

Introduction

My research program aims to understand the ecological and evolutionary genetics of traits that promote persistence in the face of environmental stress. My work predominantly uses an emergent plant model, *Ipomoea purpurea*, to investigate the process of adaptation to both the agricultural regime and scenarios of global climate change. I combine manipulative field experiments, quantitative genetics, molecular biology and bioinformatics to answer fundamental and applied questions in ecological genetics.

Previously, utilizing an experimental, quantitative genetics approach, I have examined the evolution of tolerance to glyphosate, the active ingredient in the herbicide RoundUp in *I. purpurea*. Through a series of greenhouse and field experiments, I uncovered constraints on the evolution of glyphosate tolerance; however, I also found tolerance to be a common phenomenon in nature, and one that arose prior to the herbicide's use. Given the almost complete reliance on this herbicide in present-day agriculture, this study system represents a widespread, unique experiment in evolutionary ecology.

As an assistant professor of Biological Sciences at the University of Cincinnati, I have developed a research program that utilizes the tools of computational bioinformatics and molecular biology to address questions regarding the ecological and evolutionary dynamics of plant 'weediness' and herbicide resistance. I am also investigating the community dynamics of microbes that are found in association with weedy plants using next generation sequencing. The research program that I would bring to the University of Michigan is focused on the persistence of weedy plants in the agricultural setting—a topic that bridges an important theme in evolutionary ecology to a problem of practical significance in agriculture.

Present & future work

Ecology, genetics and genomics of weedy plant persistence

Weedy plant species pose a serious threat to agriculture in that they cause crop yield and financial losses on the order of 10% per year, worldwide. Despite their importance to the world's food supply, very little is known about the evolutionary potential of traits that make a plant a weed. Less is understood about the genetics of plant 'weediness' and the ecological conditions that may select for weediness. My research program is designed to investigate these topics by the use of manipulative field experiments, quantitative genetics, molecular biology and bioinformatics. Below I briefly detail four ongoing projects in my lab.

The evolutionary ecology of plant weediness—Baker (1965) identified a list of phenotypic traits that typify weeds such as rapid growth and continuous seed production, among others. The relative importance of these traits, or these traits in aggregate, to the adaptive process is as yet unknown. My lab's 'weediness' project relies on the principles of quantitative genetics to understand the evolution of traits that permit adaptation to the agricultural selective regime. We are generating selection lines of weedy and less weedy morning glories by applying the concept of index selection to select on multiple weedy traits. Using these selection lines and manipulative field experiments, we will be able to ask basic evolutionary questions such as 'Does weediness incur a fitness trade-off?' and 'Is there a trade-off between weediness and tolerance to abiotic stresses, such as scenarios indicated in global climate change?' This line of investigation will be applicable to funding from panels at the USDA as well as NSF.

The genetics of herbicide defense & the impact of the mating system on the evolution of herbicide resistance—Weedy species are often resistant to herbicide. Another line of research that we have begun in the lab is to uncover the genes responsible for defense to herbicide using

the morning glory/glyphosate system that I have previously developed. We are using selection lines of increased/decreased herbicide resistance, and will be performing comparative cDNA sequencing *via* whole transcriptome shotgun sequencing between lines to pinpoint genes that are indicated in both herbicide resistance and herbicide response. Furthermore, I have recently been awarded a 4-year, \$500,000 USDA grant to investigate the influence of the plant mating system on the evolution of herbicide resistance in *I. purpurea*. The broad goals of this work are to assess potential and actual gene flow in weedy *I. purpurea* populations and to determine how the impacts of glyphosate resistance may be manifested through the male (pollen) and female (seed) fitness of this normally hermaphroditic species.

The evolutionary genomics of plant weediness—The gene space of 10 morning glory species, *I. purpurea* included, has recently been sequenced by the Beijing Genomics Institute, as part of the ‘1kp plant transcriptome project,’ a multinational effort to sequence the transcriptomes of 1000 plant species. These morning glory species vary for many traits such as leaf shape, mating system and floral color. Some of these species are noxious agricultural weeds, whereas others are not. As a sub-project of the 1kp transcriptome effort, and in collaboration with John Stinchcombe, Shu-mei Chang and Gane Wong, I am comparing the transcript abundance of genes from species that are ‘weedy’ to *Ipomoea* species that are ‘nonweedy.’ We have uncovered an exciting putative trade-off—weedy *Ipomoea* species exhibit a higher level of expression for genes underlying carbon fixation compared to the nonweedy *Ipomoea* species, whereas they down-regulate genes involved in stress response. This finding supports the general hypothesis that weedy and invasive plants may allocate resources away from stress tolerance and instead allocate resources to fast growth.

The plant metagenome: responses to selection in the agricultural ecosystem—Recent breakthroughs in DNA sequencing technology and bioinformatics have given fuel to the field of metagenomics, or the study of microbial diversity in environmental samples. In collaboration with Jeff Bennetzen, I am investigating the effect of the Bt transgene on the metagenomic community found in association with maize roots. By sequencing the 16S rRNA gene from replicate maize isolines with and without the Bt transgene, we have uncovered a dramatic difference in the microbial community found in association with Bt maize. Specifically, we find a decline in bacteria from the Chitinophagaceae family – those known to hydrolyze chitin. This finding shows that the introduction of a transgene can affect the community structure and potentially the community dynamics of bacteria (Baucom and Bennetzen, *unpubs data*).

We are currently addressing a similar community genetics question using *I. purpurea* in my lab. Plants of this species range in color from white to pink and dark purple—as many as 20 floral color variants have been documented in nature. While the evolution of floral color is thought to be driven by pollinators, genes impacting floral hue may have other pleiotropic plant fitness effects, such as providing defense to herbivores and/or pathogens. We are assessing the metagenome of morning glory floral color variants to determine if variation in the plant flavanoid pathway, which produces a group of important plant secondary compounds, can impact plant root/microbe interactions. We are using 16S rRNA gene surveys of the bacteria found in association with the roots of different floral color phenotypes to ask the question ‘Does the bacterial community found in association with the roots of white flowered plants differ significantly from purple, or pink flowered plants?’ We have preliminarily found significant bacterial community structure in relation to flower color, and are concurrently performing an experiment to determine if manipulations of the bacterial root community can likewise impact plant fitness.