My research is motivated by the need to predict phenotype from genotype, to understand how genome-environment interactions through natural selection and development explain climate adaptation in plants. Here I describe previous research and future directions to advance and apply plant genomics of climate adaptation.

Uncovering the functional genomics of climate adaptation

Half a century after the Green Revolution, we have learned that monumental yield increases in staple crops such as rice and wheat are attributed to specific mutations in a handful of genes. Later still we discovered that similar, naturally occurring mutations in wild plants can produce similar phenotypes. These discoveries demonstrate the power of a retroactive analysis to uncover the genes that changed history. Now, in the age of genomics and gene editing, we are poised to discover the genes that will define the future, by addressing the challenge of identifying genes responsible for adaptation at both genomic scales and functional molecular resolutions.

Traditional genome wide association scan (GWAS) approaches often fail to identify causative loci because of allelic heterogeneity and lack predictive power because of epistasis. Traditional GWAS is also indented to identify genome regions of interest rather than functionally definitive causative mutations, meaning that results cannot be readily translated into useful applications. Alternatively, a genome-wide association framework that contrasts alleles defined by functional state rather than linked SNPs can overcome allelic heterogeneity, provide a basis to empirically study epistasis, and identify targets immediately useful for hypothesis testing (Figure 1).
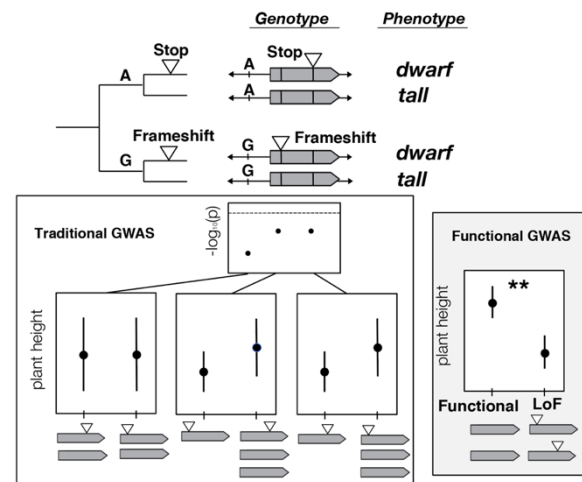

Figure 1 Theoretical illustration of a gene affecting plant height hidden from traditional GWAS, but identifiable using functional GWAS. From Monroe et al. *Invited review (in prep for Genetics).*

I have developed such a functional GWAS approach and used it to study drought adaptive loss-of-function alleles in *Arabidopsis thaliana* (Monroe *et al.* 2018*, eLife*). This work was largely supported by an NSF Doctoral Dissertation Improvement Grant. More recently, in collaboration with the International Rice Research Institute, I have applied this approach to identify targets for improving salinity tolerance in rice (Monroe *et al*. *in prep for PLoS Genetics*). With this framework we have identified >400% more candidate genes over traditional methods, with these genes being enriched in pathways previously implicated in salinity tolerance physiology. Unlike traditional GWAS, the loci identified provide immediate candidates for hypothesis testing using targeted gene knockouts. While in *Arabidopsis*, I have taken advantage of T-DNA knockout lines, the application of CRISPR based gene editing will play a major role in my future research. For example, I have immediate plans to submit an NSF Plant Genome Research Program proposal to combine functional GWAS with CRISPR based editing across diversity panels to study the epistatic basis of climate adaptation in rice. Future work will extend this approach across plant species, traits, and functional allele classes.

Novel approaches linking genes, environments, and traits

To understand the plant genomics of climate adaptation, it is important to study how genomes interact with the environment. For example, variation in functional genomic diversity along environmental gradients reflects the history of evolutionary processes such as natural selection. And during plant development, the genome provides the blueprint for phenotypic responses to environmental perturbation. By studying natural selection and development together a more mechanistic understanding of climate adaptation can be developed that links genes, environments and traits.
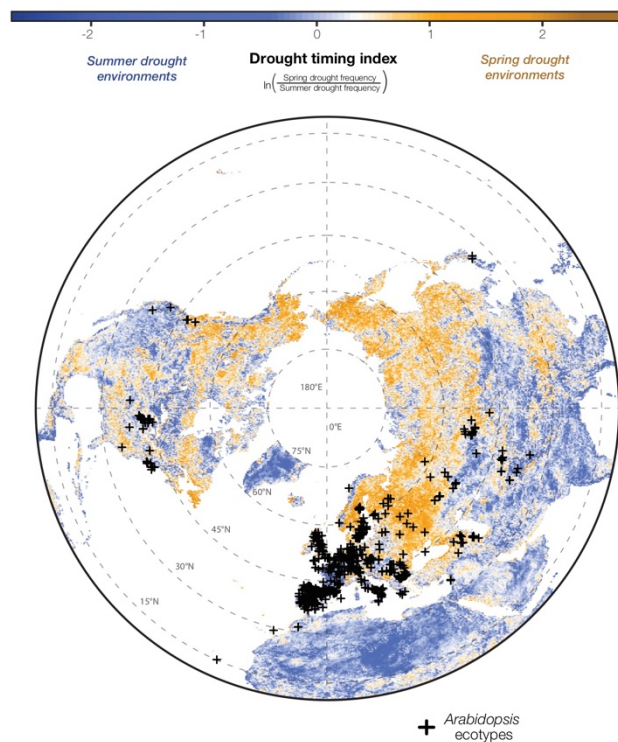
Locally adapted populations of wild plant species and land races of crops present opportunities to exploit allele-environment associations to identify genes responsible for climate adaptation. I have applied such a framework to study the genetic basis of adaptation to winter temperatures in *Arabidopsis* (Monroe *et al.* 2016, *Molecular Ecology*) and found that allele-environment associations readily predict allele-phenotype associations (Monroe *et al.* 2018*, eLife*). This approach highlights the ability to use environmental gradients to find causal loci for traits that are particularly difficult or expensive to measure. It is critical to study ecologically relevant environmental gradients. To study the genomic and phenotypic basis of drought adaptation I have pioneered the use of satellite remote sensing to characterize historic drought regimes and applied this across a number of systems (Mojica *et al.* 2016, *Plant Science*; Ditttberner *et al.* 2018 *Molecular Ecology*; Monroe *et al.* 2018*, eLife*; Monroe *et al.* 2018 *biorxv/in review at New Phytologist*). I am excited to continue this research through collaboration with the Weather Extremes group at UC Davis.

