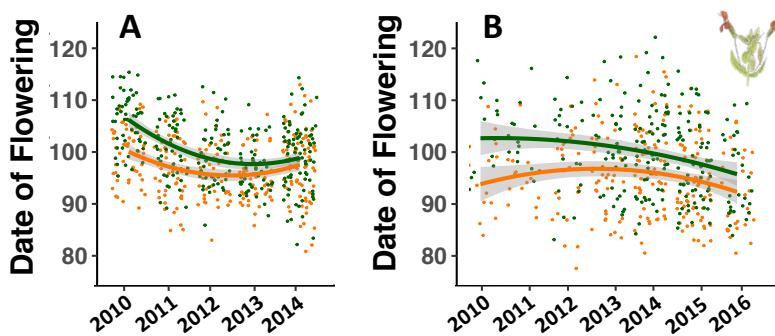


My research focuses on the evolution of ecologically important traits across environmental gradients and climate change. My lab will seek to use long-term monitoring programs to understand how evolution impacts population demography and test the need for the human mediated movement of genotypes to rescue existing populations (assisted migration). I will aim to address these issues through researching **(1) Evolutionary Rescue and Rapid Adaptation to Drought, (2) Using Landscape Genomics to Test Assumptions of Assisted Migration, and (3) Spatiotemporal Variation in Herbivory and Plant Defence.**

### (1) Evolutionary Rescue and Rapid Adaptation to Drought

Climate change is increasing the frequency and severity of extreme droughts, placing species at risk of local extinction. Population persistence may require the rapid evolution of drought avoidance and/or tolerance traits and their plasticity. This may lead to evolutionary rescue, where a decline in population size is recovered due to an increase in drought-adapted genotypes. Evolutionary rescue has been examined theoretically and demonstrated in laboratory experiments, but its prevalence in natural populations facing climate change is unknown. **My research seeks to understand how rapid evolution to drought varies across a species' range and its implications for evolutionary rescue.**

My lab will study rapid evolution in the riparian plant scarlet monkeyflower, *Mimulus cardinalis*, in response to a record-setting drought in California and Oregon. The Angert Lab has established demographic census plots spanning the range of *M. cardinalis*, and I intend to collaborate on their long-term monitoring. Seed and demographic information from 12 sites spanning the range of *M. cardinalis* will be collected yearly to determine the effect of increasingly variable climate on drought adaptations and long-term population stability. I ask **(1.1) What *M. cardinalis* traits are involved in rapid evolution to drought? (1.2) How does rapid evolution vary across the range of a plant? (1.3) Does drought adaptation have a cost to fitness during wet periods? (1.4) Does rapid evolution lead to evolutionary rescue?** Through a greenhouse common garden, I have shown evidence of drought escape through the evolution of earlier flowering time in 6 out of 12 populations (e.g. Fig.



**Fig. 1.** Evolution of (A) earlier flowering in *Mimulus cardinalis* in a population Southern California. (B) Evolution of flowering time plasticity in a population in central California.

1A; Anstett et al. 2019 in prep) and the loss of flowering time plasticity at four sites (e.g. Fig. 1B). This loss could lead to reduced fitness during wetter years, which may impede full recovery of some populations. Water content, a measure of drought tolerance, increased in four southern and central sites during the peak of the drought. Three of these four sites did not show evolution of early flowering time, indicating the evolution of different drought strategies across sites.

**Future Research** – My lab will assess the long-term impact of adaptation to drought and loss of genetic variation on population viability. With continued demography surveys and seed collections on the 12 target sites, we will be able to track the effect of past drought and future environmental change on trait evolution. Through common gardens my lab will quantify fitness during drought experiments and use this information to parametrize population demographic simulations. This will allow us to compare the expected versus realized impacts of drought on demographic viability. We will also carry out a one-time seed re-collection of 2008–2010 *M. cardinalis* seed collections range-wide across 70 sites, to assess the effect of drought on trait evolution range-wide (Fig. 3). My lab will also use targeted sequencing approaches to track genetic changes in regions associated with drought adaptation. Target regions will be acquired using genome-wide association mapping (GWAS) from the whole-genome sequencing of the 70-site dataset of *M. cardinalis* (Fig. 3; see next section

for sequencing details). The scope of this work will allow for quantification of the long-term effects of opposing selection pressures through multiple drought cycles. It will give a field-based assessment of evolutionary rescue in nature and establish this system as a case study for adaptive evolution.

