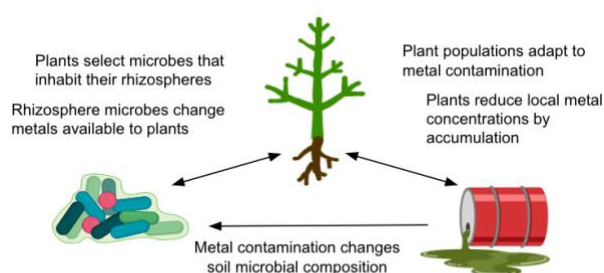


## Brook T. Moyers — Research Accomplishments and Future Plans

In my research I seek to understand the proximate causes and ultimate drivers of trait variation: why and how are individuals different from each other? To address this question I study how genetics and environment interact to influence individual and population traits, integrating techniques from evolutionary biology, genetics, ecology, engineering, and computer science. I study plants because they are critical to our culture and survival and because their traits make them particularly experimentally tractable. I focus on crops and other useful plants in order to serve human needs.

**Life history adaptation in sunflowers:** I have established two wild sunflowers as key species in the study of life history evolution. In *Helianthus argophyllus* I characterized remarkable variation in flowering time and size at maturity that is likely the result of both developmental environment and adaptation to variable selection (Moyers and Rieseberg 2016). I identified a single major genetic locus that underlies these life history traits. In this system, theoretically favorable conditions for ecological speciation (single locus, strong divergent selection) are balanced against temporally varying selection and developmental plasticity, making *H. argophyllus* a rare empirical example of how these processes interact to maintain variation within species. We also uncovered the genetic basis of ultraviolet absorptive floral patterns that are important in pollinator attraction in wild and crop species (Moyers *et al.* 2017). Finally, we find that genes putatively responsible for local adaptation are enriched for the ability to change the expression of other genes, consistent with theory for populations far from their adaptive optima (Okinedo & Moyers, *submitted*).

In *Helianthus winteri*, a newly described endemic in California, I examined the changes that accompanied its shift from herbaceous annual to woody perennial (Moyers and Rieseberg 2013). This shift conveys tolerance to extremely dry conditions in the southern exposed, shallow granite soils in the Sierra Nevada foothills. As a Plant Status Reviewer for the California Native Plant Society I helped to designate Winter's sunflower as a species of conservation concern (CNPS Rank 1B.2). **At Deep Springs** I could return to this local species.



**Figure 1.** Conceptual diagram of the interactions between plants, rhizosphere communities, and soil metal contaminants that my research addresses.

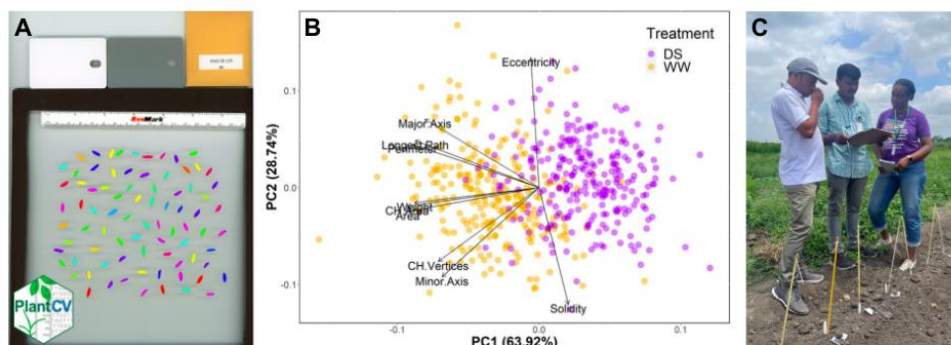
### Adaptation to heavy metal

**contamination by *Salicornia*:** Salt marshes and salt flats provide important ecosystem services but are often contaminated with toxic substances due to human activities. Little is known about how these contaminants shape population structure, adaptation, and species interactions. I am studying these

processes in pickleweeds (*Salicornia*), a genus of metal tolerant plants with a global distribution in saline environments like salt marshes and salt flats. These species have potential as both accumulators of industrial contaminants (phytoremediation) and a cultivated food source, although not at the same time of course! I am using field sampling and genetic sequencing of *Salicornia* and its root-associated bacteria (rhizosphere) to illuminate interactions among plant populations, microbial communities, and environmental contamination across salt marshes with varying histories of industrial contamination (Fig. 1).

Together with undergraduate researchers, I have developed 11 independent research projects on pickleweeds (see CV). Students are particularly interested in phytoremediation and microbial research as well as the edible nature of these species. **At Deep Springs** I would like to expand into the agricultural potential of pickleweed, which can be grown on marginal land with saline irrigation and consumed as a vegetable, seed oil, or as “green salt”. I would also like to study how *Salicornia rubra*, the nearby desert salt flat member of the genus, has adapted to environments far from the ocean of its ancestors.

**Genotype by environment interaction in rice:** Rice (*Oryza sativa*) is one of the most water-intensive crops, and water is an increasingly scarce and unpredictable resource. Rice is also an excellent model system for the study of complex traits and the interaction of genotype with the environment. My work examines how varieties in diverse populations perform across a range of stressful environments to understand the genetic and environmental drivers of trait variation. We use traditional manual measurements alongside new imaging technologies (Tanger *et al.* 2017; Marrano & Moyers 2022).



**Figure 2.** (A) Rice seeds individually segmented for shape and size analysis using a custom, open-source workflow developed with PlantCV. (B) These traits can be used for genetic discovery and to differentiate between maternal environments: trait PCA for drought stressed (DS/purple) and well-watered (WW/orange) seeds from the same recombinant inbred lines. (C) We are currently applying similar approaches in collaboration with IRRI-India.

My lab developed a low-cost, open-source method for rapid measurement of seed size and shape using digital imaging, applying it to the complex multi-parent rice Global MAGIC population under drought in field conditions (Fig. 2; Marrano & Moyers 2022), the USDA’s rice mini-core collection under heat stress in controlled conditions, and now the African rice (*O. glaberrima*, a different species domesticated in West Africa) mini-core population in collaboration with AfricaRice. This method enables cheap and rapid identification of genes and varieties with positive seed traits, making it especially valuable for crop breeders in low-resourced contexts. We are also collaborating with the International Rice Research Institute to develop a field imaging approach to identify iron deficiency stress in seedlings.

I have collaboratively developed seven undergraduate projects on rice, ranging from computer science to experimental botany (see CV). The fieldwork for these projects is conducted by my collaborators in rice-growing regions (the Philippines and India), while my contributions are smaller-scale experiments and computational analyses. **Students at Deep Springs** could easily contribute to this work. This research has the potential to provide fundamental insights to the question of how traits develop as the expression of genetic variation in variable environmental contexts. It also could have major benefits to food security for some of the poorest people in the world, especially as the climate worsens.