

2<sup>ND</sup> ANNUAL SYMBIOSIS WORKSHOP --- MAY 19-20<sup>TH</sup>, 2012



**SYMBIOSIS *WORKSHOP* 2012**

***PRELIMINARY SYMPOSIUM SCHEDULE***

**SIERRA NEVADA RESEARCH INSTITUTE**

**[HTTP://WWW.SACHSLAB.COM/SYMBIOSIS-WORKSHOP-2012.PHP](http://www.sachslab.com/symbiosis-workshop-2012.php)**

**ORGANIZED BY JOEL L. SACHS & MONICA MEDINA**

## SCHEDULE OF INVITED TALKS

### MAY 19, 2012

#### Session 1. Symbiont Communities: Diversity, specificity, and function

- 12:50-1pm Introduction and welcome to the meeting (Joel Sachs)
- 1-1:20 Angus Chandler Yeast Communities of Diverse *Drosophila* Species: Comparison of Two Symbiont Groups in the Same Hosts
- 1:20-1:40 Sharon Lafferty Doty Nitrogen-Fixing Endophytes of Poplar and Willow: Implications for Bioenergy and Agriculture
- 1:40-2:00 Nicholas Fabina Exploring coral-symbiodinium interactions with network analyses
- 2:00 – 2:20 Carolin Frank Bacterial Endophytes of Forest Conifers: Specificity and Adaptive Potential of an Unexplored Symbiosis
- 2:20-2:40 Sunshine Van Bael Interacting symbioses: leaf endophyte load and fungal garden development in leaf-cutting ants
- 2:40 – 3:00 Jesse Zaneveld Combined phylogenetic and genomic methods for studying the evolution of host-associated microbes

3:00-3:20 Break for coffee and snacks

#### Session 2. Symbiont-host conflict and evolutionary stability

- 3:20 - 3:40 Camille Paxton Cnidarian hosts can induce apoptosis independent of dinoflagellate stress
- 3:40 - 4:00 Stephanie Porter Selection in symbiosis
- 4:00 - 4:20 Allen Herre Stability and instability in Fig-Wasp mutualisms
- 4:20- 4:40 Jeff Kimbrel Conservation of type III effector genes of mutualistic rhizobia
- 4:40- 5:00 Joel Sachs Evolutionary origins and stability of proteobacterial mutualisms
  
- 5:10-5:40 Jim Lake KEYNOTE LECTURE Lake Using Genomes to Track the Evolution of Life on Earth and Beyond.
  
- 6:00-8:00 Dinner and poster session

### MAY 20, 2012

#### Session 3. Symbiosis: immunity and disturbance as mediation the host niche

- 9:00-9:20 Michelle Afkhami Mutualist-mediated niche expansion and differentiation in a wild grass-fungal endophyte symbiosis at a rangewide scale
- 9:20-9:40 Amanda Brown Population genomics of a nutritional symbiont affecting the pest status of an invasive bug: *Ishikawaella* in *Megacopta cribraria*
- 9:40 – 10:00 Allison Gregg Visualization of coral-associated bacterial respiration using biological oxygen demand optode arrays
- 10:00- 10:20 Melissa Roth Protecting the engine of coral reefs: Understanding how endosymbiotic algae cope with a fluctuating environment
- 10:20-10:40 Rebecca Vega-Thurber Viral disruption of coral-algae symbioses
- 10:40- 11:00 Virginia Weis Role of host immunity in the regulation of cnidarian-dinoflagellate mutualisms
  
- 11:15- 11:45 Doug Cook CLOSING LECTURE Elucidating the symbiotic signaling pathway in legumes

SEMINAR ABSTRACTS --- ALPHABETICAL ORDER

**Afkhami, Michelle E.**

Mutualist-mediated niche expansion and differentiation in a wild grass-fungal endophyte symbiosis at a rangewide scale