Figure 2 Geographical variation in drought timing quantified using satellite detected drought, used to identify drought adaptive loss-of-function alleles in *Arabidopsis*. From Monroe *et al.* 2018 *eLife.*

Historically, plant responses to environmental stress have been studied by growing plants under two contrasting treatments (i.e. "wet" and "dry"). While the simplicity of this approach is experimentally attractive, it overlooks the quantitative nature of plant environments and non-linear plant responses which provide necessary resolution to understand the mechanisms of stress tolerance. Working with Dave Des Marias at Harvard (now at MIT) I am designing new experimental and statistical approaches to study plant responses as a function of a continuous gradient in water availability in the model grass *Brachypodium*. This "function-valued trait" approach has revealed significant variation within and between species in the non-linearity of drought responses (Monroe *et al*. *in prep for Heredity*). These insights inspire new opportunities to scale up the study of stress tolerance physiology by exploiting naturally

occurring environmental gradients that exist among experimental sites. Then, by studying genome expression responses to environmental gradients in combination with allele-environmental associations, mechanistic links between the genomics of natural selection and trait responses can be studied. I have plans to submit a USDA proposal in collaborations with the UC Davis Agricultural Experiment Station to combine these approaches.

Applying genomics to investigate the ecosystem consequences of climate adaptation

In 1881, twenty-two years after *On the Origin of Species*, Charles Darwin published a book inspired by the idea that organism adaptation can significantly impact the environment. Since then, mounting evidence indicates that adaptive evolution, especially in plants, has altered ecosystems and the climate throughout Earth's history. Furthermore, recent work has indicated the possibility for rapid adaptation in response to anthropogenic climate change to significantly alter carbon cycling (Monroe *et al.* 2018 *Trends in Ecology and Evolution*). Studying this process is important for predicting future atmospheric carbon dioxide concentrations, developing agricultural systems that maximize ecosystem services, and is at the forefront of providing a much-needed synthesis

Figure 3 The evolution of carbon cycling traits in response to climate change. From Monroe *et al.* 2018 *Trends in Ecology and Evolution.*

between evolutionary and ecosystem ecology. As a geneticist, I am interested in applying genomic tools to this problem. In recent years, a number of advances present an opportunity for a synergistic approach to improve the ecosystem impacts of agriculture and study ecosystem consequences of contemporary climate adaptation: 1.) genomic prediction has proven a powerful approach for predicting and improving plant traits, 2.) ancient DNA obtained from herbarium specimens has been useful for reconstructing recent evolutionary history, 3.) high throughput phenotyping makes possible the large-scale study of ecosystem traits. As a PI at UC Davis, I would seek to develop a collaborative project integrating these components to study the genomic basis of carbon cycling traits in wild and crop plant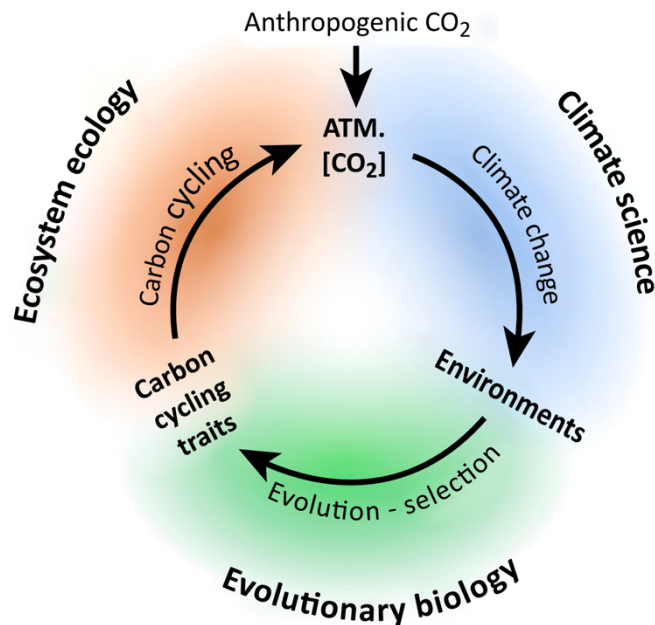 species through a DOE research grant.