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Research in Progress
Conference Room, 8:45 am

Life in the leaves: The diversity and distribution of foliar fungal endophytes

Foliar fungal endophytes (FFE) represent one of the most species rich and phylogenetically diverse guilds in the kingdom Fungi, however less than 1% are taxonomically described. FFEs symbiotically associate with all known vascular and nonvascular plant phyla from arctic to tropical ecosystems. Consequently, they represent a useful model to investigate fungal diversity patterns and plant-fungal network structure at large biogeographic scales. The latitudinal diversity gradient (i.e. increasing species richness toward the equator) is the most widely documented pattern of biodiversity across diverse assemblages of plant and animal groups and therefore represents a comprehensive biogeographical model to explore FFE diversity patterns. It has been suggested that FFE communities from various angiosperm lineages follow a similar diversity pattern using culturing methods. However, recently collected data using culture-independent methods (next-generation sequencing) strongly suggest FFE diversity does not conform to LDG and I will discuss how abiotic and biotic drivers may contribute to these patterns.

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Research in Progress
Exhibit Room, 1:30 pm

Comparing restoration methods in invaded California grasslands

Fully established *Stipa pulchra* (purple needlegrass) individuals can affect the fitness of *Centaurea solstitialis* (yellow starthistle) through competition and can prevent or reduce invasion rates of *C. solstitialis* (Morghan & Rice 2005; Morghan & Rice 2006). However, establishing *S. pulchra* populations can be difficult and costly. My research compares two different restoration methods of the perennial bunchgrass *S. pulchra* following the removal of *C. solstitialis*. I will test the efficacy and cost of plugs versus seeds over two years in a natural setting. I will additionally test the effects of planting density between the two taxa, both interspecifically and intraspecifically.

In fall of 2016, *S. pulchra* plugs and seed were planted at in replicates of five at five different densities at three sites in the Sacramento Valley. Also in fall of 2016, *S. pulchra* and *C. solstitialis* seed mixtures were planted in pots at the Chico University Farm in an addition series type experimental design. The mixtures consist of three total densities, planted at five different ratios. Data collection just began, thus there are no data to present at this time.

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Proposed Research

Conference Room, 1:45 pm

Adaptation, facilitation, and refugia in Mojave Desert mosses

Mosses are poikilohydric and desiccation-tolerant organisms, which means that their tissues quickly equilibrate to ambient water content, and they are able to recover from being completely dry. Terrestrial mosses will dehydrate and go dormant between precipitation events. Mosses that live in the desert spend most of their time in a desiccated, inert state exposed to high solar radiation in the dry summer months. Like other plants, mosses are known to have mechanisms for absorbing damaging UV or quenching excess photosynthetically active radiation. However, when dormant they have no ability to actively repair damages caused and lack thick cuticles and other structural protective seen in vascular plants. My research will investigate cellular UV protection mechanisms employed by the desert mosses of the genus *Syntrichia*. I will culture these plants in different light environments and use mass spectroscopy to characterize and compare protective UV-absorbing metabolites. Through transcriptomic analyses, I will search for candidate genes associated with UV protection and sequence candidate gene regions in other plants to explore the evolutionary history of this trait. Finally, I will compare the soil crust community of mosses, lichens, fungi, and other microorganisms at different light environments within a Mojave Desert research plot and test for evidence of facilitation between community members. This research will provide insight to the physiology, ecology, and evolution of organisms in extreme environments.

Danielle Black[†] and Scott Hodges

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Exhibit Room, 8:45 am

**Identifying the genetic basis of serpentine adaptation
in the California coastal endemic *Aquilegia eximia***

Plants in serpentine soils experience extreme nutrient limitation, elevated concentrations of heavy metals, high levels of Mg that are hypothesized to inhibit Ca uptake, among other extreme environmental factors. Serpentine ecosystems are also characterized by high levels of endemism due to plant species that have evolved a variety of mechanisms to tolerate and survive in these inhospitable environments. This project compares *Aquilegia eximia*, a serpentine endemic along the California coast, to its more widespread presumed progenitor species that lacks the ability to survive on serpentine soils, *Aquilegia formosa*. F₁ hybrids between the two species have been utilized to create F₂ and F₁-backcross populations, which will be planted in the greenhouse and phenotyped for their ability to grow on serpentine soil. This project will take advantage of the genomic resources available for *Aquilegia* to examine these two closely related species in order to elucidate the genetic basis of serpentine tolerance in *A. eximia*. I will perform a Quantitative Trait Locus (QTL) mapping study using high throughput whole genome sequencing to genotype individual plants and link the phenotypic data for serpentine tolerance to particular loci along the chromosomes. This experiment plans to utilize upwards of 2,000 plants of various genotypes for our mapping population and will allow us to examine and confirm the contribution of particular genes to serpentine tolerance in plants. This project has broader scale goals to identify new candidate genes involved in serpentine tolerance that may give insight as to how adaptations to serpentine environments evolve in natural plant systems and how presence of these genes may affect the ability of plants to tolerate inhospitable environmental conditions.