Afkhami, Michelle E. & Sharon Y. Strauss

University of California, Davis

The study of organisms' niches has been central to our understanding of ecology and evolution, driving major advances in our knowledge of species coexistence, community assembly, and speciation. However, research has focused on niche reductions caused by negative species interactions, while the possible effects of positive interactions (e.g. mutualism and facilitation) have received far less attention. In contrast to competition/predation, positive interactions can expand the realized niche of a species, possibly beyond the fundamental niche, by conferring benefits that ameliorate (a)biotic stresses. Partner-generated niche shifts could also lead to niche differentiation within a species, if individuals that associate with partners have different niches from those that do not. We take an integrative approach to examining how a fungal endophyte (*Neotyphodium* sp.) affects the niche of its California-native grass host, *Bromus laevipes*. First, we use large-scale quantitative field surveys of ~100 populations coupled with ecological niche modeling (Maxent) to create two niche models – one for symbiotic *B. laevipes* and one for non-symbiotic *B. laevipes*. By comparing these models (via niche breadth and overlap statistics) across geographic and climatic niche axes, we document significant mutualist-associated niche expansion and differentiation across the species range. Importantly, niche differentiation between symbiotic and symbiont-free plants was not only significant, but also comparable to differentiation among other species of California-native *Bromus*, providing the unexpected result that associating with mutualistic symbiont may be as important as species identity in determining the niche.

To complement this modeling approach, we designed an experiment using common gardens in northern and central California (representing >1/3 of the host's range). Endophyte levels in *B. laevipes* plants from 11 populations were experimentally manipulated (via fungicide) and then planted into common gardens at five sites (2 sites with naturally 100% symbiotic plants and 3 with naturally 0% symbiotic plants). Over the last three years, we collected data on individual plant fitness, natural enemy damage, and environmental variables to determine the impact of endophytes on *B. laevipes* performance and niche. Across all five gardens, plants with high-levels of endophyte experienced higher fitness than plants with low-levels or no endophyte, even at sites where endophyte was absent from the natural population. The fitness increase was large – ~40% more stems and leaves, ~80% greater flowering, and ~25% lower mortality – consistent with endophyte-mediated expansion. Mutualist-conferred protection against natural enemies may be underlying this increased fitness, as plants with high endophyte levels receive less damage from insects and fungal pathogens. We continue monitoring these gardens to collect the demographic data needed for evaluating lifetime fitness and population persistence. We are also conducting experiments on the impact of symbiont-conferred enemy resistance and drought tolerance to the niche.

**Brown, Amanda M. V.**

Population genomics of a nutritional symbiont affecting the pest status of an invasive bug: *Ishikawaella* in *Megacopta cribraria*

University of Montana

The gamma-proteobacterium, *Candidatus Ishikawaella capsulata*, is an obligate nutritional symbiont living in special gut crypts of the stinkbug *Megacopta cribraria* (Hemiptera: Plataspidae). These bugs were endemic to Asia and only first appeared in the U.S. in 2009, in Georgia, and have spread throughout the southeast, feeding on their native wild legume, kudzu. Since 2010, they have become a soybean pest. In Japan, where there are pest- and non-pest *Megacopta* species, experiments show it is the symbiont, *Ishikawaella*, that determines the bug's pest status. Furthermore, the U.S. bug is more closely related to the non-pest in Asia. To determine how this bug has become a soybean pest in the U.S., we did Illumina sequencing on whole *Ishikawaella* genomes, examining SNPs and polymorphic sites between bugs caught at "ground zero", in the first days of the invasion, to those across the present range, considering potential roles in amino acid, vitamin and cofactor pathways that could be associated with the bug's pest status. Results show very few SNPs, and sufficient divergence of the "ground zero" symbiont from the non-pest in Asia to support a genetic change before the bug's arrival, followed by a "sweep" of the successful pest genotype in the U.S.

**Chandler, J. Angus**

Yeast Communities of Diverse Drosophila Species: Comparison of Two Symbiont Groups in the Same Hosts

Chandler, J. Angus, Jonathan A. Eisen, and Artyom Kopp

University of California, Davis

The combination of ecological diversity with genetic and experimental tractability makes *Drosophila* a powerful model for the study of animal-associated microbial communities. Despite the known importance of yeasts in *Drosophila* physiology, behavior, and fitness, most recent work has focused on *Drosophila*-bacterial interactions. In order to get a more complete understanding of the *Drosophila* microbiome, we characterized the yeast communities associated with different *Drosophila* species collected around the world. We focused on the phylum Ascomycota because it constitutes the vast majority of the *Drosophila*-associated yeasts. Our sampling strategy allowed us to compare the distribution and structure of the yeast and bacterial communities in the same host populations. We show that yeast communities are dominated by a small number of abundant taxa, that the same yeast lineages are associated with different host species and populations, and that host diet has a greater effect than host species on the yeast community composition. These patterns closely parallel those observed in the *Drosophila* bacterial communities. However, we do not detect a significant correlation between the yeast and bacterial communities of the same host populations. Comparative analysis of different symbiont groups provides a more comprehensive picture of host-microbe interactions. Future work on the role of symbiont communities in animal physiology, ecological adaptation, and evolution would benefit from a similarly holistic approach.

