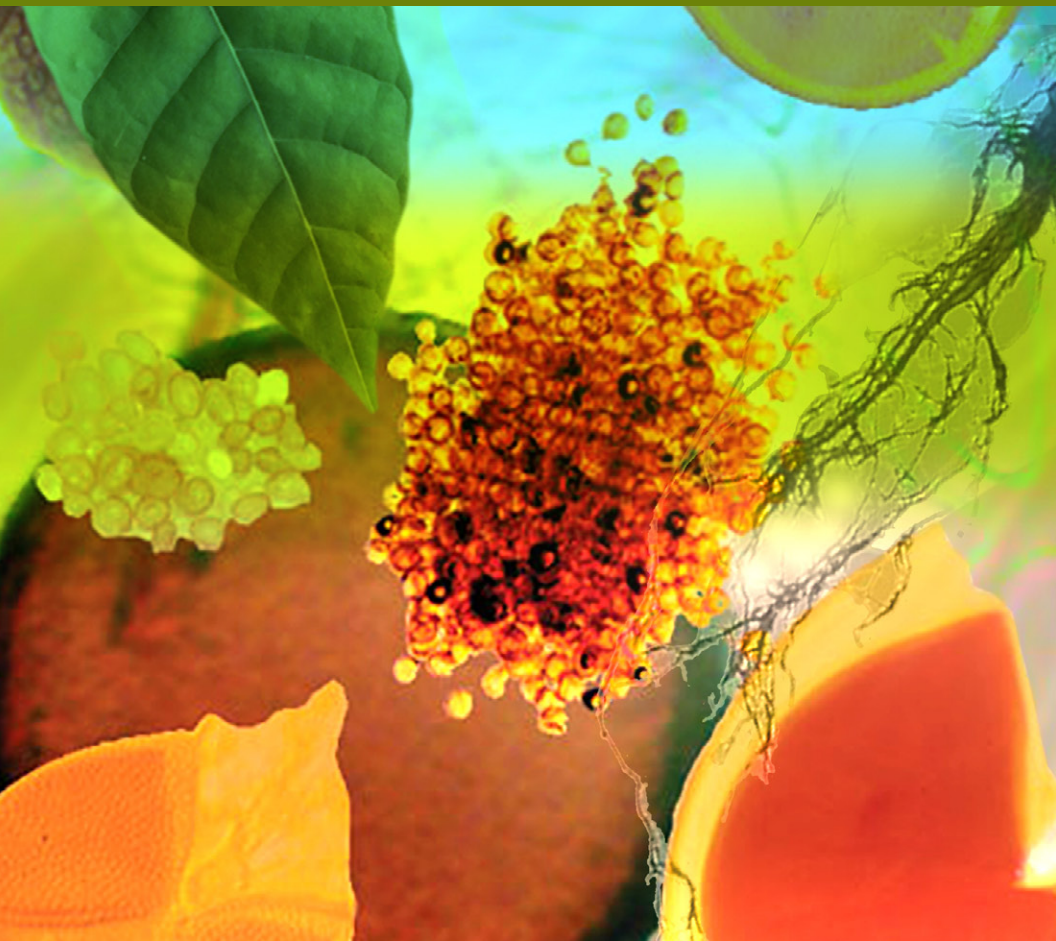




Smithsonian
Tropical Research Institute

FRONTIERS IN TROPICAL MARINE AND TERRESTRIAL MICROBIAL ECOLOGY

VIRTUAL SYMPOSIUM | MARCH 24-25, 2021



GORDON AND BETTY
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Quercus costaricensis Baru. Photo courtesy of James Dalling

SUMMARY

This symposium aims to summarize our current understanding of four interconnected themes that run through on-going work in tropical marine and terrestrial host-microbial interactions and their evolution. Despite addressing many related general questions, too often researchers who study microbial evolutionary ecology in either terrestrial or marine environments are only vaguely aware of each other's paradigms, results, and ongoing studies.

Given the increasingly clear, interconnected threats to biological diversity, ecosystem functions, and human health, it is essential that we understand the roles that fungi, bacteria, archaea and viruses play in them. There can be no question that both descriptive and functional knowledge are critical for any success in applied efforts aimed at natural habitat restoration or overall sustainability.

Twenty-seven researchers whose investigations have focused on either "surf" or "turf" organisms will outline what they consider to be important current knowledge in their fields, the outstanding questions, and key next steps for both basic and applied research. Throughout this symposium, the speakers will emphasize the profound effects that microbiomes exert on species and functional diversity across all levels of biological organization in both terrestrial and marine ecosystems.

The Smithsonian Tropical Research Institute is grateful to the Simons Foundation and the Gordon and Betty Moore Foundation for their support of microbial research in Panama.



