Figure 1: Floral diversity in Papaveraceae. From left to right: Top: *Papaver rhoeas*, *Platystemon californicus*, *Argemone munita*, Bottom: *Eschscholzia californica*, *Romneya coulteri*, *Dicentra spectabilis*

Previous Research: I began my research career as a Master's student at UC San Diego, studying genetic diversity at self-incompatibility loci in Papaveraceae. I investigated whether floral variation in Papaveraceae (Figure 1) had an effect on the site of self-incompatibility recognition. Exchanging molecular benchwork for microscopy, I showed that despite considerable variation in floral morphology, the location of self-recognition in many different poppies remained anatomically similar [1].

More recently, I have worked on a variety of projects in the Ross-Ibarra lab at UC Davis, including the development of sequence assembly methods for repetitive regions [2], finding patterns of evolutionary constraint on gene expression in maize endosperm [3], and surveying the literature on ecological genomics of maize and its wild relative, teosinte [4]. My most recent publication investigated patterns of diversity in centromeric regions of the maize genome [5]. My ongoing work in the Ross-Ibarra lab studies genome size evolution and its potential role in adaptation to altitudinal clines, and I will continue these and related projects with my already gathered data after graduation. With funding from the UC MEXUS dissertation grant, I am using the sister genera *Zea mays* and *Tripsacum dactyloides* to identify parallel patterns in genetic repeat content change and examine whether evolutionary trajectories are reproducible. In addition to identifying overall genome size trends in related taxa, my investigation identifies the specific genomic components responsible for the changes in genome size. I measure repetitive content from whole genome sequencing with a bioinformatic pipeline I assembled and identify changes across populations. I will utilize this bioinformatic pipeline and ongoing collaborations to spur maize-related undergraduate research projects in my lab at CSU Monterey Bay. Using the large quantities of sequence data from my projects in conjunction with freely available data online, I can guide students through investigations of genomic diversity, fluctuations in repetitive content, and historical population demographics with bioinformatic tools. I can also use maize and *Tripsacum* genotyping-by-sequencing (GBS) data from my project and those of collaborators to investigate the relationship between genome size diversity and kinship, providing ready research projects for undergraduates that utilize cutting edge methods.

Proposed Research: Since the discovery of DNA, genome size variation has perplexed scientists. Studies continue to find that genome size variation is extensive between and within species [6], though questions about the adaptive potential of genome size remain unanswered. Previously, scientists have posited that genome size variation may play a role in determining life history strategy and environmental adaptation [7],

but a lack of clear evidence shows further investigations are required. I propose to use the native California golden poppy, *Eschscholzia californica*, to investigate trends of genome size variation across environmental variables and life history strategies. *E. californica* is adapted to a wide range of habitats in California, spanning coastal regions near Monterey Bay to desert climates further south, while exhibiting variation in life history strategy. Though we have no estimates of genome size variation within the species, extensive genome size variation has been documented in closely related poppies [8] as well as in other plants with broad geographic distributions. To better understand the adaptive role of genome size, I propose the following:

Aim 1: Explore the eco-geographic distribution of genome size and its correlations with phenotypic traits in E. californica. I predict that genome size in *E. californica* decreases along increasing altitudinal and latitudinal gradients as has been observed in other plant species [9]. I hypothesize that genome size itself is adaptive as a mechanism to control flowering time and life history strategies, predicting larger genome sizes in populations that flower later or grow perennially. New collections will supplement readily available germplasm, and plants can be grown at campus facilities to track phenotypes such as days to flowering, life history strategy, and biomass. Multiple genome size measures will be collected per plant and used to identify within and between population variation. Students will participate in all steps of the project, from beginning local collections and field observations to greenhouse work and data analysis, as well as paper writing and revision.

Aim 2: Investigate genomic variation in invasive E. californica *from South America.* Though native and ornamental in western North America, the introduction of *E. californica* to South America has resulted in a rapid invasion of the native habitat. I propose to genotype both California and South American populations with GBS, a method for reduced representation sequencing. The relatively small reported genome size for *E. californica* (1.13 Gb; [10]) makes it an excellent candidate for GBS. A genetic analysis of *E. californica* kinship between native and invasive populations will provide valuable insight about the origin of the invasive type. The project will also provide a valuable training tool for undergraduate and graduate students, exposing them to foundational sequencing technologies and bioinformatic tools such as burrows-wheeler alignment software and R statistical programming.

Aim 3: Flowering time change under bidirectional selection for genome size Previous studies in maize showed that selection for earlier flowering time resulted in a concomitant reduction in genome size [11]. While the study provided circumstantial evidence for the role of genome size as a mitotic and developmental clock, I propose to expand the study with bidirectional selection on genome size while observing phenotypic changes. Selection will be performed toward both larger and smaller genome sizes. Complimentary experiments in which early and later flowering times are selected for in separate populations can also be performed. The ability to scale these experiments to many separate populations and repeat selection in these populations will allow for student participation and more robust scientific findings.

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