**Cook, Doug CLOSING LECTURE**

Elucidating the symbiotic signaling pathway in legumes

Brendan K. Riely<sup>1</sup>, Estibaliz Larrainzar<sup>1</sup>, Jeong-Hwan Mun<sup>2</sup>, Birinchi Sarma<sup>3</sup>, Douglas R. Cook\*<sup>1</sup>

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Legumes and rhizobia collaborate in conversion of atmospheric di-nitrogen to ammonia. On a global scale, this interaction represents a key entry point for reduced nitrogen into the biosphere, and as a consequence this symbiosis is important in both natural and agricultural systems. Symbiotic development by chito-oligosaccharide signals ("Nod factors") from the bacterium, which are perceived by the legume root and trigger development of the symbiotic nodule organ. Understanding the molecular and cellular processes that underlie Nod factor perception is one focus of research in the Cook laboratory.

To identify genes and proteins that link Nod factor perception to cellular and physiological responses we are taking two parallel approaches. In the first approach, we assume that Nod factor-induced redirection of root hair growth is achieved by perturbation of protein systems involved in normal root hair polar growth. These proteins and their respective genes become targets for reverse genetic analyses. In the second approach, we have taken a discovery-based strategy based on (1) tandem affinity purification (TAP-tagging) of symbiotic receptor proteins and their associated protein partners, and (2) large-scale transcriptional profiling. All three approaches are yielding new insights into symbiotic development and the current status of these studies will be described.

**Doty, Sharon Lafferty**

Nitrogen-Fixing Endophytes of Poplar and Willow: Implications for Bioenergy and Agriculture

SHARON LAFFERTY DOTY, Zareen Khan, Jenny Knoth, Soo-Hyung Kim, and Gregory Ettl

School of Environmental and Forest Sciences, College of the Environment, University of Washington, Seattle, USA

The interior of plants provides habitat for a wide range of bacteria and fungi, termed endophytes, that benefit the plant host in multiple ways including phytohormone production, increasing nutrient acquisition, stress tolerance, and pathogen resistance. Nitrogen fixed biologically by plant-symbiotic bacteria is ecologically friendly and has been effectively exploited for important leguminous crop species, but associations of other N-fixing (diazotrophic) bacteria with non-legume crops have been less studied. A variety of microorganisms able to grow under nitrogen-limitation were isolated from the stems of native poplar (*Populus trichocarpa*) and willow (*Salix sitchensis*). Inoculation of these poplar and willow endophytes into commercially important plants including turf grasses, rice, corn, peppers, tomatoes, and poplar trees significantly affected plant growth in the absence of fertilizer. With more study of the multiple benefits of diazotrophic endophytes on plants, we can better understand the role of endophytes in natural systems as well as utilize that information for a new revolution in agriculture that is better for the environment.

**Fabina, Nicholas**

Exploring coral-symbiodinium interactions with network analyses

Most reef-building corals in the order *Scleractinia* depend on endosymbiotic algae in the genus *Symbiodinium* for energy and survival. Significant levels of taxonomic diversity in both partners result in numerous coral-*Symbiodinium* associations with unique functional characteristics. We created and analyzed the first coral-*Symbiodinium* networks utilizing a global dataset of interaction records from corals and *Symbiodinium*. Our results reveal that the majority of coral species and *Symbiodinium* types are specialists and the specificity of a coral's symbionts is predicted by transmission mode. Globally, *Symbiodinium* types are partitioned between vertically and horizontally transmitting corals, with only a few generalist types found with both. Our results demonstrate that specificity and transmission mode are major drivers of interaction patterns, and affect the resilience of species and reefs.

