

NINTH ANNUAL

YOSEMITE SYMBIOSIS WORKSHOP



Sierra Nevada Research Institute

Yosemite National Park, May 17-19 2019

Friday May 17, 2019

Arrival & Welcome Party 7:00pm – 10:00pm

Landsneas House 2667 English Lane, Wawona CA (see attached map)

Saturday May 18

Wawona Community Center (see attached map)

Lunch 11:30pm – 12:25pm

12:25 Welcome to the 2019 Yosemite Symbiosis Workshop (Carolyn Frank, Joel Sachs)

Session I: How do host or microbe control symbiosis outcomes?

- 12:30 Joel Sachs, UC Riverside
Interspecific conflict triggers fitness costs for host investment into symbiosis
- 12:45 Alexandra J. Weisberg, Oregon State University
The genomic bases for cheating among wild populations of nodule-associated *Bradyrhizobium*
- 1:00 Gabriel Ortiz, UC Riverside
Effects of domestication in the symbiotic interaction between cowpea and rhizobia

30 minute break for coffee and snacks

Session II: What shapes symbiont community function?

- 2:00 Shayle Benjamin Matsuda, University of Hawaii,
Symbiont manipulation: Coral exposure to algal symbiont (Symbiodiniaceae) cocktail as an early life strategy to prepare for future ocean warming
- 2:15 Joshua Harrison University of Wyoming
Both dominant and infrequent endophytes affect plant traits as shown through experimentation and a new application of Dirichlet-multinomial statistical modeling
- 2:30 Chris Wall, UH Manoa
Master of polyps: Symbiodiniaceae functional diversity drives niche partitioning and isotope values in a Hawaiian reef coral
- 2:45 Carly D. Kenkel, USC
Transgenerational inheritance of shuffled symbiont communities in the coral *Montipora digitata*
- 3:00 Jamison Sydnor, CSU Chico
The Bacterial Community Associated with the Model Sea Anemone *Exaiptasia pallida*: Response to Rising Ocean Temperatures

30 minute break for coffee and snacks

Session III: How do environmental stressors modulate host-symbiont systems?

- 3:45 Jackie Shay, UC Merced
Endophyte community shifts in response to drought in monkeyflowers (*Erythranthe laciniata*) grown in native soil
- 4:00 Lorena Torres-Martínez, UC Riverside
Climate, but not symbiosis, drive local adaptation of an annual legume
- 4:15 Lauren Howe-Kerr, Rice University
Symbiont community diversity is more constrained in holobionts that tolerate diverse stressors
- 4:30 Benedicte Bachelot, Rice University
Disturbances can promote and hinder coexistence of competitors in on-going partner choice mutualisms

Beer, Wine & Snacks 4:45-5:30

Keynote Lecture Martha 'Molly' Hunter 5:30-6:30

"Environmental transmission:

Upending our assumptions about the intimacy of mutualist arthropod-microbe symbioses"

Dinner 6:30-800

Poster Session 8:00-9:30pm

SYMBIOSIS WORKSHOP SCHEDULE 2019

Sunday May 19

Breakfast in your Cabins

Session IV: How does symbiosis reshape forest ecosystems?

- 9:00 Caroline Daws, Stanford University
Landscape biogeography of plant-fungal symbioses in Populus
- 9:15 James Kupihea, UC Merced
Nitrogen Fixation by diazotrophic endophytes in Sierra lodgepole pine foliage
- 9:30 Jake Sarver, UC Santa Barbara
Exploring Foliar Fungal Endophyte Assemblage, Diversity, and Host Specialization in Pine
- 9:45 Austen Apigo, UC Santa Barbara
Life in the leaves: the diversity and distribution of foliar fungal endophytes
- 10:00 An Bui, UC Santa Barbara
Tree-fungal associations in the Anthropocene: Symbiotroph community composition in California's oak savanna along an aridity gradient

30 minute break for coffee and snacks

Session V: What mechanisms regulate symbiosis versus dysbiosis?

- 10:45 Valeri Lapacek, Oregon State University
Characterizing the role of NADPH oxidase during heat stress in the symbiotic sea anemone *Aiptasia*
- 11:10 Raphael Ritson-Williams, California Academy of Science
Variability in Gene Expression Drives the Susceptibility of Coral Symbiosis to Bleaching
- 11:15 Lorraine Ling, Stanford University
Localization and dynamics of a glucose transporter putatively involved in Cnidarian-dinoflagellate symbiosis

Session VI: How does altering partners change a symbiosis?

- 11:30 Mark Sistrom, UC Merced
Probiotics as vectors of antibiotic resistance in the human microbiome
- 11:45 Sarah Hammarlund, University of Minnesota
A shared limiting resource leads to competitive exclusion in a microbial mutualism
- 12:00 Samuel A. Bedgood, UC Irvine
Spatial subsidies change the interaction between host sea anemones and their algal symbionts

Lunch 12:30-1:30

End of conference

Talk Abstracts

1. Austen Apigo, UC, Santa Barbara aapigo@ucsb.edu
Life in the leaves: the diversity and distribution of foliar fungal endophytes
 Austen Apigo, Rodolfo Salas-Lizana, Jose Rubén Montés, Edward Allen Herre, Luis Mejía, Ryoko Oono
 Foliar fungal endophytes (abbreviated as 'endophytes') are a species-rich and phylogenetically diverse guild of microfungi that asymptotically inhabit the aboveground, tissues of all land plants. Endophytes are distributed worldwide across every terrestrial biome and it has been suggested they compose much of the undiscovered biodiversity within the kingdom Fungi. However, their apparent 'hyperdiversity' has yet to be quantified (1) across the diversity of ecosystems in which they occur, (2) with culture-independent methods (i.e., high-throughput sequencing) that capture rare and unculturable fungal species and (3) with analyses that account for host community structure. To understand how the structure of these complex symbioses vary as a function of climate and the plant host community, we surveyed endophyte communities from 21 temperate and tropical forests (5°N - 64°N) by intensively sampling all co-occurring plant host species within five 50 m² quadrats per site during the summers of 2016 and 2017. We then sequenced the internal transcribed spacer 1 region on the Illumina MiSeq platform to directly characterize fungal community structure from host leaf tissue (n = 2,424 plant samples). Previous culture-dependent studies suggest endophytes are highly abundant and diverse in the tropics and follow the widely documented pattern in many plants and animals where species richness increases towards the equator - the latitudinal diversity gradient. Our preliminary high-throughput data (12 of 21 sites) suggest that endophyte diversity is bimodal as a function of latitude. I will discuss how plant community structure and host specificity may contribute to observed endophyte diversity patterns and the implications of endophyte diversity on our understanding of global fungal biodiversity.