## (2) Using Landscape Genomics to Test Assumptions of Assisted Migration

Assisted migration is a bold technique that has been proposed to carry out evolutionary rescue on species threatened by climate change. While this idea is controversial for multiple reasons, the lack of data needed to design effective implementation hinders future use. **My lab will use the landscape genomics of *M. cardinalis* over a period of extreme drought to test the viability of assisted migration as a conservation strategy.** I will test two important assumptions of assisted migration: **(3.1) Assisted migration assumes the needed genotypes are not already present in declining populations. (3.2) Assisted migration also assumes that certain places on today's landscape will provide the needed genetic variation for future climates (space-for-time equivalency).** With a Genome BC grant I am sequencing ~800 whole genomes at 15X coverage across 70 sites (Fig. 3). I will carry out GWAS using environmental variables to find regions associated with drought severity and increased temperature. To test for the presence of needed genotypes in at-risk populations (3.1), I will determine the frequency of each adaptive allele or its distance away from each northern site. This will provide the first detailed analysis of the need for assisted migration. To test for space-for-time equivalency (3.2), the increase in frequency of drought-associated alleles will be tracked across a seven-year time series comprising 385 genomes from twelve sites. Finding concordant patterns across many adaptive loci would provide evidence in favor of the space-for-time assumption. In conjunction, these analyses will assess the need and benefits of utilizing assisted migration.

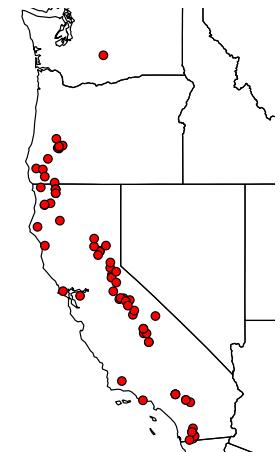


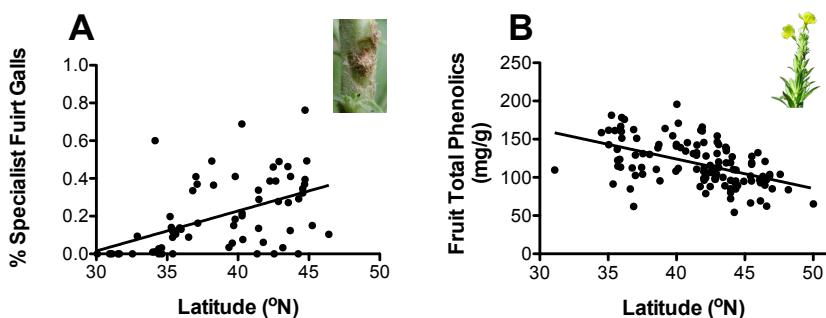
Fig. 3. Locations of 70 populations sampled across the range of *Mimulus cardinalis* prior to severe drought. Each location will be re-sampled in the near future to assess effects of climate change through resurrection experiments.

Establishing a landscape genomics pipeline for determining the need for assisted migration will allow broader applications to species at risk. My lab's approach will use the decreasing costs of sequencing to assess the distribution of putatively adaptive variation across a significant portion of a species' range, with the goal of identifying regions of increased conservation importance, and potential for assisted migration. The exact determination of target species will be based on the needs and prior work of local and regional government and conservation agencies. Through this collaboration I will be able to both advance the study of landscape genomics and help find conservation solutions for multiple species at-risk due to climate change and environmental degradation. Due to its clear broader impacts this work will be competitive for NSF and for applied funding sources.

