

Project Description

Working title: Quantitative genomic architecture of function-valued traits in Balsam Poplar.

Introduction/Motivation

Adaptation to historical climate conditions often lead to constraints in current conditions (Etterson & Shaw 2001; Weins 2004), particularly if populations are exposed to novel environments such as those brought about by climate change (IPCC). **In response to a changing environment, what mechanisms lead populations to become resilient or susceptible?** Long-lived perennial plant species that experience significant environmental variation within their lifespan must rely on the pre-existing genetic architecture to produce functional traits that match shifting environments in order to persist (Scheiner 1993; Gilchrist 1995). This genotype by environmental interaction that produce phenotypes often manifests in non-linear responses that can be represented as mathematical expression, known as a *function-valued trait* (Kingsolver et al. 2001). **Visualizing a trait as such offers insights on the nature of trade-offs (Kingsolver et al. 2015), for example, genotypes may perform highest at specific windows of the environmental gradient (low-high trade-off) or operate over wider or shorter windows (generalist-specialist trade-off).** Unfortunately, we have very little understanding for how complex environmental axes modulates trade-offs in function-valued traits, both at the phenotypic and genomic levels, which critically impairs predictions of species responses to climate change.

Poplar is an exemplary model to understand the quantitative genomic architecture of trade offs in growth, imagined as a function-valued trait, across environmental gradients. Poplar represents a DOE flagship genus that provide key ecosystem services and are utilized as an alternative energy source. Therefore, growth is a functional trait of ecological and economical significance.

Research Objectives

Objectives

I propose to detail and uncover the genetic constraints on woody biomass production of balsam poplar when exposed to varying growing season lengths (GSL) and soil moisture. Genetic constraints will be explored in two approaches **1) Quantify the shifts in the genetic architecture in growth performance both at the phenotypic and genomic levels and 2) Quantify any changes in the effects of previously identified quantitative loci associated with shifts in the genetic architecture and predict performance within natural populations.**

Experimental Approach

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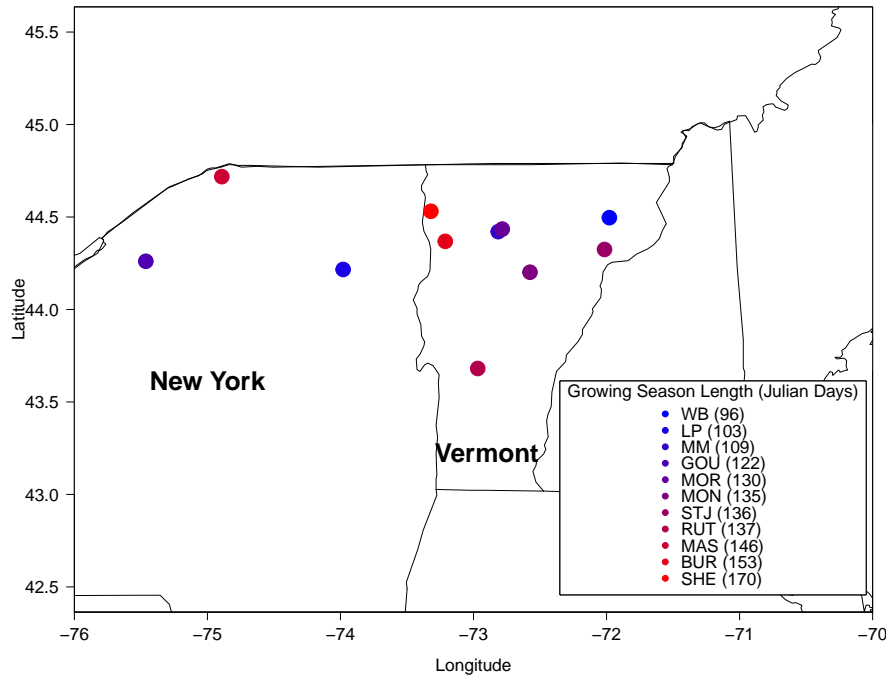


Figure 1. 11 sites vary in their growing season length (Julian Days) with very similar climate in New York and Vermont.

Anticipated Major Outcomes

The outcome of this work will inform growing practices. If we observe **overall variation** in growth, then the top cultivar operates the highest over many latitudes (Figure 2 A,B). However, if there are constraints between **lower-higher** growing season length, then only particular cultivars should be chosen at a given latitude (Figure 2 C,D). Finally, **generalist-specialist variation** would indicate that specific latitudes should utilize a certain cultivar (Figure 2 E,F).