**Frank, Carolin**

Bacterial Endophytes of Forest Conifers: Specificity and Adaptive Potential of an Unexplored Symbiosis

University of California, Merced

The relationship between forest trees and symbiotic bacteria called endophytes dwelling throughout their tissues is likely to be one of the world's most wide-spread symbioses, yet it is largely unexplored. Research on agricultural crops has shown that some bacterial endophytes beneficially affect host development and growth, and provide stress protection. Bacterial endophytes of forest trees are also likely to play important roles in host biology, but to date, the ecological significance of this symbiosis is unknown. The aim of this study was to identify long-term and context-dependent associations between subalpine pine trees and endophytes. We wanted to know if specific symbionts with potentially important roles in host biology are shared across individual trees, or alternatively, if there is a high turnover of random 'visitors' with little importance in host biology. Using 16S pyrosequencing to profile the endophytic community in needles of adult limber pine (*Pinus flexilis*), we compared the bacterial community within and across individual trees, and across geographic locations. We found that there is high consistency in the bacterial needle community across samples. All trees are dominated by bacteria belonging to the genus *Gluconacetobacter*, pointing to a adaptive and specific relationship between *P. flexilis* and these bacteria. *Gluconacetobacter* and related genera are capable of N<sub>2</sub>-fixation in the rhizosphere (the area surrounding plant roots) and as endophytes of crops such as sugarcane and coffee. Subalpine forest ecosystems have naturally low N availability due to slow turnover of organic nitrogen. To our knowledge, the possibility of endophytic N<sub>2</sub> fixation in this ecosystem has not been explored. A capacity to fix N<sub>2</sub> would explain the high relative abundance of *Gluconacetobacter* sp. in all limber pine samples.

**Gregg, Allison**

Visualization of coral-associated bacterial respiration using biological oxygen demand optode arrays

A.K. Gregg<sup>1</sup>, M. Hatay<sup>2</sup>, K. Barott<sup>1</sup>, A. F. Haas<sup>3</sup>, D. Coffee<sup>3</sup>, M. J. A. Vermeij<sup>4,5</sup>, K. Marhaver<sup>4,6</sup>, A. Hewitt<sup>7</sup>, and F. Rohwer<sup>1</sup>

San Diego State University

Coral health is reduced when in close proximity to many types of algae, and algal-derived dissolved organic matter can cause microbially-mediated mortality of reef building corals. The proposed killing mechanism is hypoxia caused by rapidly growing microbes. Hypoxia has been observed where corals are in contact with turf algae; however, this is not observed when coral is in contact with crustose coralline algae (CCA). The tested hypothesis was bacterial communities associated with the coral species *Montastraea annularis* consume more oxygen when exposed to organic matter released by turf algae than that of CCA. This study employed biological oxygen demand (BOD) optodes embedded with a microbial community cultured from coral mucus to visualize bacterial respiration when exposed to exudates generated by turf algae and CCA. These data indicate that exudates from turf algae stimulated the highest oxygen draw down by coral bacterial communities compared to CCA exudate and seawater. When introduced to turf algal exudates, bacterial communities isolated from coral, turf algae, and CCA responded similarly in terms of oxygen consumption. These results demonstrate that exudates from turf algae may contribute to hypoxia-induced coral stress due to increased microbial respiration, regardless of whether the bacteria are associated with coral, turf algae, or CCA.

**Herre, Allen H.**

Stability and instability in Fig-Wasp mutualisms **ABSTRACT TBA**  
Smithsonian Tropical Research Institute

**Kimbrel, Jeff**

Conservation of type III effector genes of mutualistic rhizobia **ABSTRACT TBA**  
Oregon State University

**Lake, James KEYNOTE LECTURE**

**Using Genomes to Track the Evolution of Life on Earth and Beyond.**

MCD Biology and Human Genetics, UCLA

Today Evolutionary Genomics is in a state of crisis because we mistakenly assumed that once complete genome became available – the complete tree of life on Earth could be easily reconstructed in considerable detail. Instead, all of us in the field agree that we cannot easily determine a single tree. Different genes have different histories. However, everyone seems to have different reasons for why they think that this happens. Here, I'll make the case that Darwinian tree like evolution, and the "survival of the fittest" metaphor give an incomplete view of evolution and that we need to focus more upon **both** tree like evolution and cooperation between organisms (endosymbioses and other types of gene sharing).

Trees are easy to calculate from genomic data, but we must combine "survival of the fittest" and "cooperation", if we are to reconstruct the evolution of life on Earth. Methods to do this are vastly more complex and are just being developed. Here I'll describe the remarkable findings that are now being obtained using new methods.