Peter Breslin

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Research in Progress

Exhibit Room, 2:30 pm

Spatially-explicit Population Viability Analysis using species distribution modeling for an island endemic cactus species in Baja California Sur

Many threatened plant species occur in isolated, restricted ranges that are characterized by patches or clusters of individuals. Yet, there is a continuing gap in accurate extent of occurrence (EOO) mapping and area of occupancy (AOO) mapping for plant species thought to be rare. In addition to this basic mapping information, there is a lack of data regarding smaller scale patterns of clustering on the landscape and data-rich species distribution modeling for many of these threatened plants. For example, the 3-dimensional and map projected EOO and AOO, patch density patterns, within-patch population densities, and other essential geospatial data are partially or entirely unknown for Baja California's *Cocheminea halei*, an island endemic plant species in the Cactaceae. Yet this species was recently assessed by the IUCN as being threatened and having declining population numbers. Determining the possible causes and effects of both the patchy and fragmented distribution is crucial to understanding the threats faced by *C. halei*. The combination of incidence data and abiotic variables such as soil type, texture, slope aspect, slope angle and microclimate profiles will be used to construct species distribution models, both maximum entropy presence-only models and presence/absence generalized linear mixed models. These models illuminate current and historical dispersal, interaction effects limiting site occupation, possible effects of climate change on distribution, and spatial patterns of pollination and gene flow. Specifically in regard to edaphic factors, the study site of Islas Magdalena and Santa Margarita includes extensive areas of serpentine rock and derived aggregates. Serpentine soil is known to drive plant endemism along the California coast, but this phenomenon has not been studied in Baja California, nor in general for endemic cactus species.

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Research in Progress

Conference Room, 2:15 pm

Characterization of the microbiome in *Asclepias* spp.

The flowers of native and non-native *Asclepias* species vary in size, color, and blooming time, and presumably also in pollinator types. Studies have shown microbiomes that exist in the nectar of flowers and which have been introduced by pollinators. We hypothesized that the microbes that live in the nectar may also vary based on plant species or location due to differences in pollinators. We bagged whole inflorescences before the flowers open at South Coast Botanic Garden, CSUDH nature garden, and a home in Anaheim and watered the plants for two days to encourage as much nectar production as possible. We then exposed the newly opened flowers to pollinators for one day before re-bagging them. We extracted the remaining nectar, and isolated the genomic DNA. Sequencing libraries were prepared for whole metagenomic shotgun sequencing in July 2017 and 16S rRNA sequencing in October 2017. Using MG-RAST, the taxonomic units of organisms present in the nectar of native and non-native *Asclepias* were analyzed. The most striking observation was that much larger diversity was found in non-native nectar as compared to native nectar and the most common microbe genus found in floral nectar of native and non-native species was *Acinetobacter*. Using 16S rRNA sequencing, we found that the native *Asclepias* species had a much larger diversity. We also found greater amounts of *Burkholderia*, which was not previously found in metagenomics shotgun sequencing. We plan to expand our sampling across the urban environment as well as observe floral visitors and isolate nectar bacteria after single pollinator visits to further elucidate the relationship between the pollinators and the nectar microbiome.

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Research in Progress
Conference Room, 9:30 am

**Biogeography, ecology and phylogeny of the
Orthotrichum lyellii (Orthotrichaceae, Musci) species complex**

The *Orthotrichum lyellii* (Orthotrichaceae, Musci) complex is known from Western Europe, and west of the the North American Rocky Mountains from Cedros Island, Baja California to Southwest Alaska. It is an ecologically dominant epiphyte on hardwood trees throughout coastal portions of its range. The most common form (subsp. *lyellii*) commonly reproduces clonally through asexual propagules, but other forms have been described in which such propagules are completely absent (subsp. *pappilosum*). In addition, the North American and European populations exhibit interesting differences in ecology, size, and morphology. The reproductive, morphological and ecological diversity of the *O. lyellii* complex throughout its range has led some authors to divide the taxon into as many as 5 separate species, subspecies, or varieties. Each of these forms seems to differ in characters such as habitat preference, morphology, and reproduction. However, the necessary integrated morphological and molecular systematic work on the group has been lacking. As a result, it remains unclear whether this complex is truly a variable and wide-ranging disjunct species, two geographically-separate clades, or up to five “cryptic species”. This high degree of variation may thus stem from plasticity, ecotypes, local adaptation, or a even an unnoticed adaptive radiation. A further wrinkle is that this dioecious plant is sexually dimorphic, and each sex seems to have slightly different habitat preferences. As part of my PhD thesis, I hope to use a combination of molecular, morphological and ecophysiological data to clarify relationships within this wide-ranging clade.

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Research in Progress
Conference Room, 2:30 pm

The inhibitory effects of juglone on microorganisms

Juglone is an allelopathic compound exuded by members of the Juglandaceae, particularly walnuts. Many people groups around the world have noticed this noteworthy phenomenon. Juglone also seems to exhibit some level of microorganism inhibition. High concentrations of juglone is found in all tissues throughout the plant, but particularly high in the husk of the fruit. I extracted pure juglone and transformed it into a stable powder. The powder was redissolved in ethanol and diluted with sterile distilled water. Different cultures of pathogenic fungus and bacteria grown on media dishes were exposed in a bioassay to varying levels of juglone. Preliminary results indicate a sensitivity by bacillus and fusarium microbes. Minimal Inhibitory Assays also indicate visible inhibition at 30µg/mL.