2. Benedicte Bachelot, Rice University bb32@rice.edu
Disturbances can promote and hinder coexistence of competitors in on-going partner choice mutualisms
 Coauthor: Charlotte Lee
 Disturbances can promote and hinder coexistence of competitors in on-going partner choice mutualisms
 Ecosystems are under threat from anthropogenic and natural disturbances, yet little is known about how these disturbances alter mutualistic interactions. Most mutualistic interactions are highly context-dependent and dynamic due to "on-going" partner choice, impeding our understanding of how disturbances might influence these interactions. Previously we showed that, in the absence of additional known mechanisms of competitive coexistence, mutualistic fungi can coexist in a system where the plant community associated dynamically with two empirically-defined arbuscular mycorrhizal fungal types: a cheap kind that provides low nutrient benefits and an expensive type that provides high nutrient benefits. We built on this framework to ask how disturbances of different types, frequencies, amplitudes, and predictability alter on-going partner choice and thereby influence the coexistence of mutualists. Disturbance can disrupt mutualist coexistence by enabling hosts to more efficiently exclude partners that behave as parasites. Disturbance can also promote coexistence by altering the strength and direction of consumer-resource interactions. Predicting the effects of disturbance on the mutualist community therefore requires us to understand better the consumer-resource relationships under various environmental conditions. We showed that, through such context-dependent effects, disturbance and on-going partner choice can together generate relative nonlinearity and investment in future benefit, introducing fluctuation-dependent mechanisms of competitive coexistence. We found that the effects of disturbances depend on the type, amplitude, and predictability of disturbances, but not their frequency. Our findings support a broadening of the conceptual framework regarding disturbances and competition to include fluctuation-dependent mechanisms alongside the spatiotemporal Intermediate Disturbance Hypothesis.

3. Samuel A. Bedgood, UC Irvine sbedgood@uci.edu
Spatial subsidies change the interaction between host sea anemones and their algal symbionts
 Matthew E. S. Bracken
 Three congeneric species of sea anemone (genus *Anthopleura*) that are hosts to symbiotic unicellular algae (family Symbiodiniaceae) co-occur in rocky intertidal habitats on the central coast of California. The sea anemones provide their intracellular symbionts with abundant nitrogen and carbon dioxide for growth, while the symbionts provide the sea anemone with dietary carbon in the form of translocated sugars and lipids. However, symbionts do not provide the only dietary carbon source available to the host. Sea anemones are passive suspension feeders, consuming items that come in contact with their tentacles. The availability of prey in their intertidal environment is highly variable,

and many prey items originate from outside the local system. How these spatial subsidies influence the relationship between the sea anemone and its symbionts is unknown. By manipulating the amount of food received by *Anthopleura sola* and *A. xanthogrammica* in situ, we found that algal symbiont density, chlorophyll a, photosynthetic efficiency, and symbiont biovolume were all affected by diet. However, the response depended on the species of sea anemone. Implications for this response include the ability of sea anemones to maximize the benefit from their symbionts, keeping them at high density when prey is scarce and expelling them when resources are abundant. However, an increase in symbiont volume and a decrease in density resulted in a conserved total symbiont biovolume, which could keep the contribution from symbionts constant despite fluctuating prey availability.

4. An Bui, UC Santa Barbara an.bui@lifesci.ucsb.edu

Tree-fungal associations in the Anthropocene: Symbiotroph community composition in California's oak savanna along an aridity gradient

Coauthors: Holly Moeller, Devyn Orr, Michelle Lepori-Bui, Hillary Young

The functioning of forested systems depends in no small part on the relationships between trees and their fungal symbionts, which account for two-thirds of tree root carbon inputs into soil and 80% of soil N mineralization in forested systems (Zhang et al. 2018). However, these relationships are imperiled by the impacts of climate change – in particular, California's ecosystems are now subject to increasingly warmer, dryer years. Changing climates could mean shifting species community composition of symbionts, with further implications for ecosystem function. To test the hypothesis that symbiotroph community composition is shaped by aridity, we sampled fungal communities along an aridity gradient within oak (*Quercus* spp.) savanna in the Tehachapi Mountains of California. We then used Illumina sequencing methods to characterize the fungal community and identify fungal species. Using fungal trait databases, we were able to link species identity to functional group. In this talk, I demonstrate that there is a graded shift in fungal community composition across aridity and explore the implications of these dissimilarities for fungal community function.

5. Caroline Daws, Stanford University, cdaws@stanford.edu

Landscape biogeography of plant-fungal symbioses in Populus

Coauthors: Michael Van Nuland, Kabir Peay

Landscape biogeography of plant-fungal symbioses in *Populus*. The fungal mycobiome consists of a complex community of plant-associated symbionts (spanning mutualists to pathogens) involved in many processes that govern community dynamics and ecosystem function. For instance, the presence of certain leaf endophyte fungi can affect plant disease susceptibility and drought tolerance, root fungi help determine the recruitment success of tree seedlings, and soil fungi influence the decomposition rate of plant organic material. We know that the diversity of these plant-associated mycobiomes can be highly variable both across different tissues of a single host and across the range of single host species. However, it is yet unclear how fungal diversity is linked between above and belowground tissues of a specific host species, and how environmental and topographical factors affect the dispersal of these microbes across large spatial gradients. Because the mycobiome alters the fitness and environmental tolerance of host plants (i.e., their ecological niche), characterizing how fungal communities differ across wide environmental gradients is critical for understanding the impact of these symbioses on plant biogeography and species responses to environmental change. Here, we assess the diversity of the above and belowground mycobiome of five *Populus* species (*P. angustifolia*, *P. deltoides*, *P. fremontii*, *P. trichocarpa*, and *P. tremuloides*) from sites across their geographic ranges in the continental US. *Populus* is a widespread tree genus, which allows us to control for phylogenetic effects and focus on the environment/dispersal effects on variation in host-fungal symbioses. Specifically, we incorporate plant traits, soil chemistry, and climate measurements to ask two central questions: 1) How is the diversity of plant-associated fungi distributed across host tissue compartments (i.e. leaves, roots, and soils) and across the range of a host species? 2) What environmental and topographical characteristics of the landscape best predict changes in fungal diversity? We characterized the fungal mycobiome by extracting DNA from leaf, root, and soil material from mature *Populus* trees at each site (N = 94 sites), and sequencing the ITS1 region of the fungal ribosomal RNA genes on the Illumina MiSeq sequencing platform. We employed spatially-explicit cost modeling to determine where fungal diversity turns over most dramatically across the landscape, and to investigate what environmental and geographical characteristics predict these rapid shifts in community composition. We find evidence for tissue-specific and host species-specific variability in fungal community turnover, suggesting that both the identity of the host and the mode of dispersal and colonization in above and belowground symbioses are important in determining mycobiome composition. Furthermore, we find that environmental factors such as precipitation and temperature and topographic barriers such as host range connectivity are equally important to host identity in determining fungal symbiont community composition across

large spatial gradients. Our work suggests that symbioses that are often studied in isolation (i.e. mycorrhizal partnerships or pathogen outbreaks) are implicated in a complex network of interactions that is governed both by host microbiome properties and by environmental characteristics across the range of the host