**Paxton, Camille**

Cnidarian hosts can induce apoptosis independent of dinoflagellate stress  
Oregon State University

Coral bleaching occurs when there is a breakdown in symbiosis between cnidarian hosts and resident Symbiodinium. Multiple mechanisms for the bleaching process have been identified including apoptosis and autophagy and most focus has centered on Symbiodinium as the initiator of the bleaching cascade. In this work we show that it is possible for host cells to initiate apoptosis leading to death of the Symbiodinium. First we used colchicine, a known elicitor of apoptosis in other animals, to show that it causes cell death in host cells but not in Symbiodinium cell in culture. In contrast, when symbiotic *A. pallida* were incubated in colchicine cell death in resident Symbiodinium was observed. Via live cell confocal imaging of macerated symbiotic cell isolates we identified a pattern of the initiation of host cell death followed by death of resident Symbiodinium. This same pattern was observed in symbiotic host cells that were subject to a temperature stress: initiation of host cell death followed by resident Symbiodinium death. This research indicates destruction of symbionts during temperature-induced bleaching can be initiated by host apoptosis.

**Porter, Stephanie, S.**

Selection in symbiosis  
University of California, Davis  
Porter, Stephanie S. & Kevin J. Rice

Mutualistic plant-microbe symbiosis can provide critical fitness benefits for both partners. However, host and symbiont combinations may experience conflict over outcomes that favor reproduction of one partner at the expense of the other. The microbial mutualists that colonize plants can affect the expression of plant traits. This may generate conflict between microbes and the host over plant trait values. We investigate this conflict in the legume-rhizobium symbiosis and ask whether environmental context affects the intensity of conflict. Using a greenhouse experiment, we raised experimentally cross-inoculated legume-rhizobium combinations in both harsh serpentine soil and more benign non-serpentine soil. We demonstrate that both plant and rhizobium genotype affects traits such as reproductive output, symbiotic investment, phenology, and structural investment. Selection analysis was used to analyze the trait values and reproductive outputs of both partners. Phenotypic selection differentials and genotypic selection gradients suggest that legumes and rhizobia can be under selection for conflicting trait optima. In addition, the quality of the growth environment can affect the intensity of this conflict. These results highlight the role biotic interactions may play in constraining environmental adaptation.

**Roth, Melissa S.**

Protecting the engine of coral reefs: Understanding how endosymbiotic algae cope with a fluctuating environment

Melissa S. Roth<sup>1,2</sup>, Dimitri D. Deheyn<sup>3</sup>, and Krishna K. Niyogi<sup>1,2,4</sup>

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The survival and success of coral reef ecosystems depend on the symbiosis between corals and dinoflagellates. Photosynthetic products produced by the dinoflagellates provide corals with most of their energy. Like all photosynthetic organisms, the dinoflagellates rely on a delicate balance of sunlight absorbed and processed through photochemistry. Therefore, environmental stressors such as changes in temperature and light can easily disrupt this equilibrium. We found that cold causes acute stress in the reef-building coral *Acropora yongei*, but heat is ultimately more deleterious. These trends were identical to what was observed in their algal symbionts. We also found that both the coral host and their endosymbionts employ photoacclimation strategies to adjust to changes in light intensity. Currently, our research is focused on the photoprotective mechanisms in different clades of endosymbiotic dinoflagellates. We are generating mutant algae that are deficient in non-photochemical quenching and plan to infect cnidarian hosts with these mutants. Elucidating photoprotection in dinoflagellates may be a key component to understanding the susceptibility of the coral-algal symbiosis to environmental disturbances.

**Sachs, Joel L.**

Evolutionary origins and stability of proteobacterial mutualisms

Sachs, J. L., Skophammer, R.G., Bansal, N., and Stajich, J.E. University of California, Riverside, CA 92521

Mutualist bacteria infect most eukaryotic species in nearly every biome. Nonetheless, the evolution of these bacterial mutualisms is poorly understood. Two key dilemmas remain unresolved: how do mutualist phenotypes first arise in bacterial lineages and to what degree are these traits resistant to mutants that parasitize hosts or abandon host-association entirely? Here, we reconstruct a Bayesian phylogeny of the phylum proteobacteria and map host-association phenotypes onto the tree. Using ancestral state reconstruction we investigate the origins and evolutionary stability of mutualistic bacterial phenotypes in deep evolutionary time. We inferred a minimum of 37 independent origins of mutualist phenotypes in proteobacteria, revealing the relative ease in which bacteria can evolve traits that enhance fitness of eukaryote hosts. We found proteobacterial mutualists to be more frequently nested in parasitic than in free living lineages, consistent with the common but untested hypothesis that bacterial mutualists often evolve from pathogens. Strikingly, our ancestral state reconstructions revealed that mutualistic phenotypes in proteobacteria rarely reverse to parasitism or free-living status. This result is contrary to the longstanding paradigm, which predicts that faster-evolving microbes evolve to exploit and or abandon their eukaryotic hosts. One possible explanation for our data is that bacterial-eukaryote mutualisms only emerge as stable interactions when hosts exhibit traits to limit symbiont exploitation. Another model posits that genomic constraints can hinder evolutionary transitions between mutualist and parasite phenotypes. Our dataset provides a key set of well-resolved evolutionary transitions to begin to test these and other alternate hypotheses in a comparative phylogenomic framework.

