github*, with fully documented workflows to facilitate repeatable analyses.