6. Sarah Hammarlund, University of Minnesota hamma111@umn.edu
A shared limiting resource leads to competitive exclusion in a microbial mutualism
 Coauthors: Jeremy Chacon, Will Harcombe
 Species interactions and coexistence are often dependent upon environmental conditions. Many microbial communities are organized into webs of cross-feeding interactions, in which species rely on nutrients excreted by others. When two cross-feeding bacteria exchange essential nutrients, the addition of a cross-fed nutrient to the environment can release one species from its mutualistic dependence on the other. Previous studies suggest that continued coexistence depends on relative growth rates: coexistence is maintained if the slower-growing species is released from its dependence on the other, but if the faster-growing species is released, the slower-growing species will be lost (a hypothesis that we call 'feed the faster grower' or FFG). Using invasion-from-rare experiments with two reciprocally cross-feeding bacteria, genome-scale metabolic modelling and classical ecological models, we explored the potential for coexistence when one cross-feeder became independent. We found that whether nutrient addition shifted an interaction from mutualism to commensalism or parasitism depended on whether the nutrient that limited total growth was required by one or both species. Parasitism resulted when both species required the growth-limiting resource. Importantly, coexistence was only lost when the interaction became parasitism, and the obligate species had a slower growth rate. Under these restricted conditions, the FFG hypothesis applied. Our results contribute to a mechanistic understanding of how resources can be manipulated to alter interactions and coexistence in microbial communities.

7. Joshua Harrison, University of Wyoming jgharrison1982@gmail.com
Both dominant and infrequent endophytes affect plant traits as shown through experimentation and a new application of Dirichlet-multinomial statistical modeling
 Coauthors: C. Alex Buerkle, Lyra Beltran, W. John Calder, Daniel Cook, Dale Gardiner, Thomas L. Parchman, Matthew L. Forister
 Endophytes are microbes that live, for at least a portion of their life history, within plant tissues. The ways in which most endophytes affect host phenotype are unknown and it is often assumed that the rare members of endophytic consortia have minor ecological influence. To understand the effect of endophytes within differing abundance categories on their hosts, we manipulate both the suite of rare foliar endophytes and *Alternaria fulva*—a dominant, heritable fungus—within the Fabaceous forb, *Astragalus lentiginosus*. We report that rare endophytes, despite likely occupying only a small amount of host tissue, affected host size and foliar N %, but only when the dominant fungal endophyte was not present. *A. fulva* also reduced plant size and N %, but these deleterious effects on the host could be offset by a striking antagonism we observed between this heritable fungus and a foliar pathogen. Analyses involved a new application of Bayesian statistical modeling using the Dirichlet and multinomial distributions. We briefly present results from a simulation experiment confirming the benefits of this technique over popular differential expression testing methods.

8. Lauren Howe-Kerr, Rice University lih2@rice.edu
Symbiont community diversity is more constrained in holobionts that tolerate diverse stressors
 Coauthors: Benedicte Bachelot, Rachel M. Wright, Carly D. Kenkel, Line K. Bay, Adrienne M.S. Correa
 Coral reefs are experiencing global declines as climate change and other stressors cause environmental conditions to exceed the physiological tolerances of host organisms and their microbial symbionts (collectively termed the holobiont). To assess the role of symbiont community composition in holobiont stress tolerance, diversity metrics and abundances of obligate dinoflagellate endosymbionts (Family: Symbiodiniaceae) were quantified from eight *Acropora millepora* coral colonies (hereafter called genet) that thrived under or responded poorly to various stressors. Four 'best performer' coral genet were selected for analysis because they survived 10 days of high temperature, high $p\text{CO}_2$, bacterial addition, or combined stressors, whereas four 'worst performer' coral genet were analyzed because they experienced significant mortality under these stressors. At the end of the experimental period, seven of eight coral genet mainly hosted *Cladocopium* symbionts, but also contained *Brevolium*, *Durusdinium*, and/or *Gerakladinium* symbionts at lower abundances (<0.1% of the total community). After 10 days of stress, symbiont communities varied significantly among host genet, but not stress treatments, based on alpha and beta diversity metrics. A generalized joint attribute model (GJAM) also predicted that symbiont communities were primarily sensitive to host genet at regional scales. Symbiodiniaceae communities exhibited higher richness

and variance (beta diversity) in the worst performing genets. Indicator species analysis and the regional GJAM model identified significant associations among particular symbionts and host genet performance. Specifically, *Cladocopium* 3k contributed to the success of best performer host genets under various stressful conditions, whereas *Durusdinium glynnii* and *Durusdinium trenchii* were significantly associated with one worst performer genet. *Cladocopium* 3k dominance should be more broadly investigated as a potential predictor of stress resistance in *Acropora millepora* populations across their geographic range. The experimental approach and analyses employed here can be broadly applied to identify beneficial symbiont community properties in hosts central to diverse disciplines, from agriculture to medicine.

9. Carly D. Kenkel, USC ckenkel@usc.edu

Transgenerational inheritance of shuffled symbiont communities in the coral *Montipora digitata*

Coauthors: Kate M. Quigley, Bette L. Willis

Adult organisms may “prime” their offspring for environmental change through a number of genetic and non-genetic mechanisms, termed parental effects. Some coral species can alter their thermal tolerance by shuffling the proportions of Symbiodiniaceae types within their endosymbiotic communities, but it is unclear if this plasticity is transferred to offspring in corals that have maternal symbiont transmission. We evaluated symbiont community composition in tagged colonies of *Montipora digitata* over two successive annual spawning seasons and the 2016 bleaching event on the Great Barrier Reef. ITS2 amplicon sequencing was applied to four families (maternal colonies and 10-12 eggs per family) to characterize shuffling potential and determine if shuffled abundances were preserved in gametes. Symbiont densities and photochemical efficiencies differed significantly among adults in 2016, suggesting differential responses to increased temperatures. Low-abundance (“background”) symbionts differed more among years than between maternal colonies and offspring. Results indicate that shuffling can occur in a canonically ‘stable’ symbiosis, and that such plastic changes to the symbiont community are heritable. Although previously hypothesized, to our knowledge, this is the first evidence that shuffled Symbiodiniaceae communities can be inherited by offspring and supports the hypothesis that plastic changes in microbial communities may serve as a mechanism of rapid coral acclimation to changing environmental conditions.

