

# Project Summary

## Overview

How does historical selection on natural variation lead to contemporary constraints on growth and productivity under novel environments? Low standing genetic variation in these functional traits may be the key limiting factor in response to novel selection regimes. On the other hand, even if standing genetic variation is large, negative correlations between 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 genomic basis when expressed under different environments, yet we understand very little about this process. Thus, significant gene by environment interaction leads to difficulty in predicting genotype growth to new environments, which are particularly challenging when responses are non-linear.

**I propose to investigate the quantitative genetics and genomics bases of gene by environment interactions** in a DEO flagship genus, *Populus*, known for their economical and ecological significance. In a close relative to the model *P. trichocarpa*, *P. basamifera* show 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* also is ideal for assessing genotypic responses 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 in woody biomass production across an environmental gradient of GSL while controlling for photoperiod** and **2) uncover the genomic landscape of trade-offs associated with GSL**. that provide a powerful system to understand the impact of historical selection and gene by environment interactions on productivity.

## Intellectual Merit

This work will contribute to understanding the limits of adaptation and productivity to novel environments such as climate change, particularly when the genetic architecture of adaptation involves trade-offs the same trait measured among different environments. Linking quantitative genetic theory with the genomic underpinnings of an ecological and economically important trait: woody biomass production. Therefore, proper identification of trade-offs not only aide 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

Following a trickle down approach, 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 my 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 undergraduate researchers in the plant biology department at the University of Vermont in this research with the goal of leading them to co-authored publications. Since Burlington, Vermont is a resettlement site for refugee from Nepal, Vietnam, and Africa, I will host 2 week hands on workshops for local high schools in our common garden plots where they will actively participate in sampling with the aim of fostering appreciation for the importance of

sustaining plant productivity under climate change and providing real life experiences of how science works. I will further disseminate the outcomes of the proposed work to scientists at conferences and poplar breeders. Finally, for full transparency in uncovering findings, all data generated from this project will be stored and shared on open data repositories such as NCBI SRA, iPlant, and open access data repositories, with fully documented workflows to facilitate repeatable analyses.