Project Description

Introduction

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 2007). **The degree to which organisms can alter their functional traits, known as phenotypic plasticity, across shifting climate gradients dictates whether they are resilient or susceptible, which is especially important for long-lived species** that experience significant environmental variation within their lifetimes (Gilchrist 1995). Typically, phenotypic plasticity is reduced during climate adaptation such that physiological mechanisms that were once induced become fixed (Waddington 1953; Pigliucci et al. 2006), resulting in trade-offs between historical and contemporary environments that may indicate susceptibility to climate change. However, changes in the environment may interact in unique ways with genotypes such that trade-offs lessen or may even completely reversed (Messina & Fry 2003), resulting in resiliency to environmental perturbations. Yet, **we know very little about the complex dynamics of trade-offs** because many experimental approaches (Wu et al. 1992; Wu & Stettler 1997; Zalesney et al. 2005) do not include environmental manipulations that are continuous in natur which may severely underestimate the genotype by environmental influences (Stinchcombe et al. 2012).

Genotype by environmental interaction that produce phenotypes (Yamada 1962) often manifest in non-linear responses that can be represented as mathmetical expression, known as a *function-valued trait* (Gomulkiewicz & Kirkpatrick 1992; Kingsolver et al. 2001). **Visualizing a trait as such offers insights on the nature of trade-offs**, for example, genotypes may perform highest at specific windows of the environmental gradient (*short-long trade-off*) or perform higher over wider or shorter windows (*generalist-specialist trade-off*; Kingsolver et al. 2015). 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 (Gienapp et al. 2008; Fitzpatrick & Keller 2014).

Shifting climate may potentially negatively impact **Poplar, a DOE flagship genus with long-lived species** that provide key ecosystem services (Schimel et al. 1998) and are utilized as an alternative energy source (Stanton et al. 2010). Poplar is an exemplary model to understand how historical selection regimes have shaped populations can result in either resiliency or susceptibility to future climate change. In particular, populations of balsam poplar (*Populus basamifera*) display strong signatures of historical selection on productivity (Kellet et al. 2011) and genetic based clines in phenology in natural populations (Keller et al. 2012) and under common gardens (Keller et al., unpublished). **However, growing season length (GSL) cues driven by photoperiod or temperature are confounded and future experimental work needs to disentangle both forces** (Keller et al., unpublished?). Furthermore, since climate change will bring about more complex shifts such as more variable precipitation regimes (Mueller & Seneviratne 2012), whether optimal hydration status can rescue or reinforce trade-offs in GSL is currently unknown, especially since soil moisture is a critical parameter of growth for balsam poplar (Larchevêque et al. 2011). Luckily, balsam poplar readily propogate clonally and in fact, clonal selection is the principal mode used by plant breeders (Stanton et al. 2010). Therefore, balsam poplar are amenable to quantitative genetics and genomics techniques that will improve predictions to future climate shifts (Stanton et al. 2010; Fitzpatrick & Keller 2014).

Research Objectives

My overall goal is to determine the quantitative genetic architecture of trade offs in growth,

imagined as a function-valued trait, across 2 continuous environmental axes: GSL and soil moisture. Genetic constraints will be determined with two approaches: **1)** Assess 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 broadly to natural populations.

Experimental Approach

With the aide of **high school students, undergraduate researchers, and local botany groups (New England Wild Flower Society and Burlington Garden Club)**, we will establish 8-12 common gardens that span a GSL gradient spanning 2.5 months (Figure 1) using a quantitative genetic clonal design. In addition, we will vary soil moisture at 2 levels, high or low, at each common garden. Within each common garden and moisture level, we will randomly plant 30-50 unique genotypes with 3-5 replicates per genotypeat 1-2 meter spacing. Prior to planting, genotypes will be clonally propogated utilizing the University of Vermont's greenhouse to initially control for growth conditions and ensure enough material for replication. Genotypes will be selected from regions spanning the whole climate gradient of their native range and have pre-existing genomic resources/information. **In total, the community will have established 1,440-6,000 poplar plants**.