10. James Kupihea, UC Merced jkupihea@ucmerced.edu

Nitrogen Fixation by diazotrophic endophytes in Sierra lodgepole pine foliage

Oscar A. Elias

Growing evidence supports the hypothesis that foliar diazotrophic endophytes are present in the needles of conifers, and that they may contribute to host-tree nitrogen (N) budgets in N limited ecosystems. Sierra lodgepole pine (*Pinus contorta* var. *murrayana*) are long-lived conifers that thrive in a broad spectrum of soil types ranging from water-logged organic soils to well-drained glacial outwash. Interestingly, they often dominate wet and poorly drained N limited soils unable to support most plant species. Biological nitrogen fixation (BNF) by diazotrophic endophytes may help explain how Sierra lodgepole pine persists on N poor soils. However, rates of BNF in lodgepole pine foliage is poorly understood, as is how rates vary across the development of the host-tree. We sought to address the following questions: 1) Can we observe nitrogenase activity in the foliage of lodgepole pine, and 2) Does nitrogenase activity vary with host-plant age? We conducted a series of acetylene reduction assays (ARA) with Sierra lodgepole pine in Yosemite National Park from 2016-2018 to assess the rate of BNF by foliar diazotrophic endophytes in seedlings and mature branches (Aug 2016), intermediate-aged trees (Aug 2017), and again for all size classes (Aug – Nov 2018). We measured the conversion of acetylene to ethylene in 500+ seedlings, and the needles of ten mature and intermediate-aged Sierra lodgepole pine. Foliage samples (above the hypocotyl for seedlings) were excised and incubated in 16 oz septa-fitted mason jars (volume = 473ml) for two hours in a 10% v/v acetylene atmosphere. Gas samples were analyzed for ethylene concentration on a Shimadzu-GC with an FID. The conversion rate of acetylene to ethylene is equal to the net increase in moles of ethylene in the headspace during the 2-hour incubation.

EARLY RESULTS (ANALYSIS IN PROGRESS - Positive rates of ethylene production were detected in Sierra lodgepole pine seedlings (0-8.68 $\mu\text{mol C}_2\text{H}_4 \text{ gdw}^{-1} \text{ hr}^{-1}$), intermediate aged trees (0.5-1.5 $\mu\text{mol C}_2\text{H}_4 \text{ gdw}^{-1} \text{ hr}^{-1}$), and mature trees (0-0.94 $\mu\text{mol C}_2\text{H}_4 \text{ gdw}^{-1} \text{ hr}^{-1}$) compared to controls. Endogenous ethylene production in samples were below detection limit. Seedlings contained the highest rate and broadest range of ethylene production, while mature trees showed the lowest rates of ethylene production across the narrowest range. Our data reflects rates higher than previously reported values observed in limber pine (*Pinus flexilis*) in Niwot, CO (0.22 \pm 0.02 $\text{nmol C}_2\text{H}_4 \text{ g}^{-1} \text{ needle hr}^{-1}$), and were also greater than the 30-110 $\text{mmol C}_2\text{H}_4 \text{ gdw}^{-1}$ observed in deciduous white cottonwood (*Populus trichocarpa*) foliage. Overall, our results indicate that nitrogenase activity occurs in the needles of Sierra lodgepole pine, and that rates of ethylene production may decline with host tree age.

11. Valeri Lapacek, Oregon State University lapacekv@oregonstate.edu
Characterizing the role of NADPH oxidase during heat stress in the symbiotic sea anemone *Aiptasia*
 Angela Poole, and Virginia Weis
 Persistent elevated ocean temperatures stress the cnidarian-dinoflagellate symbiosis causing symbiotic dysregulation (dysbiosis), commonly known as coral bleaching. In corals and anemones, increased expression of NADPH oxidase (NOX) has been observed in bleaching and heat-stressed animals. NOX produces reactive oxygen species (ROS) that perform essential roles in stress-response and immune responses against microorganisms. These enzymes transport electrons across various membranes in a cell to generate an oxidative burst of superoxide and other downstream ROS. Oxidative stress has been shown to play a role in cnidarian bleaching, however, the role of NOX in dysbiosis remains unclear. The goals of this study were to characterize NADPH oxidase components in the genome of the tropical sea anemone, *Aiptasia*, a model system for the study of cnidarian-dinoflagellate symbiosis. The NADPH oxidase complex is present across the Metazoa as a multiunit protein, comprised of membrane and cytosolic components. Membrane-bound (NOX2-like and p22phox) and cytosolic (p67phox) genes were identified and expressed in symbiotic and aposymbiotic anemones. The research presented here will focus on NOX gene expression during thermal stress to assimilate NADPH oxidase's role in symbiotic dysfunction. In addition, data presented will include the localization of p67phox during bleaching in tissues of whole-mount anemones and dissociated tentacle cells.
12. Lorraine Ling, Stanford University loriling@stanford.edu
Localization and dynamics of a glucose transporter putatively involved in Cnidarian-dinoflagellate symbiosis
 Coauthors: Cory Krediet, John Pringle
 Many corals, sea anemones, and other cnidarians form mutualistic symbioses with dinoflagellate algae (Symbiodinium). The animal hosts provide inorganic nutrients and protection, while the algae provide photosynthetic products such as glucose and other fixed-carbon compounds. Within the host gastrodermal cells, the endosymbiotic algae are surrounded by the host-derived symbiosome membrane, across which all communication and metabolite trafficking occur. We previously identified a predicted glucose transporter (GLUT8) that is upregulated in the symbiotic relative to the aposymbiotic state of the sea anemone *Aiptasia*, a model system for study of this symbiosis (1). We generated a monoclonal antibody to *Aiptasia* Glut8 and verified its specificity by peptide competition. We then characterized protein localization in adult polyps via immunofluorescence and protein dynamics in response to heat stress via western blotting. We observed that Glut8 staining was qualitatively higher in gastrodermal than epidermal tissue within symbiotic *Aiptasia* and higher in symbiotic than in non-symbiotic animals. In addition, Glut8 staining was observed around algae freshly isolated from tentacle-cell macerates, but not around cultured axenic Symbiodinium. During thermal stress at 34°C, Glut8 protein abundance decreased at a rate roughly similar to that of the loss of the algal symbionts. These results support the transcriptome data, show that Glut8 protein levels are higher in symbiotic anemones, and show that Glut8 protein is intimately present around endosymbiotic algae. Taken together, the data suggest that Glut8 is involved in the key transport of glucose from Symbiodinium to its host cells and perhaps also to animal cells that lack direct access to food.
13. Gabriel Ortiz, UC Riverside gorti010@ucr.edu
Effects of domestication in the symbiotic interaction between cowpea and rhizobia
 Coauthors: Sierra Neal, Fizzah Khairi, Tarek Soubra, Paola Cardenas, Jerry Trinh, Angela Porter, Arafat Rahman, Lorena Torres, Joel Sachs
 In an ideal world, agricultural practices would support growing populations while protecting the environment. Crop domestication has modified wild plant species into altered forms to meet human needs. However, breeding practices focus on traits such as fruits, seeds, and disease resistance that manifest mainly in above ground plant tissues, but has largely ignored belowground traits of nutrient acquisition from microbiota. Legume – rhizobia symbiosis is an untapped resource for crop improvement as atmospheric nitrogen fixed by bacteria could reduce the current dependence on nitrogen fertilizers while improving crop performance. We investigated the effect of domestication on the evolution of symbiotic specificity between cultivated and wild cowpea genotypes. We tested twenty wild and cultivated cowpea genotypes in single and co-inoculations of two root nodule forming *Bradyrhizobium* strains that were efficient and inefficient nitrogen fixers. We measured traits of host fitness and whether the host possess a control system that modulates symbiont fitness based on the amount of fixed nitrogen provided. Our data suggests that cowpeas possess a sanctions mechanism against ineffective rhizobia and that cultivated and wild cowpeas accessions exhibit segregating variation for key symbiosis functions.