Dylan Cohen

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Research in Progress
Conference Room, 11:00 am

Systematics, taxonomy, and biogeography of *Loasa* s.l. and *Blumenbachia* (Loasaceae)

A primary goal of evolutionary biology is to understand the processes that have generated diversity observed today. Allopatric speciation is one of the most frequently cited modes of generating diversity and often involves speciation as a result of a vicariant or a dispersal event followed by isolation. Mountain uplifting creates new habitats and also can act as a barrier to gene flow. The Andes of South America are among the youngest, longest, and highest mountain ranges in the world. *Loasa* s.l. and *Blumenbachia* (Loasaceae) are distributed across the southern Andes. Species level taxonomy within these genera has been problematic for more than one hundred years. Phenotypic plasticity and very similar floral or leaf morphologies have no doubt contributed to taxonomic confusion. In my research, I seek to elucidate species boundaries and relationships by using a combination of molecular (RAD-Seq), morphological, and biogeographic data. Historical biogeography will be analyzed to infer events that may have generated diversity within this south Andean clade. New specimen based documentation, revised taxonomic keys and species descriptions, and identification of putative dispersal corridors, areas of refugia and patterns of endemism are among the outcomes to be generated by this research.

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Completed Research
Exhibit Room, 9:15 am

Seedling recruitment of *Atriplex polycarpa* (Chenopodiaceae) in the San Joaquin Valley of California: The roles of invasive grass competition and residual dry matter

Invasive grasses dominate large areas in the arid and semi-arid regions of the western United States. In the San Joaquin Valley of California, much of the now-invaded habitat was historically dominated by Valley Saltbush Shrub (*Atriplex polycarpa*) communities, and remnants patches are found throughout the area. The presence of the grasses may inhibit saltbush recruitment and survival, thereby transforming these communities. One way this could happen is due to competition for resources between the grasses and saltbush seedlings. Another possibility is that the dense cover of residual dry matter (RDM) produced by the grasses alters the habitat. We hypothesized that dense populations of grasses and RDM alters the water status and temperature of the soil and that these changes diminish germination and survival of saltbush seedlings, limiting the succession of grass-dominated areas to saltbush shrublands.

A manipulative weeding experiment was used to test the effect of competition on seedling germination, as well as a shading experiment to manipulate the effect of RDM shading on seedling survival. We measured the species density and coverage in each of six competition/ shade treatments for one year, and monitored soil moisture and temperature. We found that both competition and RDM significantly inhibited the germination and survival of *A. polycarpa* seedlings, but no interaction between the two factors. However, we did not find a significant difference in soil moisture or temperature between the treatments, indicating that the grasses may reduce germination and survival in ways independent of soil moisture or temperature. Overall, we found that the presence of RDM was the primary factor governing germination and survival of *A. polycarpa*, with competition serving as a secondary factor. Management tools that can reduce RDM and grass competitive ability may aid saltbush seedling recruitment.

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Exhibit Room, 11:00 am

Causes and community-level consequences for clinal adaptation in a foundational plant species

As sessile organisms, plants experience strong selection pressures imposed by local environmental conditions. However, plant adaptation to both the abiotic and biotic environment is not well understood. To this end, environmental gradients can serve as powerful tools to understand plant adaptation to abiotic clines, providing insight into how populations could respond to future conditions. We established a common garden of *Artemisia californica* sourced from 20 populations along a 5° latitudinal gradient, where precipitation is on average lower in the south. We found genetically based variation in *A. californica* functional traits including growth rate, timing of flowering, specific leaf area, water use efficiency, and nitrogen and terpene content. This work provides strong evidence that this species is locally adapted to the steep clinal variation in precipitation and temperature that occurs along California's coast. Concurrent with this study of local adaptation in *A. californica*, we characterized the canopy arthropod community (insects and spiders), and how genetic variation in *A. californica* in turn leads to variation in arthropod density and community composition. We found that variation in *A. californica* traits in turn led to variation in the arthropod communities; plants sourced from the northern populations supported higher densities of both herbivorous and predatory insects (as compared to southern populations), and insect species composition differed as well. These results suggest that landscape-scale genetic variation plays an important role in structuring plant-arthropod interactions.

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Conference Room, 10:45 am

Phylogeny and taxonomy of the *Bouteloua annua* – *B. aristidoides* (Poaceae) clade based on molecular data and leaf micromorphology

Bouteloua annua and *B. aristidoides* are annual, sister grass species distributed natively in the New World. *Bouteloua aristidoides* is widespread whereas *B. annua* is restricted to Baja California Sur. Within *B. aristidoides* two varieties have been recognized, the widespread var. *aristidoides* and the more narrowly distributed var. *arizonica*. The goal of our project was to evaluate variation within and among these three taxa and to test the classification. A total of 63 specimens were studied using morphometrics, leaf micromorphology, and molecular phylogenetic analyses. Results support elevation of *B. aristidoides* var. *arizonica* to the rank of species. Analyses revealed phylogenetic structure within *B. aristidoides* var. *aristidoides*. *Bouteloua annua* differs from *B. aristidoides* in a number of traits, including fewer autogamous flowers. The monophyletic *B. arizonica* differs from *B. aristidoides* by having more spikelets per branch and shorter branch extensions and lemmas. Further, scanning electron microscopy revealed the presence of papillae on the leaves in *B. arizonica* and macrohairs on the leaves of members of a clade within *B. aristidoides*.

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Research in Progress
Conference Room, 9:00 am

**Reconstructing chromosome evolution in Onagraceae
using a novel stochastic character mapping approach**

The first application of phylogenetic ancestral state reconstruction was to study chromosome evolution in *Drosophila*, by Dobzhansky and Sturtevant. In this work I examine chromosome evolution of the plant family Onagraceae using a novel ancestral state reconstruction method. This new approach overcomes limitations to the widely used stochastic character mapping method by sampling character histories directly from their joint distribution, conditional on the observed tip data and the parameters of the model of character evolution. To illustrate the usefulness of this approach I apply recently developed phylogenetic models of chromosome evolution to a densely sampled 340 taxa phylogeny of Onagraceae estimated using 8 genetic loci and 4 fossil calibrations. I compare the timing, number, and mode of chromosome changes estimated over the phylogeny with the many hypotheses of Onagraceae chromosome evolution published by Peter Raven, Ledyard Stebbins, and others.