**Vega-Thurber, Rebecca L.**

Viral disruption of coral-algae symbioses

Rebecca L. Vega Thurber<sup>1,2\*</sup>, Adrienne M.S. Correa<sup>1,2</sup>, and Rory M. Welsh<sup>1,2</sup>

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Scleractinian corals and their dinoflagellate algal endosymbionts (*Symbiodinium* spp.) are ecosystem engineers of coral reefs; therefore disruption to this symbiosis may result in negative impacts to reef health and resilience. Coral bleaching is the loss of *Symbiodinium* and/or chlorophyll from coral tissues, and results in the pale or white appearance of colonies. Bleaching most commonly results from the accumulation of oxidative stress within symbiont chloroplasts following damage to Photosystem II, which can trigger the expulsion of algae from coral tissues via unresolved mechanisms. Although environmental stressors and microbial-mediated disease are documented to disrupt this important symbiosis, viral infection also has been hypothesized to trigger coral-*Symbiodinium* dissociation, but few studies have been conducted on coral viruses and their effects on coral symbiosis and health. Here, we present the first evidence of active viral infections of *Symbiodinium* within coral colonies and in culture. We identified and annotated +ssRNA and dsDNA virus-like transcripts in cDNA viromes of the coral, *Montastraea cavernosa*, and in EST libraries generated from *Symbiodinium* cultures. In the *M. cavernosa* viromes, sequence similarities to the major capsid protein of the dinoflagellate-infecting +ssRNA virus, *Heterocapsa circularisquama* RNA virus (HcRNAV), were observed. Alignments to known HcRNAV mcp amino acid sequences suggested that a highly novel dinornavirus infects the symbiotic dinoflagellates in corals. Therefore we have designated this putative virus as 'Symbiodinium RNA virus' (SRNAV). Further, similarities to dsDNA viruses (e.g., Phycodnaviridae) dominated (~69%) eukaryotic viral similarities in the *M. cavernosa* viromes, and homologies to these same sequences were found in two independently generated *Symbiodinium* EST libraries. Phylogenetic reconstructions substantiate that these transcripts are undescribed members of the nucleocytoplasmic large DNA virus (NCLDVs) group. Combined our evidence indicates that the novel NCLDVs and SRNAV identified here infect the endosymbionts of corals, and not coral tissues themselves. Furthermore, empirical studies are confirming that these viruses disrupt coral-algae symbioses by reducing the abundance of functional *Symbiodinium* cells in the holobiont.

**Van Bael, Sunshine**

Interacting symbioses: leaf endophyte load and fungal garden development in leaf-cutting ants

Plants and insects host a wide diversity of symbiotic fungi, with some symbionts being essential to host survival. Previous studies have focused largely on the reciprocal costs and benefits within a particular host-symbiont pair, but have rarely investigated the multiple interactions among pairs of symbionts and their hosts. Because most organisms participate in symbioses, such symbiont-symbiont interactions must occur often but in a cryptic fashion. Our research focuses on the fungal-fungal interactions among two symbiotic pairs: (i) leaf-cutting ants and their symbiotic fungal gardens, and (ii) tropical plants and their foliar endophytes, the cryptic symbiotic fungi within their leaf tissue. The former involves farming ants and the fungus they cultivate as a food crop. The latter is a widespread association; in some cases endophytes are known to provide benefits by chemically defending leaves against herbivores. Previous work has shown that leaf-cutting ants prefer to cut leaf material that is relatively low in fungal endophyte content. Such a preference suggests that fungal endophytes exact a cost on the ants or on the development of their colonies. It also suggests that endophytes may play a factor in their host plants' defense against leaf-cutting ants. The endophyte-leaf-cutter ant interaction may parallel constitutive defenses in plants, whereby endophytes reduce the rate of colony development when its risk of mortality is greatest.