14. Shayle Benjamin Matsuda, University of Hawaii shayle@hawaii.edu
Symbiont manipulation: Coral exposure to algal symbiont (Symbiodiniaceae) cocktail as an early life strategy to prepare for future ocean warming
 Coauthors: Ruth D Gates
 Scleractinian reef corals live within a few degrees from their upper thermal limit, and are therefore threatened by episodic and seasonal ocean warming that disrupts their mutualistic symbiosis with Symbiodiniaceae, a process known as coral bleaching. In recent years, global bleaching events have contributed to massive coral die-offs. Both Symbiodiniaceae and bacterial communities play an integral role in holobiont nutrition, defense, and physiology, and have been shown to affect the performance of reef corals during (and following) temperature stress. Here, we examine how thermal stress affects the host-Symbiodiniaceae-bacterial symbioses and the overall holobiont health in four coral species in Kāneʻohe Bay, Hawaiʻi (*Montipora capitata*, *Porites compressa*, *Pocillopora acuta*, and *Pavona varians*) differing in key functional traits (skeletal morphology, tissue thickness, and Symbiodiniaceae fidelity and transmission mode). Twelve genotypes (n=5 ramets genotype⁻¹) of each species were collected and exposed to ambient (ca. 28°C) or high (ca. 31°C) temperature treatments for 2 weeks, and then held at 28°C for one month for physiological recovery. Bleaching responses were assessed via multiple physiological assays, including: PAM fluorometry, algal cell counts, coral growth, and biomass proteins. DNA was assayed at three time points (prior to heat stress, after high temperature exposure, and after recovery period) and treatment effects on microbial community assemblages were identified through amplicon sequencing of ITS2 (Symbiodiniaceae) and 16S (Bacteria). Of the four species, *Montipora capitata* was the most resistant to thermal stress, showing no significant decrease in Symbiodiniaceae cell counts and the smallest drop in photochemical efficiency. ITS2 profiles did not change in response to thermal stress or experimental time points, however, ITS2 profiles remained consistent by genotype (for example, *Porites compressa*, that associates primarily with *Cladocopium spp.* (ITS2 C15), exhibited one of three different C15-dominant ITS2 profiles by genotype, not treatment or time point). Similarly, after heat stress, bacterial profiles from stressed coral nubbins within a coral species more closely resembled those of their conspecific ambient counterparts than those of other species under thermal stress. *Porites compressa* showed the largest change in bacterial community structure at 31°C compared to 28°C controls. Our results show that heat stress can have minimal effects on some coral species, their symbionts and microbes, whereas more microbial communities in temperature sensitive species are disrupted within the coral holobiont and may contribute to coral disease, mortality, and loss of coral function that requires prolonged periods of post-stress recovery.
15. Raphael Ritson-Williams, California Academy of Science rritson-williams@calacademy.org
Variability in Gene Expression Drives the Susceptibility of Coral Symbiosis to Bleaching
 Coauthors: Stuart Willis, and Rebecca Albright
 Coral bleaching is a breakdown of coral symbiosis with endosymbiotic dinoflagellates that can be caused by warming seawater temperatures. Understanding the causes and consequences of coral bleaching has been a topic of research for the past 40 years, yet we still have a poor understanding of how some corals resist bleaching. In 2014 there was an extensive coral bleaching event on Oahu, Hawaii, USA and we found some coral colonies that resisted bleaching, even though they were found in the same environment as the corals that did bleach. Corals were tagged as pairs, one individual colony that bleached adjacent to another colony of the same species that resisted dysbiosis. RNAseq conducted on eight pairs of *Montipora capitata* colonies that hosted the same type of *Symbiodiniaceae* showed extensive gene expression variability among individual coral colonies regardless of location. Despite this variation, we found differential gene expression in over 1,800 genes between those corals that bleached and those that did not. We also found differences in expression in over 6,000 genes from the *Symbiodiniaceae* that were in bleached or resistant coral colonies. This variation in gene expression is providing critical data to understand the contributions of host and symbiont physiology to holobiont resistance to the modern impacts of climate change.
16. Joel Sachs, UC Riverside joels@ucr.edu
Interspecific conflict triggers fitness costs for host investment into symbiosis
 Kenjiro W. Quides Fathi Salaheldine, Ruchi Jariwala,
 Microbial mutualists provide substantial benefits to hosts that can feed back to enhance fitness of the associated microbes. But conflict is predicted to emerge over the magnitude of individual resource expenditures by each partner into the mutualism. We investigated the scope of conflict in the association between *Lotus japonicus* and its root-nodulating symbiont, *Mesorhizobium loti*. We employed experimental inoculations with near isogenic host and symbiont variants and analyzed fitness effects on each partner over a range of host investment into symbiotic root nodules. Consistent with fixed costs but diminishing benefits of root nodule formation, we found that *L. japonicus* hosts exhibited a unimodal fitness function for nodulation. Conversely, the fitness of the symbiont *M. loti* increased

linearly as the host plant formed additional root nodules, revealing host-symbiont conflict over the joint phenotype of number of nodules formed. These data highlight the often overlooked conflict in mutualistic interactions..

17. Jake Sarver, UC Santa Barbara jake_sarver@ucsb.edu
Exploring Foliar Fungal Endophyte Assemblage, Diversity, and Host Specialization in Pine
 Jake Sarver, Rodolfo Salas-Lizana, Austen Apigo, David S. Gernandt, and Ryoko Oono
 Host specialization of foliar fungal endophytes (FFE's) remains a cryptic and uncommon phenomenon. Since patterns of host specialization are sensitive to host taxonomic and spatial scales, a field study that investigates the fungal endophytic community of pines (Pinaceae), a taxonomically well-defined and diverse group, across a wide geographic range spanning much of North America, was conducted. Pines have a high incidence of FFE infection, likely due to the longevity of their evergreen foliage as well as their dominance in some ecosystems. Furthermore, *Lophodermium* (Rhytismataceae), a well-studied FFE genus that seems to be common within needles of the Pinaceae family, indicates high phylogenetic host specificity that is rarely documented in other FFE's. In total, 6 taxa from *Pinaceae* were sampled from 8 different localities across the Northeastern United States. Illumina MiSeq sequences were collected on the community assemblage of FFE's with a closer investigation of *Lophodermium* OTU's. Host specificity of common OTU's were analyzed and compared across geographic and taxonomic groups of pines. These findings will be crucial in furthering our understanding of the evolutionary and ecological nature of these mysterious microfungi on their hosts.