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Research in Progress
Conference Room, 11:30 am

**Preferential parasitism of the desert mistletoe
Phoradendron californicum in the Mojave Desert**

Mistletoes are obligate, hemiparasitic shrubs that use haustoria to invade host stems and steal water. Desert mistletoe, *Phoradendron californicum*, parasitizes leguminous trees in southwestern North America and uses avian frugivory for seed dispersal. While previous research suggests that populations of desert mistletoe may specialize on different host species, this idea is controversial. We investigated host utilization in desert mistletoe in Afton Canyon, CA, where two potential hosts co-occur. At this site, mistletoe infected *Prosopis glandulosa* var. *torreyana* (honey mesquite) but not another documented host, *Senegalia greggii* (catclaw acacia). To explain this pattern, we hypothesized that either mistletoe seeds are not dispersed to acacia, or that mesquite's phenotype is more susceptible to parasitism by desert mistletoe. We measured mesquite and acacia size in three 30m × 40m plots. We also measured pre-dawn and mid-day water potentials, percent infestation per unit area, bark thickness and branch diameter, and seed counts on acacia.

Mesquite was significantly taller and occupied more area than acacia. Plant height was positively correlated with heavier infestation in mesquite, and the relative bark thickness was significantly thinner in mesquite than in acacia. Mid-day water potential was significantly lower than pre-dawn measurements in mesquite, but not in acacia. We found over 600 mistletoe seeds on acacia and rejected the hypothesis that mistletoe is dispersal limited in Afton Canyon. These results provide evidence supporting the presence of a host race limited to mesquite at this site. With the current prolonged drought and a changing climate, parasitism may disproportionately affect mesquite, shifting ecological interactions in Afton Canyon. Genetic analyses of desert mistletoe population structure is now underway.

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Research in Progress

Exhibit Room, 11:15 am

Patterns of woody plant mortality in *Tamarix*

Patterns of woody plant mortality have been linked to environmental changes, such as increased moisture deficits, salinity, and episodic outbreaks of insect herbivores. While many studies have focused on specific stresses, site variation in susceptibility raises a less studied question of whether local adaptation to stress creates variation in carbon allocation that can influence plant susceptibility to herbivory. *Tamarix* spp. are a group of dominant, non-native tree species in western North America that are experiencing dieback driven by episodic herbivory of the introduced tamarisk leaf beetle (*Diorhabda carinulata*). As beetles have spread, variation in mortality appears to be driven by carbon starvation, including across areas with different salinities. Here I ask whether plants from sites with increasing salinities have different patterns of gas exchange, productivity and carbon allocation when grown in a common garden. I evaluated these traits using reciprocal salinity treatments with asexually propagated plants from adjacent high and low salinity sites along the Colorado River in southeastern California. Plants were grown in a greenhouse and traits were evaluated under increasing salinity. I anticipated that *Tamarix* is adapted to its local environment, and local adaptation to specific conditions will yield predictable responses to episodic herbivory.

Both in situ collections and greenhouse trials suggest that local adaptation to salinity exists and is manifested in different allocation patterns. For example plants from high salinity sites allocated relatively greater amounts of resources to belowground biomass in the greenhouse regardless of the salinity they were grown in ($p = 0.055$). Plant material collected in situ from the low and high salinity sites during the dormant season showed increased allocation to labile carbon storage ($p = 0.027$). In the greenhouse, plants from high salinity sites had reduced photosynthetic rates ($p = 0.002$), while at the same time exhibiting greater water uptake, resulting in a lower water use efficiency. Future studies will evaluate how resource allocation patterns to storage or growth in response to increased salinity interact with episodic herbivory. The results from these studies suggest that *Tamarix* is experiencing environmental selection across small spatial scale gradients, and that the heterogeneous rates of mortality from herbivory across the landscape may be linked to heritable traits related to carbon allocation in response to salinity and other site factors.

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Completed Research

Conference Room, 2:15 pm

Importance of microsites in rare plant introductions

It is well known that rare plant introduction efforts often fail due to hasty efforts that do not fully evaluate the specific habitat requirements of the introduced species. For *Lupinus nipomensis*, we manipulated abiotic factors in order to evaluate which microsite conditions were beneficial or required for its establishment. We selected a variety of sites from the Black Lake Ecological Area, which provided a heterogeneous landscape but which allowed for manipulation of topography and aspect. Seeds were sown over the span of two years, subject to pre-treatment and included various degrees of caging in order to determine ideal conditions for establishing *L. nipomensis*. We found that aspect and duration the seed spent in the ground were the two most important factors in the establishment success of *L. nipomensis*. Although our results are specific to *L. nipomensis*, careful consideration of microhabitat conditions can be utilized widely in order to increase establishment success for rare plant introductions.