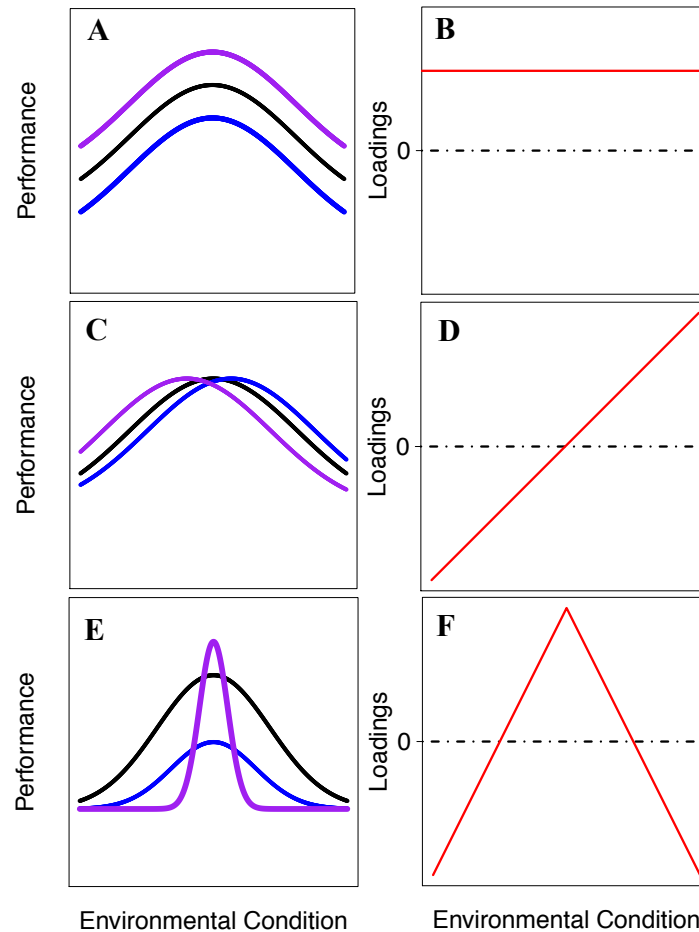


Figure 2. Predictions for the outcome of common garden experiment which vary in growing season length. The left panels illustrates different types of performance curves (growth) as a function of growing season length for three mock cultivars. The accompanying right panel figures illustrates the genetic correlation between growth and environmental condition using quantitative genetics techniques (Kingsolver 2001; Kingsolver et al. 2015). If **overall variation in growth is not constrained (A)**, then growth is genetically correlated among all GSL conditions (**B**). However, if there is a **trade-offs between shorter-longer GSL (C)**, then there will be opposing correlational structuring of performance among growing length conditions (**D**). Lastly, if there is **generalist-specialist trade-offs (E)**, then performance at intermediate GSL are negatively correlated with extreme GSL (**F**).

Significance

Training Objectives

The training objectives I have developed involve **3 general goals**: 1) Establish a solid foundation in ecological genomics and apply these principles to a new system plant systems; 2) Acquire more statistical and bioinformatic tools to uncover complex biological patterns associated with genomic and phenotypic datasets; 3) Optimally communicate science to diverse backgrounds.

Goal 1:

One of the first steps in applying theory is knowing your organism. Therefore, a foundation in natural history of balsam poplar will be absolutely critical for how I approach analyzing data. To achieve this goal, I will not only delve into the primary literature (or should I have done this by now?) but also aide in ongoing common gardens in Burlington, Vt and Indian head Canada, which will also involve interacting with experts in the field.

Goal 2: Although I have worked with next-generation genomic data in my dissertation, there is much more to learn, particularly with respect to creating genotype-phenotype maps across varying season lengths. To aide in this goal, I will consult and meet with my post-doctoral advisor on a weekly basis when data are ready to be analyzed.

Goal 3: Science will solve pressing issues that we face today, such as the negative effects of climate change. Therefore, it is my firm belief that science should be shared to all people, whether a student, a farmer, or other scientists. Therefore, I will usher in the next wave of scientists by mentoring high school and undergraduate researchers. I will communicate my findings with poplar farmers. I will present my findings at scientific meetings to obtain feedback and create a scientific network that is cohesive.

Career Development

Funding will facilitate my long term goal: **discover and uncover novel trends in biological systems/processes**, whether as an academic, consultant, or data scientist. I find enjoyment in analyzing data, sharing it in a digestable manner, and applying the outcomes to solve real world problems. Today's problems often involve handling big-data and synthesis between fields. Funding for the proposed work will allow me create explicit links between two fields: quantitative genetics and the molecular bases of complex traits. To create these links, I will further develop my statistical and bioninformatic capabilities to analyze large datasets generated from next-generation sequencing.