**Weis, Virginia**

Role of host immunity in the regulation of cnidarian-dinoflagellate mutualisms

Oregon State University

Cnidarians such as reef-building corals engage in a mutualistic symbiosis with intracellular photosynthetic dinoflagellates. This intimate partnership forms the trophic and structural foundation of coral reef ecosystems. This presentation will examine the cellular and molecular mechanisms underlying the establishment, maintenance and breakdown of the symbiosis in coral- and anemone-dinoflagellate partnerships. There is increasing evidence from both genomics and functional studies that host innate immunity and symbiont strategies for modulating this immune response are central to the stability of the symbiosis. During onset of symbiosis these mechanisms include, lectin-glycan signaling, host innate immunity, host cell apoptosis and changes in host membrane trafficking. Coral bleaching, a severe threat to the health of reefs worldwide, results from the dysfunction and collapse of the symbiosis. Several studies suggest that coral bleaching is a host innate immune response to a symbiont compromised by severe oxidative stress. This evidence includes increased nitric oxide levels, and host cell apoptosis and autophagy in heat-stressed animals, all well-known immune mechanisms in other systems to eliminate detrimental microbial invaders.

**Zaneveld, Jesse**

Combined phylogenetic and genomic methods for studying the evolution of host-associated microbes

Oregon State University

Symbiotic associations between microbes and their multi-cellular hosts play important roles in medicine, agriculture, and ecology. We are investigating the complex microbial community associated with corals, which includes both photosynthetic algal Symbiodinium symbionts, and a variety of bacteria, archaea, fungi, viruses and phage. We hypothesize that this coral microbiota plays an important role in mediating the effects of human impacts such as agricultural runoff and overfishing on coral health. To test this hypothesis, we are currently analyzing a large (>1300 sample) library of coral mucous DNA samples collected during a multi-year in situ experimental intervention. The top-down ecological effects of herbivore removal (e.g. from overfishing) were tested by enclosing coral subplots with cages, while the bottom-up effects of inorganic nitrogen and phosphorous addition (e.g. from agricultural runoff) are tested by addition of a nail carrying a fertilizer diffuser. The results thus far suggest species-specific differences in the composition of the coral microbiota and its response to environmental perturbation. We are interested in combining these surveys of the coral microbiota with available genomic evidence in order to better understand the genomic changes that allow microorganisms to initiate, switch, or end association with particular hosts. Previous work using combined phylogenetic and genomic evidence identified a distinct evolutionary signature of host-adaptation in the gene content of bacteria adapted to the human gut. Based on these findings, I will discuss a novel phylogenetic approach that aims to reconstruct the sets of genomic changes that accompany microbial adaptation to life in association with corals or other hosts.

--- POSTER PRESENTERS ---

**Asgharian, Hosseinali**

Transcriptomic study of Wolbachia-induced male feminization in the leafhopper *Zyginidia pullula*  
University of Southern California

**Buschiazzo, Emmanuel**

Evolutionary and Community Genetics in the Reef: Shaping the Coral Holobiont  
University of California, Merced

**Datta, Jhuma**

Towards the elucidation of protein interaction networks regulating early host responses to Rhizobium  
University of California, Davis

**Diaz, Erika**

*Cassiopeia xamachana* as a model to study symbiosis  
University of California, Merced

**Greenspan, Alex**

Rhizobial strain selectivity in wild and cultivated chickpea  
University of California, Davis

**Klueter, Anke**

Metabolic profiles of Symbiodinium spp. in variable light and temperature regimes: A perspective for invertebrate-algal symbiosis  
SUNY Buffalo

**Petitfils, Michelle**

CFTR-like gene found in Hydra, a freshwater Cnidarian  
San Diego State University

**Poole, Angela**

The role of complement in cnidarian-dinoflagellate symbiosis  
Oregon State University

**Rachmawati, Rita**

Differential responses of Indonesian Corals to Bleaching Events  
University of California, Los Angeles

**Simms, Ellen**

Local spatial structure of Bradyrhizobium populations  
University of California, Berkeley

**Welch, Rebecca**

Dispersal regimes and infection competence in Symbiotic and freeliving Nostoclean Cyanobacteria  
University of California, Berkeley

**Wilson, Emily**

Bacterial endophytes of conifer buds  
University of California, Merced