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Completed Research
Conference Room, 9:45 am

Using population genetic analyses to distinguish between two similar species of rush lilies (*Hastingsia*, Agavaceae)

Integrative taxonomy allows us to evaluate multiple lines of evidence used to differentiate difficult-to-distinguish species. The rush lilies (*Hastingsia*, Agavaceae) are one such group. *Hastingsia alba* and *H. serpentinicola* were recognized as separate species fairly recently (1989) based on geographic location and plant size. *Hastingsia alba* is found in the Trinity Mountains and northern Sierra Nevada of California and Oregon. *Hastingsia serpentinicola* is found farther north in the Klamath Mountains and as suggested by its name, is limited to serpentine soils. Unlike *H. serpentinicola*, *H. alba* is not restricted to serpentine soils, but is often found near them. Morphologically, the two species typically differ in size with *H. alba* having an overall larger stature than *H. serpentinicola*. *Hastingsia alba* also develops more flowers and greater raceme density than *H. serpentinicola*. However, recent phylogenetic studies failed to distinguish between these taxa. In this study, we evaluated the extent of genetic diversification and gene flow across multiple populations of *H. alba* and *H. serpentinicola* using microsatellite markers. We collected leaf material from a total of eight populations in Oregon and northern California, which span nearly the complete range of these taxa. Sixteen to thirty individuals were sampled from each population and full morphological measurements were taken whenever possible. Twelve microsatellite loci were evaluated for population genetic structure, as well as evidence of gene flow between populations of *H. alba* and *H. serpentinicola*. We compared these population genetic results with the field-collected morphological measurements to evaluate species boundaries.

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Research in Progress
Exhibit Room, 2:00 pm

Encouraging chaparral recovery in degraded landscapes

Chaparral is a dominant vegetation type in the southern California mountains. It is characterized by evergreen, sclerophyllous shrubs adapted to a Mediterranean climate and infrequent wildfire. However, wildfires are becoming more frequent due to an increase in anthropogenic ignitions, causing many chaparral communities to be at risk of type conversion, defined here as a change from native shrubland to invasive annual grassland. While these type converted landscapes are abundant, few studies have focused on restoring chaparral to its historical range or have investigated best management practices that lead to successful restoration. In this study, we aim to take early steps to determine how feasible chaparral restoration is, keeping the goals of land managers in mind, and what steps can be taken to promote restoration success. Our field design includes twelve degraded chaparral study sites in Piru, California. Our restoration treatments include: planting 3+ month old seedlings, sowing seeds, and scarifying the topsoil before sowing seeds. Invasive competition is also controlled within each treatment at: full removal, half removal, or no removal. Our findings on restoration success will be helpful to researchers and land managers alike in planning chaparral restoration efforts and by providing techniques that will promote the reestablishment of native chaparral species to the landscape.

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Research in Progress

Conference Room, 1:30 pm

Botany on the edge: A flora of Point Arena National Monument

Although California has a rich history of botanical exploration, many areas of the state remain understudied in terms of their floristic diversity. Focused inventories of previously under-botanized landscapes are important for elucidating patterns of plant diversity and endemism, understanding range sizes, and monitoring the spread of potential invasive species in California. The newly designated Point Arena National Monument consists of 1655 acres of pristine coastal dunes, bluffs, and prairie that were made public by President Obama in 2013. The Point Arena lands lie west of the San Andreas fault, and are geographically isolated, and are therefore of interest botanically because they may harbor floristic oddities or disjunct populations. Historical botanizing on these lands is scant but includes well-documented traditional ecological uses of plants by the Miwok Pomo, a federally recognized tribe that manages reservation lands immediately south. Additionally, Clare R. Wheeler made collections in protest of a proposed nuclear power plant construction in the 1970s. In 2016, the University of California Botanical Garden began a floristic inventory of this area that has already added hundreds of occurrence records about rare, invasive, and native plants. These efforts are helping the Bureau of Land Management plan recreational infrastructure for the national monument and contributing to understanding of plant diversity and endemism patterns on the north coast.

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Completed Research

Exhibit Room, 11:45 am

Spatial vegetation modeling suggests a novel transmission pathway of the invasive forest pathogen *Phytophthora ramorum*

The pathogen *Phytophthora ramorum*, the causal agent of Sudden Oak Death (SOD), is responsible for the rapid deaths of millions of oak (*Quercus* spp.) and tanoak (*Notholithocarpus densiflorus*) trees in California and Oregon. To date, researchers have concluded that dispersal of this pathogen occurs primarily via wind, fog, and rain splash, and most management strategies are based on this premise. Interestingly, however, a common method of early detection in SOD monitoring programs includes baiting host leaves in infected waterways, yet researchers have concluded that stream-to-land dispersal of *P. ramorum* has not occurred in any epidemiologically significant situation. Here, we present the first evidence of epidemiologically significant stream-to-land spread of *P. ramorum*. We show laboratory-confirmed *P. ramorum* positive infections along a creek in Redwood National Park in California appear to be isolated events and include low-hanging branches with debris concealing cankers on infected hosts. In addition, an established epidemiological model of SOD which assumes only terrestrial dispersal grossly underestimated the observed spread of the pathogen. This work points to a critical dispersal mode for an important forest pathogen and highlights the need to determine the prevalence of this dispersal mechanism across the range of the pathogen.