Although the research theme is similar, the proposed work is substantially different from my dissertation. My dissertation focused on how molecular level processes explains diversity at the species-level and utilizing this information to predict ant species responses to climate change. However, species comprise of many populations, whose responses may vary themselves. Therefore, as an NSF post-doctoral fellow, I hope to approach climate change adaptation at the population-level using a completely different system, such as balsam poplar.

Choice of Sponsoring Scientists

In collaboration with **Dr. Stephen Keller at the University of Vermont**, I will be able to explore my ideas in bridging links between quantitative genetics and the genomic basis of function-valued traits on an economically and ecologically important cottonwood tree species (balsam poplar). Trees do not move, unlike the ants, and are amenable to quantitative genetic analyses because they clonally propagated. Dr. Keller has been working on balsam poplar for X years and has established an immense amount of genomic resources through the funding of the **National Plant Genome Initiative (NPGI)**. Over the span of his career, Dr. Keller has published **27 peer-reviewed manuscripts**, whose track record I wish to one day achieve. This high productivity uncovered shifts in population structure due to historical climate change which is reflected in their phenological traits with strong signatures of selection for critical loci relating to growth and phenology. Therefore, Dr. Keller utilizes diverse approaches such as field surveys, lab work, and computational skills (genomic analyses) to answer pressing issues that we face today and he has established himself as a pioneer and leader in climate change biology.

Broader Impacts and Timetable

The proposed activities will increase our understanding of how gene x environment interactions shape critically important phenotypes, such woody biomass production which is of economical importance. Furthermore, the proposed work will foster and develop my own skill sets and allow me to contribute to the development of others. First, I plan to work closely with my NSF postdoctoral mentor, Dr. Stephen Keller, to learn a brand new study system, balsam poplar. Together, we will establish 6-12 common garden sites in 2017 and quantify woody biomass production over the next field seasons (2018-2020 summers; Table 1, #1). We will also pair phenotypic results with genomic analyses to uncover the molecular bases of constraints starting the fall of the first phenotyping (Fall 2018; Table 1, #1). Concomittantly, I will begin writing methods (2018), results (2019), and submit findings as a manuscript (2020) in open access journals so that findings reach all scientists and layperson. I will also implement strong data management strategies (2017) such as version control, online notebooking for absolute transparency, and open access so that any scientist or even layperson may recaptulate critical results. To dessiminate my work further with other scientists, I will attend conferences such as Evolution and Molecular Biology and Evolution (MBE; 2019 and 2020). To dessiminate my work to a much broader audience, I will create an interactive “Shiny” Web Application all of the proposed work (Table 1, #7).

To complete my goal of ushering the next wave of scientific minds, I will involve both high school and undergraduate students as activate participants in our proposed project. Additional phsyiological metrics such as stress tolerance and phenology will pair nicely with the current scope of the project. For undergraduate students, I will develop projects with them as well as instill strong data management practices and eventually transfer their outcomes into first author publications in open access journals. Since the University of Vermont strongly supports undergraduate investigators to showcase their research, I will bring them to conferences so they can present posters and/or oral presentations (Table 1, #5). I will collaborate with local high schools by hosting workshops to involve students with the proposed work (Table 1, #6). Specifically, Burlington High School has a 2 week period for students to explore an array of interests and I will recruit students to assist in sampling in our common gardens. Since Burlington is a target site for refugees from African countries (~20), Nepal, and Vietnam, students with diverse backgrounds will surely be represented.

Table 1: Time table of yearly goals

Tasks and Goals	2017	2018	2019	2020
1) Common Garden/Field	Set up common gardens	Phenotype	Phenotype	Phenotype
2) Genomic Analyses		Initiate QTL mapping of phenotypes		Complete QTL mapping of phenotypes
3) Attend Conferences			Present poster at Evolution and MBE	Present talk at Evolution and MBE

Tasks and Goals	2017	2018	2019	2020
4) Manuscripts		Write methods	Write methods and results	Finish manuscript and submit
5) Mentoring	Develop projects with undergraduates	Implement projects	Write up findings	Submit manuscripts with undergraduate researchers as primary authors
6) Public Outreach	Set up 1 common garden with high school students	Involve high school students in phenotyping	Involve high school students in phenotyping	Involve high school students in phenotyping
7) Data Management	Initiate project and share on Github	Utilize github repository to track progress and back up data		Create interactive Shiny App