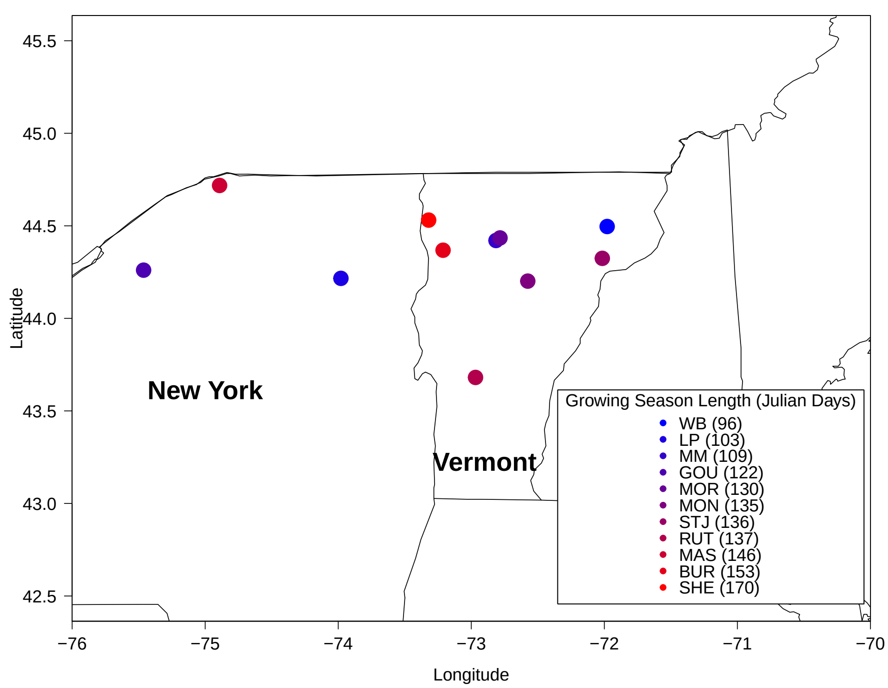

Figure 1. 11 sites vary in their growing season length (Julian Days) with very similar climate in New York and Vermont.

Anticipated Major Outcomes

When reared along a GSL gradient, genotypes may exhibit no constraints at all in growth (Figure 2 A,B), or two types of trade-offs in growth: shorter-longer (Figure 2 C,D), or generalist-specialist (Figure 2 E,F). Elevated soil moisture may either **lessen trade-offs** (i.e. slope in shorter-longer variation becomes less steep, Figure 2 D), **shift between trade-offs** (shorter-longer to generalist-specialist), or even **reverse trade-offs** (i.e. shorter-longer variation at one moisture level and generalist-specialist),

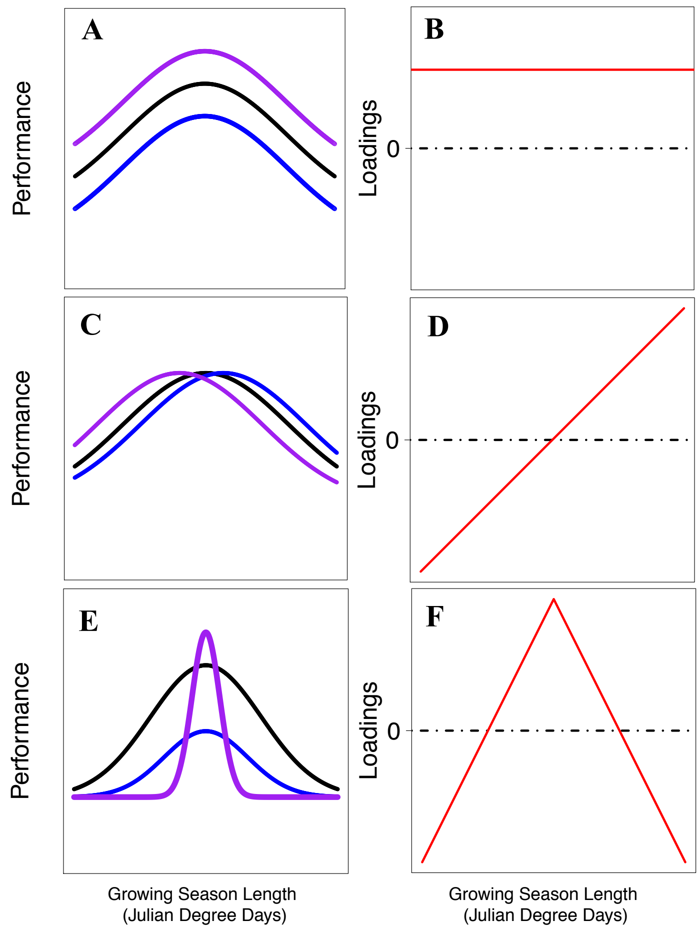

Figure 2. Predictions for the outcome of common garden experiment which vary in growing season length (GSL). The left panels illustrates different types of performance curves (growth) as a function of GSL for three mock clones. The accompanying right panels illustrates the genetic correlation (loadings from multivariate analyses) between growth and GSL 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 condtions (**D**). Lastly, if there is **generalist-specialist trade-offs** (**E**), then performance at intermediate GSL are negatively correlated with extreme GSL (**F**).