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Research in Progress
Exhibit Room, 1:45 pm

Changes in native and exotic species richness on exposed sediments following large dam removal on the Elwha River, Washington

Rapidly aging American dam infrastructure has motivated calls for dam removal as a way to cut costs, improve safety, restore riparian habitats and improve fish passage. Despite the crucial role vegetation plays in creating riparian habitats, the scarce studies on the ecological effects of dam removal rarely consider its effects on vegetation. The largest dam removal to date on the took place on the Elwha River (Washington, USA) and was completed on the downstream reservoir in 2012, and upstream in 2014, exposing a cumulative 2.76 km² of previously inundated sediment surface. The revegetation of reservoir beds on the Elwha is a unique opportunity to study vegetation restoration following dam removal. Our objective is to determine how reservoirs and landform surfaces differed in terms of riparian vegetation succession in the absence of active restoration, and to compare naturally-revegetating areas to actively planted parts of the reservoirs. We surveyed vascular plant species richness and cover in 65 100m² permanent plots in 2013, 2014, and 2016. The plots are located on 10 transects perpendicular to river flow and randomly stratified across reservoir landforms (terrace, valley wall, and active channel). We compared changes in native and nonnative species richness and cover over time across the different landforms and reservoirs using mixed linear models. Species richness declined on the valley walls and terraces of Aldwell Reservoir, while cover of exotic species increased significantly on these landforms. Concurrently, species richness increased in the active channels of Aldwell Reservoir, probably due to the combination of frequent disturbances and seed rain. This is consistent with predictions about successional stage of the landforms. Future monitoring will investigate differences between actively planted and naturally revegetating areas in the reservoirs.

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Research in Progress
Exhibit Room, 10:45 am

Common garden evidence for local climate adaptation in blue oak

Two common gardens planted 25 years ago from acorns collected across the range of California blue oak (*Quercus douglasii*) provide an opportunity to disentangle the effects of genetic variation and phenotypic plasticity in this famously variable species. Surveys of leaf emergence, leaf senescence, and cumulative growth each reveal population-level effects based on acorn provenance populations. Analyses with climate of the provenance locations indicate that these effects may be climate adaptations that serve to reinforce local environmental effects.

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Research in Progress
Exhibit Room, 10:30 am

Predicting responses of wild plant populations to climate change: Integrating climatic and biological factors influencing the ecology and evolution of floral attraction

80-90% of flowering plant species rely on the services of pollinators such as insects, birds, and bats for successful reproduction. This requirement generates strong selection for floral traits that both attract efficient pollinators and enable them to distinguish the flowers of one species from other co-occurring species and from the surrounding environment. Research that aims to identify visual cues used in pollinator decision-making requires an investigation of color, as it is perceived by pollinating insects. The retinal photoreceptors of bees allow them to perceive blue, green, and ultraviolet (UV) light. Specifically, the spatial patterns in which flowers reflect and absorb UV light affect the behavior of potential pollinators. A variety of floral UV-absorption patterns (e.g., ‘bulls-eyes’) attract and guide insects, thereby promoting efficient pollination. UV floral patterns are ubiquitous in flowering plants and may vary both within and among populations. Quantifying variation in flower color within a species, across floral development, and across geographic space can inform investigations of the ecological function of flower color and the fitness consequences of variation. In my thesis work I use an ‘eco-evo’ framework within the natural laboratories of the UC Reserves and California parks to (1) describe geographic variation in floral pigment and pattern in *Clarkia unguiculata* using a novel image analysis method, and (2) determine the quantitative genetic basis and ecological function of a suite of floral attraction traits, including a poorly understood and previously cryptic trait, ultraviolet floral patterns.

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Research in Progress
Conference Room, 2:00 pm

Flower scent as a potential reproductive barrier in a Hawaiian plant lineage

In flowering plants, chemical communication often facilitates pollinator specificity, which may affect whether populations diverge or hybridize. Species possessing divergent floral scents may attract distinct pollinators, limiting interspecific pollen transfer. Conversely, shared volatiles that attract the same pollinator could reduce prezygotic isolation. Furthermore, ability of pollinators to recognize hybrid scent could mediate gene flow between hybrids and parental species. After recombination, hybrids may produce novel volatile compounds, novel blends, or reduced emissions. Alternatively, overlap between hybrid and parental scent could enhance uni- or bi-directional backcrossing and gene flow.

The genus *Schiedea* (Caryophyllaceae) has radiated rapidly across the Hawaiian Islands, producing interfertile species with diverse pollen vectors (moth, bird, wind, selfing). We investigated the floral scent of two sympatric species from different clades (*S. kaalae* and *S. hookeri*) and their artificial hybrids. These species are visited by the same microlepidopteran pollinator, and when artificially pollinated produce viable hybrid seeds and vigorous F₁ hybrids in the greenhouse. However, we have no evidence of natural hybridization or past genetic introgression, suggesting other barriers. We hypothesized that parental species differ in scent due to their phylogenetic distance yet share volatile compounds to attract their common pollinator, and that F₁ hybrid plants will have intermediate floral volatile composition. Alternatively, F₁ hybrids could lack attractants and/or produce novel compounds.

We grew *S. kaalae*, *S. hookeri*, and F₁ hybrids in the greenhouse from seeds and cuttings. Floral volatiles were characterized and quantified by dynamic headspace sampling and thermal desorption GC-MS, with overlap determined by qualitative comparison (compounds in ≥4 samples), PERMANOVA, and constrained analysis of principal coordinates (CAP). Parental species shared 58 of the 113 volatile compounds produced by the two species. As a group, artificial hybrids produced 57 of these 58 shared compounds, 11/17 compounds unique to *S. kaalae*, 36/36 compounds unique to *S. hookeri*, and 2 novel compounds, some of which (1-octen-2-ol, linalool) are known insect attractants. Quantitative scent composition differed between parents, hybrids were intermediate in their scent composition, and hybrids differed from parental species in scent composition.