18. Jackie Shay, UC Merced jshay@ucmerced.edu
Endophyte community shifts in response to drought in monkeyflowers (*Erythranthe laciniata*)
 Coauthors: Lauren Brooks, Mo Kaze, Carolin Frank, Jason Sexton, Mark Sistrom
 All plants have a community of asymptomatic microbes inhabiting their tissue known as endophytes. Increasing evidence suggests that microbes are an extension of plant host phenotype and can ultimately help them adapt in response to stress, including drought (Compant *et al.* 2010). Additionally, stressful conditions may select for distinct endophyte taxa with specific functions (Lemanceau *et al.* 2017). Further understanding of how the structure of endophytes shift in response to drought is a potentially important avenue for identifying significant biotic interactions that may play a role in stress response to climate change and perhaps predicting species distribution shifts. The aim of this project is to examine changes in endophyte communities in plants suffering from drought. We ask, does drought alter microbiome composition, and if so, what part of the plant is changing and are there specific taxa that come into play? We sampled both roots and shoots of *E. laciniata* plants grown in native soil in laboratory 1) controlled and 2) drought conditions. Plant tissues were sampled at two time points in the plant life cycle to account for any shifts over time. All tissue was analyzed for bacterial and fungal taxa. Preliminary results indicate strong differences in endophyte between plant compartments (e.g. roots and shoots), suggesting that root communities are more impacted by the effects of drought than shoot communities. The diversity of endophytes was also greater in the root communities than in the shoot, suggesting transmission of endophytes from their native soil.

19. Mark Sistrom, UC Merced msistrom@ucmerced.edu
Probiotics as vectors of antibiotic resistance in the human microbiome
 Mo Kaze, Tricia Van Laar, Emmanuel Flores
 Probiotic use and the number of conditions they are purported to treat are growing at a rapid rate. Many of the species of bacteria used in probiotics have been observed to carry antibiotic resistance (AR) genes and display AR phenotypes. Additionally, many multispecies probiotic products have been observed to contain non-target bacterial species. Our lab has investigated the commercial multi-strain products and found probiotics with AR to multiple classes of antibiotic drugs, including last resort antibiotic drugs, as well as multiple non-target species. AR genes in common probiotic strains of bacteria can horizontally transfer to the bacteria in the gut, leading to an increase in the AR of the patient's microbiome. This has the potential to result in two distinct phenomena with significant health implications: 1) the gut microbiota may become resistant to antibiotics, meaning the inadvertent impact of antibiotics on this community may be beneficially reduced; and 2) opportunistic pathogens that are normal constituents of the healthy gut microbiome may become resistant and thus much more difficult to treat in the instance of an infection.

20. Jamison Sydnor, CSU Chico jsydnor@mail.csuchico.edu
The Bacterial Community Associated with the Model Sea Anemone *Exaiptasia pallida*: Response to Rising Ocean Temperatures

Kelsey Dani, Cawa Tran

The sea anemone *Exaiptasia pallida* (Aiptasia) is a model organism for studying the symbiotic relationship between corals and photosynthetic dinoflagellates belonging to the family Symbiodiniaceae. With climate change driving ocean temperatures to rapidly increase, thermal stress is implicated as the primary culprit disrupting the cnidarian-dinoflagellate symbiosis. As dinoflagellates vacate their host in response to thermal stress, the symbiosis collapses, causing bleaching to occur. In the worst cases, large-scale bleaching events wipe out the framework for entire ecosystems. To address this increasingly dire issue, researchers have adopted a new approach to understanding these processes by shifting focus to the bacteria associated with Aiptasia. We hypothesized that the bacterial community associated with Aiptasia changes in response to thermal stress. Symbiotic and aposymbiotic (lacking algae) anemones were subjected to both control (27°C) and thermal-stress (34°C) temperatures to emulate their natural environment and bleaching threshold respectively. 16S rDNA gene sequencing was then performed to determine community composition and trends in bacterial abundance with respect to symbiotic state and bleaching progression. Distinct bacterial taxa are closely linked to symbiotic state, as well as either the animal itself or its seawater environment. Specifically, predominant genera (*Alteromonas* and *Pelobacter*) show notable changes in heat-stressed symbiotic Aiptasia. This study inspires the development of marine probiotics by allowing us to identify potentially beneficial bacteria that may help the animal host adapt to heat stress in the face of climate change.

21. Lorena Torres-Martínez UC Riverside lorenat@ucr.edu

Climate, but not symbiosis, drive local adaptation of an annual legume

Camille Wendlandt, Jessica Purcell, Joel Sachs

The ability to associate with rhizobia enables legumes to colonize habitats where nitrogen is a limited resource. However, it is still under debate if this association could modulate plant population adaptation to local conditions. Here, we evaluated the hypothesis that local adaptation in legumes is largely driven by landscape features that relate to symbiosis, including the local pool of rhizobial mutualists and soil nitrogen levels. We estimated patterns of genetic differentiation among populations of the native California legume *Acmispon strigosus*. We genotyped a total of 75 individuals from seven different locations across the species range using double-digest RADseq. To estimate signatures of population adaptation to local environmental conditions we tested if patterns of genetic variation across the California range of *A. strigosus* could be associated with local communities of rhizobia, soil nitrogen concentrations, and local climatological features. Based on a total of 3164 genome-wide SNPs we observed high levels of population differentiation and inbreeding within each location. Climate more than levels of nitrogen deposition explained patterns of genetic variation among *A. strigosus* populations. Individual genotypes from wet and cooler northern locations were positively associated to high annual precipitation and seasonality, while populations from desert-like locations were related with lower annual precipitation and seasonality. Additionally, a total of 115 SNPs were found to be under selection and associated with annual precipitation and seasonality. Our results suggest that the symbiotic association of legumes with rhizobia might help maintain similar input nitrogen levels across populations, and thus relaxing this abiotic condition as a selective factor. Instead, precipitation might have a stronger selective pressure that in combination with genetic isolation and inbreeding are driving the local adaptation of *A. strigosus* natural populations.

22. Chris Wall, UH Manoa cbwall@hawaii.edu

Master of polyyps: Symbiodiniaceae functional diversity drives niche partitioning and isotope values in a Hawaiian reef coral (*Montipora capitata*)

Coauthors: M Kaluhiokalani, M Donahue

Reef corals are mixotrophic organisms that meet metabolic demands through symbiont-derived photoautotrophy and the capture of particles/prey from seawater (collectively, heterotrophy). However, some symbiont genotypes (Family: Symbiodiniaceae) display environmentally mediated or genetically fixed opportunistic tendencies to the detriment of host nutrition and growth. In addition, the capacity for corals to exploit heterotrophy under normal and stressed conditions varies among coral species and the composition and integrity of the symbiont community. To better understand symbiont community effects on the biology and nutrition of reef corals, we sampled *Montipora capitata* from a human impacted Hawaiian coral reef ecosystem (Kāneʻohe Bay), where *M. capitata* associates with *Cladocopium* and *Durusdinium* symbionts (hereafter, C- and D-colonies) that partition with depth. We observed significant changes in the biology and $\delta^{13}\text{C}$ isotopic values of *M. capitata* and its symbiont algae over a relatively small depth zone (<1–8m) during two seasons with distinct patterns in host-symbiont interactions (symbiont densities, photopigmentation) and isotopic values dependent on symbiont community. D-colonies had higher symbiont densities, lower photopigments/cell and lower $\delta^{13}\text{C}$ values in host and symbiont tissues, consistent with lower carbon translocation rates and/or greater isotope fractionation. While $\delta^{13}\text{C}$ values declined with depth,

neither holobiont showed indications of greater heterotrophy or nutritional plasticity. These results indicate D-colonies may experience nutritional tradeoffs and hosting *Durusdinium* may be energetically taxing for coral hosts. These findings provide insight into the ecology of the coral-Symbiodiniaceae symbiosis and the abiotic and biotic influences on stable isotope proxies for coral nutrition.