Significance

The proposed work will illuminate the nature of trade-offs for two critical environmental axes (GSL and water availability). **Determining whether trade-offs can be alleviaed or reversed has significant applied value** because poplar growers may enact management practices to maximize yield, particularly for an ecologically and economically important species within poplar, a DOE flagship genus. 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 **shorter-longer GSL**, then only particular cultivars should be chosen at a given latitude (Figure 2 C,D). Finally, **generalist-specialist GSL** would indicate that specific latitudes should utilize a certain cultivar (Figure 2 E,F).

Training Objectives

I have **3 general training objectives**: 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) Effectively communicate science to diverse backgrounds.

Goal 1: A foundation in the natural history of balsam poplar and population genetic theory will be absolutely critical for carrying out the proposed work. To achieve this goal, I will aide in ongoing common gardens in Burlington, VT and Indian Head, Canada, which will allow me to become familiar with poplar and interact with experts in the field. I will lead journal clubs specific to population genetic papers in order to solidify my scientific purview. After all, I learn best by talking and doing science.

Goal 2: Although I have worked with next-generation genomic data in my dissertation, there is much more to learn. In particular I will need to create genotype-phenotype maps, project genomic predictions, and manage large datasets. 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: Because science will solve pressing issues that we face today, it is my firm belief that science should be shared to all people from different walks of life. I will develop undergraduate projects and offer one on one mentoring. Next, I will actively include local high school students in their 2 week **Year End Semester (YES) program** and **members from the New England Wild Flower Society (http://www.newenglandwild.org/) and Burlington Garden Club (http://www.bgcvt.org/)** into our common garden in order to cultivate citizen scientists. I will communicate my findings to poplar farmers. As a member of the **Burlington Data Science Meetup (http://www.meetup.com/Burlington-Data-Scientists/)**, I will host a **Hackathon** where local data scientists from diverse professions may propose novel methods for uncovering biological patterns.

Career Development

Funding will facilitate my long term goal: **discover and uncover novel patterns in biological 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 inolve 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 informatic skills 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 in the plant biology department** 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 I am accustomed to, and are amenable to quantitative genetic analyses because they clonally propogate. 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**, utilizing diverse approaches such as field surveys, lab work, and computational skills (genomic analyses) to answer pressing issues that we face today. This high productivity and track record, which I strive to emulate, identified significant climate adaptation for phenology in balsam poplar with strong signatures of selection for loci relating to growth and phenology. Therefore, Dr. Keller 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 by environment interactions shape critically important functional traits, 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 8-12 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 through the Github platform (https://github.com/adnguyen), so that any scientist or even layperson may recaptiulate our findings. To dessiminate my work further with other scientists, I will present posters initially (2019) and oral presentations (2020) at conferences such as Evolution and Plant and Animal Genome (PAG). 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).

Public Involvement: Students

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**.

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.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, #2).

Public Involvement: Local Data Scientists
Public Involvement: Poplar farmers

Table 1: Time table of yearly goals

Tasks and Goals	2017	2018	2019	2020
1) Common Garden	Set up common gardens	Phenotype	Phenotype	Phenotype
2) Public Involvement	Initiate **Year End Semester (YES) program**: Set up common garden with high school students and local citizen scientists	Involve high school students and citizen scientists in phenotyping	Involve high school students and citizen scientists in phenotyping	Involve high school students and citizen scientists in phenotyping
		Create interactive Shiny App	**Host Hackathon** with local Data Science Meetup group	Engage poplar farmers
3) Mentoring	Develop projects with undergraduates	Implement projects	Write up findings	Submit manuscripts with undergraduate researchers as primary authors
4) Data Management	Initiate project and share on Github	Utilize github repository to track progress and back up data		
5) Genomic Analyses			Gather RNA-seq data	Genomic analyses and prediction
6) Attend Conferences			Present poster at 2 conferences	Present poster at 2 conferences
7) Manuscripts		Write methods	Write results	Finish and submit manuscript