Despite sharing a pollinator, parental species differed in floral volatile composition. Implications for isolation are equivocal because the two parental species and hybrids produced both shared and distinct floral volatiles. Future work will identify compounds critical for moth attraction and their role in pre- and post-zygotic reproductive isolation.

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Research in Progress
Conference Room, 11:45 am

Host-to-parasite horizontal gene transfer and its utility in time-calibrating the Orobanchaceae phylogeny

Horizontal gene transfer (HGT) from autotrophic plants to their heterotrophic parasites has been observed in several independent lineages. Here, I will present phylogenetic evidence of HGT of the gene *rbcL* (RuBsCO large subunit) into the ancestor of the recently described species of the holoparasitic genus *Aphyllon* (Orobanchaceae) from the plastid of its *Galium* host. Differences in sequencing coverage between other plastid genes in *Aphyllon* and the horizontally derived *rbcL* paralog, suggest that it has not been integrated into the parasite plastome, however, additional study is needed to verify its location in the genome.

Previous research has shown host to parasite HGT of a different gene, *albumin1*, in the common ancestor of *Aphyllon* and its Old World relative, *Orobanche*. Due to the extensive fossil record of its leguminous host, these researchers were able to infer the timing of the HGT event and subsequent diversification events. Using this point as a secondary calibration, I reconstructed a dated phylogeny for the Orobanchaceae, overcoming the limitations of a depauperate fossil record and accelerated rates of molecular evolution.

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Research in Progress
Exhibit Room, 11:30 am

Drought, fungi, and death in *Arctostaphylos glauca*

Synergies between extreme climate events and pathogens may lead to dramatic changes in plant communities. In the Santa Ynez mountain range in Santa Barbara County, the widespread and classically drought-tolerant shrub, big berry manzanita (*Arctostaphylos glauca*), is experiencing dramatic dieback related to two factors: a multi-year drought and pathogenic infection from latent fungal pathogens in the Botryosphaeriaceae family. In winter 2016-2017, a greenhouse experiment was conducted to identify the individual and interacting influences of drought and fungal infection on shrub mortality. The goal was to determine if a common fungal pathogen by itself could cause *A. glauca* dieback and whether drought exacerbated the influence of the pathogen. Using the fungal species *Neofusicoccum australe*, which I cultured from field samples, I conducted a full factorial experiment to test the influence of extreme drought (watered versus drought) and fungi (+ vs -) on shrub performance and mortality. Data were collected on a weekly basis for 90 days to measure onset of disease, changes in photosynthetic output (A_{max}), and time until mortality. Results show a significant difference between treatment groups, with the drought and fungus treatment group exhibiting the fastest decline in photosynthesis, onset of symptoms, and subsequent mortality. This was followed by the watered and inoculated group, and then the drought without inoculation group. All individuals in the control group survived while only two other individuals survived (one in the drought only treatment group and one in the watered with inoculation group). These results indicate a possible synergy between drought and fungal infection in influencing the rate of *A. glauca* mortality. The data further suggest that *N. australe* is itself highly virulent and causes mortality fairly quickly, at least in small individuals, even in non-drought stressed plants.

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Research in Progress
 Conference Room, 11:15 am

**Phylogenetic investigation of the genus *Hechtia*,
 an understudied group of succulent Mexican bromeliads**

The genus *Hechtia* (Bromeliaceae), with nearly 80 described species mostly restricted to Mexico, is an understudied and poorly understood genus that lacks a comprehensive taxonomic treatment—not surprising since nearly 40% of the species have been described in the past eight years. This genus of dioecious plants has interesting characters that including a range of ovary positions, different points of origin for their inflorescence, and different floral morphology that make them an exciting subject for evolutionary studies. My project is utilizing genome skimming to assemble complete plastomes and the nrDNA cistron to infer phylogenetic relationships within the genus. A goal is to propose the first infrageneric classification. With a total of 65 specimens sampled from the genus, the study includes over 50% of the described species and 16 putative, undescribed species. The sample covers the geographic and morphological breadth of the genus. While there are the expected strong geographic associations, natural morphological groups are well supported. For example, the species with serrulate leaves and those producing inflorescences from leaf axils forming well supported clades—the latter group covering nearly the entire north-south range of the genus. There are a few surprising results suggesting introgression that will need to be investigated in the future.

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Research in Progress
 Conference Room, 9:15 am

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**A window into land plant evolution through the first complete
 annotated fern genomes of *Azolla filiculoides* and *Salvinia cucullata***

Ferns are one of the few remaining embryophyte lineages for which a complete nuclear genome sequence is not available. To remedy this gap, we have sequenced and annotated the nuclear genomes of the heterosporous water ferns *Azolla filiculoides* and *Salvinia cucullata*. *Azolla* is a fast growing plant that forms a symbiotic relationship with an obligate nitrogen-fixing cyanobacterial symbiont and has huge potential for carbon sequestration, providing nitrogen-rich feedstock, and as a sustainable biofertilizer. *Salvinia* has no roots and a genome one-third the size of *Azolla*, the smallest known of any fern. *Azolla* and *Salvinia* will serve as critical lineages of comparative genomic analyses of land plants, will further our understanding of the evolution of symbioses, genome size, heterospory, and roots. Using extensive transcript and homologous protein evidence, a custom repeat library, and ab initio predictions, we annotated protein-coding genes and repeats in *Azolla* and *Salvinia* using the MAKER-P pipeline. *Azolla* has nearly twice as many genes as *Salvinia* and a greater proportion of its genome is comprised of mobile genetic elements. Ongoing analyses of gene function and repeat content will help identify genomic contributions to the biological differences of *Azolla* and *Salvinia*.