23. Alexandra J. Weisberg, Oregon State University weisbeal@oregonstate.edu

The genomic bases for cheating among wild populations of nodule-associated *Bradyrhizobium*

Jeff H. Chang, and Joel Sachs

Nitrogen-fixing rhizobia can form mutualistic relationships with legumes. In this interaction, rhizobia occupy plant nodules and fix nitrogen for the plant in exchange for carbon. The fitness cost associated with fixing nitrogen is high, and given the large population sizes and short life cycle of the symbiont, can lead to the evolution of “cheaters” and a break down in mutualism. In this scenario, the bacteria can still induce nodules and gain carbon without reciprocating fixed nitrogen. To understand the bases for the cheater phenotype, we cultured and characterized 88 strains of *Bradyrhizobium* isolated from root nodules of *Acemison strigosus* sampled across southern California. Most isolates could induce nodules and fix nitrogen. However a number of isolates failed to elicit nodules. A third set were cheaters that could induce nodules on *A. strigosus* but did not fix nitrogen. Analyses of whole genome sequences revealed that cheaters are closely related to beneficial isolates and are predicted to be capable of fixing nitrogen on the basis of having all conserved nodulation (*nod*) and nitrogen fixation (*nif/fix*) genes. However, multiple cheater lineages vary in their repertoire of secretion system loci, which have been previously shown to influence symbioses. Long-read DNA sequencing was also employed and analyses revealed other large-scale changes, including variation in plasmids that are also implicated in influencing symbiosis.

POSTERS

1. Emily Aguirre University of Southern California emilyagu@usc.edu

Host-specific microbial associates of the endangered coral, *Acropora cervicornis*

Cory Krediet, Carly Kenkel

Microbial associates (bacteria, protists, archaea and viruses) contribute to coral health, resilience and fitness. However, characterizing microbial functional roles remains a challenge due to coral holobiont diversity. Recent microbiome studies across taxa have revealed the influence of host genotype on microbial recruitment and maintenance, yet studies exploring host-specific associates in scleractinian corals is scant. This project aims to identify bacterial biomarkers of health by examining the core and transient microbiota in the mucus of ten, healthy *Acropora cervicornis* genets. We sampled mucus from 30 fragments of each *A. cervicornis* genet (n=300) inhabiting a common garden nursery environment in the Florida Keys, followed by 16SrRNA tag-sequencing to assess microbial variability between fragments of the same genet (alpha-diversity) as well as between genets (beta-diversity). A thorough analysis of the microbial composition among and within *A. cervicornis* genets will inform on the role of host genotype vs environment on microbial communities.

2. Rebekah Bryant, Rice University rlb10@rice.edu

Preliminary evidence that heat stress alters coral photosymbiont health and viral diversity

Coauthors: Carsten Grupstra, Adrienne M.S. Correa

Rising ocean temperatures threaten coral reefs by causing scleractinian corals to lose their dinoflagellate photosymbionts (Family: Symbiodiniaceae) in a process called coral bleaching, which often kills the coral host. While stressors that induce bleaching are relatively well documented, the physiological mechanism(s) underlying the bleaching process remain disputed. Viruses associated with coral colonies potentially cause some bleaching signs by lysing coral photosymbionts. This study tracks the abundance of virus-like particles as well as photosymbiont health using transmission electron microscopy on one of five colonies of the stony coral *Pocillopora verrucosa* exposed to heat stress for five days. The presence of viruses in the family *Alvernaviridae* was confirmed in our coral samples based on major capsid protein gene amplicon sequencing data. Increased photosymbiont degradation signs were observed visibly and through TEM images throughout the experiment, and virus-like particles appeared in photosymbionts in corals regardless of whether or not heat was applied. The findings presented here can help clarify the role of viruses in coral bleaching signs.

3. Brooke Hoffe, California State University, Chico bahoffe@mail.csuchico.edu

Establishment of symbiosis in the sea anemone *Exaiptasia pallida*: Analyzing host specificity of dinoflagellate uptake under heat stress

Coauthors: Kelli Thorup, Cawa Tran

The vast ecosystems of coral reefs depend on the symbiotic relationship between cnidarians (such as corals, sea anemones, jellyfish) and dinoflagellates (algal symbionts). Due to changing environmental conditions, such as rising ocean temperatures, the symbiotic relationship can break down, leading to expulsion of algae. As a result of this breakdown in corals, the host tissue dies, leaving behind the calcium carbonate skeleton, a process referred to as coral bleaching. In this study, we utilized a sea-anemone model, *Exaiptasia pallida* (Aiptasia), to investigate algal colonization of cnidarian tissue. The goal of this study was to better understand the dynamics of algal uptake and proliferation while the host is experiencing heat stress. We hypothesized that heat stress will result in a decrease of initial uptake of algae, coupled with an increased selectivity, resulting in a slower proliferation of algae over time. Our results have shown that heat-stressed anemones take up algae and maintain them through 8 days; however, the symbiosis is not successfully maintained past this point, as the algae do not proliferate within host tissues. After 20 days, heat-stressed anemones do not contain any algal symbionts. Compatibility between the host and algae is even more critical under heat-stressed than normal conditions. By investigating the cellular dynamics of symbiosis establishment under heat stress in a cnidarian model, this study enhances our understanding of how corals may potentially re-establish symbiosis after a bleaching event.