## (3) Spatiotemporal Variation in Herbivory and Plant Defence

Climate change is leading to a longer growing season, higher temperatures and increased drought. These conditions are likely to increase insect population sizes, activity, and number of generations within a season, as well as encourage northward spread and host shifts within native and invasive insects. It is likely that herbivore pressure will increase, placing plant populations under pressure to rapidly evolve greater defences against herbivores. **My lab seeks to quantify change in herbivory over time and the potential rapid evolution of increased plant defences across multiple taxonomically and geographically diverse systems.**

**(3.1) Does herbivory increase over time?** My lab will measure change in herbivory over time across a latitudinal gradient in *Oenothera biennis* and *M. cardinalis*. In 2012, I assessed latitudinal gradients in herbivory in *O. biennis* across 79 populations<sup>1</sup>, forming a baseline for future comparisons. Strikingly I found increased herbivory at higher latitudes in fruit tissues (Fig. 2A), possibly already capturing increases due to



**Fig. 2. Latitudinal gradients in *Oenothera biennis*.** (A) Increased specialist fruit galls at higher latitudes in a latitudinal survey. (B) Plant chemical defences are lower at higher latitudes across 137 genotypes of *O. biennis*.

**(3.2) How do genetically based plant defences change across the range of a plant?** To assess changes in plant defences over time my lab will carry out a resurrection program using (A) *O. biennis*, (B) *M. cardinalis*, and (C) 12 species from Project Baseline<sup>2</sup>. Previous work I carried out on a range-wide seed collection of *O. biennis* showed increased plant defences at lower latitudes (Fig 2B) and measured at total of 24 plant resistance traits<sup>3</sup>. My lab will compare results from these genotypes, collected in 2002-2008, with new seed collections carried out in 2021. Through greenhouse and common garden experiments, my lab will assess changes in physical and chemical defences, induced defences, and herbivory tolerance. In *M. cardinalis* we will leverage the on-going seed collection efforts to assess trade-offs between adaptation to drought tolerance and evolution of plant defence. Specifically, will compare trichome evolution (which is an adaptation to both drought and herbivory) with chemical defences (phenylpropanoid glycosides).

My lab will assess change in plant defences using Project Baseline<sup>2</sup>, a repository of range-wide seed collections for use in climate change research. Initially we will select collections of 12 annual species across multiple plant families (Asteraceae, Balsaminaceae, Brassicaceae, Campanulaceae, Fabaceae, Onagraceae, Phrymaceae). Baseline collections from 2014 through to 2018 will be compared to re-surveyed seeds which my lab will collect at least 5-years after initial collections. Evolution of plant defences will be assessed using resurrection experiments by growing past and future genotypes in greenhouses and common gardens. Plant defences and tolerance to herbivory will be broadly assessed through feeding trials with generalist and when possible specialist insects. Physical defences (e.g. trichome number), and broad-based chemical defences (e.g. total phenolics) will be assessed across all target species. More specialized chemical defences (e.g. glucosinolates, phenylpropanoid glycosides) will be assessed within taxa where they are relevant. For genera where molecular resources are available and chemical defence genes are described (e.g. *Brassica*, *Helianthus*), I would consider exploring genomic evidence of adaptation through candidate gene and GWAS approaches if these species show change in plant defences over time. This study would eventually also focus on perennial species once these seeds become available from project baseline (~2028-2030). Overall, the variability in the biogeography and evolutionary history of the target species will help ensure any observed patterns are generalizable, and variation attributable to differences in biology and geography.

## References

1. Anstett, D. N., Naujokaitis-Lewis, I. & Johnson, M. T. J. Latitudinal gradients in herbivory on *Oenothera biennis* vary according to herbivore guild and specialization. *Ecology* **95**, 2915-2923 (2014).
2. Baseline, P. <http://www.baselineseedbank.org>.
3. Anstett, D. N. et al. Can genetically based clines in plant defence explain greater herbivory at higher latitudes? *Ecol. Lett.* **18**, 1376–1386 (2015).

climate change. My lab will resurvey these latitudinal gradients for two years to search for changes in herbivory in individual regions and across a N-S transect of the species range. My lab will also add an herbivory monitoring program to our *M. cardinalis* demography surveys, allowing us to track herbivory changes over the next 20 years and of this herbivory on population demography.