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Completed Research

Conference Room, 10:30 am

Resolving the anomaly: *Lomatium triternatum* var. *anomalum*

Lomatium, of the family Apiaceae, is a genus within one of the largest endemic plant radiations in North America: The Perennial Endemic North American (PENA) clade. *Lomatium* is of particular interest due to its complex and poorly understood evolutionary history. Recent phylogenetic analyses of *Lomatium* have demonstrated that many of the morphological characters used to delimit taxa have arisen multiple times and that most taxa are para- or polyphyletic. Here we examine one of the clades recovered in the *Lomatium* group of taxa that includes *L. triternatum* and *L. triternatum* var. *anomalum*. Through analysis of morphometric, phylogenetic, and ecological parameters, we have improved support for evolutionary relationships and resolved species boundaries, illuminating two potentially novel *Lomatium* species from the ambiguously classified *L. triternatum* var. *anomalum* group. *Lomatium* is a prime example of a useful endemic as indigenous people have depended upon it for both medicinal and dietary uses; thus, documenting *Lomatium* species diversity may benefit humanity on a multidisciplinary level.

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Research in Progress

Exhibit Room, 9:45 am

Effects of renewable energy development on annual plant seed bank dynamics

California's deserts support 171 CRPR-listed taxa that may be affected by renewable energy development, with permanent structures changing natural light and water regimes in ways that may strongly affect plant performance. Annual species may be most sensitive to these effects, because persistence depends on regeneration from a seed bank. Work in other systems has shown higher seed mortality with decreasing light and increasing moisture, abiotic shifts likely to occur under arrays. These changes may also favor some species over others, with invasive plant infestations increasing where infrastructure creates conditions favoring their success. Design and siting of facilities to minimize impacts thus requires understanding how altered abiotic conditions affect belowground seed reserves as well as aboveground life stages, for exotic species as well as rare and common natives. Sensitivity analyses of existing demographic models for a rare and common native species pair show population growth estimates improve with higher seed bank survival rates, but little is known about how solar infrastructure affects belowground processes. In our current work, we create artificial seed banks, assessing seed survival and germination rates for seed of different ages in control and shade plots. Because moisture is known to negatively affect seed survival in other systems, possibly by facilitating fungal attack, we subject half of our seed banks to a fungicidal treatment. We have also added a third focal species to our study, the invasive Sahara mustard, to allow comparison of aboveground and belowground response by both native and exotic species. This work will shed light on population-level impacts of solar development on multiple species, and contribute to understanding of seed bank dynamics and microhabitat factors affecting seed longevity.

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Research in Progress
Exhibit Room, 9:00 am

Next-generation population genetics in California rare plants

The state of California has the largest number of rare, threatened, and endangered plant species in the United States. Many of these species are narrowly endemic to California, have populations that are fragmented, or currently inhabit a fraction of their historical ranges. As populations of rare plants decline, their genetic health and variability needs to be assessed so that appropriate conservation plans can be developed. Recent advances in genome sequencing technology allow for the rapid development of population genetic markers for non-model organisms in a high throughput and economical way. This new technology provides exciting new opportunities to study conservation genetics in California rare plants. We have initially targeted 9 rare plants identified by the United States Fish and Wildlife Service as being in need of genetic research. We are using next-generation shotgun genome sequencing to develop microsatellite markers for the following species: *Ambrosia pumila*, *Brodiaea filifolia*, *Ceanothus ophiochilus*, *Chorizanthe orcuttiana*, *Dudleya stolonifera*, *Eriastrum densifolium* subsp. *sanctorum*, *Fremontodendron mexicanum*, *Navarretia fossalis*, and *Verbesina dissita*. Candidate microsatellite loci will be evaluated and tested for amplification. Microsatellite primers will be made publically available to the plant science community for use in conservation projects. We welcome feedback and collaboration with individuals and organizations interested in rare plant conservation and land management planning.

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Research in Progress
Exhibit Room, 9:30 am

The effect of increasing forest density and compositional shifts on seedling survival in a Sierra Nevada mixed-conifer forest

Fire suppression, management, and altered disturbance regimes have changed the structure and composition of western forests, which influences the suitability of seedling regeneration sites. Historic datasets are often used to identify such changes, but few studies compare the effects of establishment site on seedlings abundance through time. We used a historic dataset from the mixed conifer forest of the western Sierra Nevada to examine the effect of the regeneration environment and shrub community on the abundance of *Pinus*, *Abies*, and *Calocedrus* spp. seedlings. We re-measured four US Forest Service Methods of Cutting plots originally established in 1929 to track the influence of different harvest practices on forest composition. Foresters mapped the overstory, regeneration, and understory prior to treatment in 1929 and periodically until 1947. We resampled the plots in 2016 following original methodologies to track changes over the last 85+ years. Diversity metrics indicate similar understory diversity in 1931 and 2016, but species composition has changed. A zero inflated negative binomial model identified shrub cover as positively associated with white fir and incense cedar in 1931 and burned area as negatively associated with fir and cedar. In 2016, trees per hectare was negatively associated with fir and cedar and soil moisture was positively associated with cedar. Pine seedling abundance was not inhibited nor facilitated by any factors, with low densities across all plots. Altered forest conditions have caused a decrease in pine and fir seedlings and an increase in cedar densities over the last 85 years. Climate change, altered fire regimes, and beetle outbreaks will further influence seedling survival, forest characteristics, and future community composition.