4. Christopher Ivey California State University, Chico ctivey@csuchico.edu
Phenological synchrony, not plant vigor, explains variation in defense against symbiotic galling insects of valley oak (*Quercus lobata*) in a large common garden experiment.
Christopher T. Ivey, Constantin Raether, Jessica W. Wright, and Victoria L. Sork
Because of their ability to convert carbon dioxide into carbohydrates, plants suffer an unyielding siege from diverse natural enemies. An enduring question is thus why variation in damage from herbivores is commonplace. The “Plant Vigor Hypothesis” proposes that robust or vigorously growing individuals are preferred hosts of herbivorous insects and therefore more likely to experience attack. The non-mutually exclusive “Phenological Synchrony Hypothesis” suggests that attack depends on a match between plant and herbivore developmental stages. We tested these hypotheses in a recently established provenance trial of the iconic keystone species of California’s central valley, *Quercus lobata*, involving 672 maternal families collected throughout its range and fully replicated in two field sites. Oaks are hosts to a diverse fauna of symbiotic galling herbivores of the wasp family Cynipidae, which induce tumor-like outgrowths on leaves and stems that house and nourish juvenile wasp life stages. On each of over 6,500 trees the abundance of leaf- and stem-galls was scored as a measure of vulnerability to herbivore attack. In each of two years, tree height was measured at the end of the growing season, from which relative growth rate was calculated as a measure of plant vigor. In addition, leaf emergence was scored weekly throughout the spring growing season as a measure of plant phenological stage. We predicted that a positive relationship between gall abundance and relative growth rate would indicate support for the Plant Vigor Hypothesis. Instead, at both sites, we found negative relationships between abundance of the most common gall species and relative growth rate. In addition, we found a negative relationship between gall species richness and relative growth rate at the site where diversity of galls was highest. These results fail to support the Plant Vigor Hypothesis, and may indicate a negative effect of galling insects on oak growth rates or an inability of plants with high growth rates to defend against galling insects. We predicted that a nonlinear quadratic relationship between leaf phenology and gall abundance or diversity would indicate support for the Phenological Synchrony Hypothesis. We found significant negative quadratic terms for models of the relationship between leaf phenology and gall abundance as well as gall diversity. These results indicate that trees with extreme rapid or slow development are better defended against galling herbivores, which is consistent with the Phenological Synchrony Hypothesis. We will discuss the extent to which gall abundance can be explained by tree maternal genotype as well as the climate and geography of the maternal seed source.

5. Max Miao, University of Wisconsin mjmiao@wisc.edu
Examining Potato (*Solanum Tuberosum*) Domestication to composition and function of its Rhizosphere Microbiome
Coauthor: Richard Lankau
The rhizosphere microbiome and its respective plant host have an intimate relationship. Plants have adapted to rely on their rhizosphere microbiome to address environmental challenges such as abiotic stress, non-innate plant immunity, and nutrient uptake. The potato plant (*Solanum tuberosum*) has undergone natural and more importantly artificial selection since exiting its native Andean range. The changes in host genetics due to plant domestication may have inadvertently changed the functionality and composition of the rhizosphere microbiome as a result. Here,

we hypothesized more ancient landraces of *S. tuberosum* 1) recruit distinct microbiomes compared to modern varieties, and 2) show greater relative benefit in tuber yield from their associated microbiome, especially in nutrient poor conditions. To test our hypothesis, 17 genotypes that represent different points in the evolutionary history of potato domestication were grown in a greenhouse experiment in pots inoculated with microbially rich and microbially depauperate communities, obtained from a relatively undisturbed virgin prairie versus heavy managed potato field respectively, or in non-inoculated pots, fully crossed with high and low nutrient conditions. We collected root tips for eventual amplicon sequencing and measured plant phenotype looking at above and below ground biomass, tuber yield, shoot length and width. We saw that in nutrient poor environments, landraces performed better in terms of tuber yield in prairie microbial inocula while modern varieties performed worse, relative to sterilized soil. However, we observed the opposite pattern in pots inoculated with the agricultural field microbial community. Furthermore, regardless of microbial inoculation source we observed a clear divergence in microbial communities between landraces and those of their modern descendants in low nutrient conditions. Our findings indicate that domestication of potato has resulted in changes in the structure and function of its associated microbiome, with potential consequences for potato production in high versus low input agriculture.

6. Iolanda Ramalho da Silva, UC Merced iramalhodasilva@ucmerced.edu

Arbuscular mycorrhizal fungal communities in the rhizosphere of typical plant species of the Caatinga, a Brazilian dry forest

Coauthors: José Hilton dos Passos, Jailma Alves da Silva, Leonor Costa Maia

Host plant species and environmental filtering are two of the primary drivers of arbuscular mycorrhizal (AM) fungal community composition assembly in ecosystems, but our current knowledge about the drivers of these communities in Brazilian semiarid areas (known as Caatinga) is still incipient. In this study, we examined AM fungal community composition in the rhizosphere of three plant species [*Jatropha mollissima* (Pohl) Baill., *Jatropha mutabilis* (Pohl) Baill and *Mimosa tenuiflora* (Willd.) Poir.] occurring on crystalline and/or sedimentary basins in the Caatinga. Fifty soil samples were collected at the end of the rainy season (January 2018) and AM fungal spores were extracted from 100 g of each soil sample. We identified the AM fungal species by morphology-based taxonomy and evaluated the effects of host plant species, geological environments (crystalline and sedimentary), climate (maximum and minimum temperature and accumulated precipitation) and spatial variables (elevation, latitude and longitude) on these fungal communities. In total, 59 taxa belonging to 19 genera and 13 families were detected. The AM fungal community composition differed significantly between geological environments (crystalline and sedimentary) as well as among plant species (*M. tenuiflora* vs. *J. mutabilis*). Elevation was strongly related with the resulting NDMS site scores. Our preliminary results suggest that the AM fungal community composition is influenced by host plant species (10% of variation explained in AM fungal community) and geological basins (8%). The unexplained variance can be related to variables not yet analyzed (for example, soil attributes) and/or stochastic processes, which have been pointed as drivers of AM fungal community structure in different ecosystems.

7. Ellen L. Simms, UC Berkeley esimms@berkeley.edu

Bacteriophages of native and non-native Bradyrhizobium isolates

Coauthor: Jannick Van Cauwenberghe

Biological invasions are both fascinating and troublesome ecological phenomena. Successful invasions have been blamed on propagule pressure, disturbance, competitive ability, novel weapons, and release from natural enemies. Less attention has been paid to how beneficial partnerships affect biological invasions. Highly invasive legumes provide particularly instructive models. Legumes that depend on mutualistic root infection by soil-dwelling bacteria called rhizobia are less likely to establish in non-native regions compared to rhizobia-independent legumes. In other cases, rhizobia were co-introduced with legume hosts and facilitated their successful invasion. Thus, understanding legume invasion requires investigating rhizobium invasion.

Like most bacteria, rhizobium populations are strongly controlled by viruses called bacteriophages. We hypothesize that successful invasion by rhizobia-dependent legumes depends in part on rhizobium interactions with bacteriophages. We consider three relevant ecological theories, the enemy-release hypothesis, the parasite spillover hypothesis, and the parasite spillback hypothesis. To evaluate how bacteriophages might influence rhizobium-legume co-invasion, we are isolating bacteriophages associated with rhizobia found in California on the European invader, *Genista monspessulana*, and the native legume, *Lupinus arboreus*. Our initial goal is to compare the host ranges of these bacteriophages on a panel of native and non-native Bradyrhizobium genotypes found on these host plants.

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