FRONTIERS IN TROPICAL MARINE AND TERRESTRIAL MICROBIAL ECOLOGY AGENDA

VIRTUAL
SYMPOSIUM
MARCH
24-25
2021

 [Zoom link HERE](#) | Meeting ID: 821 4930 9456 | Passcode: 651987

WEDNESDAY MARCH 24

9:00am* **Welcome remarks**
ORIS SANJUR, ACTING DIRECTOR
SMITHSONIAN TROPICAL RESEARCH INSTITUTE


9:05am **Symposium introduction**
ALLEN HERRE
SMITHSONIAN TROPICAL RESEARCH INSTITUTE

9:10am **PLENARY TALK** | 30 minutes
Seeing the forest for the microbes: how important are plant-microbe interactions to the maintenance of forest biodiversity?
▶ JOSEPH LAMANNA, MARQUETTE UNIVERSITY

 9:40am **Q&A** | 10 minutes

 9:50am **BREAK** | 10 minutes

 **MORNING SESSION MODERATOR:**
ALLEN HERRE, SMITHSONIAN TROPICAL RESEARCH INSTITUTE

 10:00am **SESSION 1 | The Evolutionary Ecology of Host Immune Systems: the Interface/Playground for Hosts and their Microbiomes**
Prerecorded lightning talks | 6 minutes each

Ecological and evolutionary interactions with enemies shapes diversity and divergence of defenses in a genus of rainforest trees
▶ PHYLLIS D. COLEY, UNIVERSITY OF UTAH

Plant immune pathways and the genetics affecting disease resistance and microbiome assembly
▶ LUIS MEJÍA, CENTER FOR BIODIVERSITY AND DRUG DISCOVERY, INDICASAT-AIP, PANAMA

Investigating interactions between the Pocillopora coral innate immune system and coral-associated bacteria communities
▶ MICHAEL CONNELLY, UNIVERSITY OF MIAMI

WEDNESDAY MARCH 24

1 MORNING SESSION 1 CONTINUED

When and why do insects need microbiomes for immune function?

▶ TOBIN J. HAMMER, UNIVERSITY OF TEXAS AT AUSTIN

Tiers of defense of multicellular host taxa

▶ ANDREA L. GRAHAM, PRINCETON UNIVERSITY

The sponge holobiont from the host perspective

▶ LUCIA PITA, GEOMAR HELMHOLTZ CENTER FOR OCEAN RESEARCH KIEL

//// 10:50am **BREAK** | 10 minutes

 11:00am – 12:30pm **Live Discussion SESSION 1**
speakers and questions from audience

.....
12:30pm – 2:00pm **BREAK**
.....

AFTERNOON SESSION MODERATOR:

KRISTIN SALTONSTALL, SMITHSONIAN TROPICAL RESEARCH INSTITUTE

2 2:00pm **SESSION 2 | Spatial and Temporal Scale in the Function and Physiology of Host-Microbial Interactions**

Prerecorded lightning talks | 6 minutes each

400 million years of symbiosis: Marine lucinid clams and the symbionts that feed them

▶ BENEDICT YUEN, UNIVERSITY OF VIENNA

Exploring the microenvironmental landscape of aquatic symbioses

▶ MICHAEL KÜHL, UNIVERSITY OF COPENHAGEN

3D bioprinted coral host microenvironments

▶ DANIEL WANGPRASEURT, UNIVERSITY OF CALIFORNIA SAN DIEGO AND SCRIPPS INSTITUTION OF OCEANOGRAPHY

Multi-host pathogens and the maintenance of forest diversity

▶ ERIN SPEAR, SMITHSONIAN TROPICAL RESEARCH INSTITUTE

A continental divide? Contrasting apparent benefits of ectomycorrhizal fungi in neotropical and paleotropical forests

▶ JAMES DALLING, UNIVERSITY OF ILLINOIS

WEDNESDAY MARCH 24

2 AFTERNOON SESSION 2 CONTINUED

Interactions of root inhabiting fungi determine contrasting patterns of dominance and diversity among tropical ectomycorrhizal and arbuscular mycorrhizal trees

▶ DAVID BURSLEM, UNIVERSITY OF ABERDEEN

A microbiological view of the causes and consequences of coral decline

▶ REBECCA VEGA THURBER, OREGON STATE UNIVERSITY

//// 2:50pm **BREAK** | 10 minutes

 3:00pm – 4:30pm **Live Discussion SESSION 2**
speakers and questions from audience

DAY 1 WRAP UP

THURSDAY MARCH 25

9:00am* **Welcome and introductions**
ALLEN HERRE
SMITHSONIAN TROPICAL RESEARCH INSTITUTE

9:10am **PLENARY TALK** | 30 minutes
Microbial symbioses and the future of coral reefs
▶ NANCY KNOWLTON, SMITHSONIAN INSTITUTION

 9:40am **Q&A** | 10 minutes

//// 9:50am **BREAK** | 10 minutes

 **MORNING SESSION MODERATOR:**
DAVID KLINE, SMITHSONIAN TROPICAL RESEARCH INSTITUTE

3 10:00am **SESSION 3 | Evolutionary Ecology of Microbial Symbioses**
Prerecorded lightning talks | 6 minutes each

The formation of the Isthmus of Panama: a natural experiment in marine host-microbe ecology and evolution

▶ MATTHIEU LERAY, SMITHSONIAN TROPICAL RESEARCH INSTITUTE

THURSDAY MARCH 25

3 MORNING SESSION 3 CONTINUED

Examining the natural and anthropogenic drivers affecting host-parasite interactions in marine systems

- ▶ KATRINA LOHAN, SMITHSONIAN ENVIRONMENTAL RESEARCH CENTER

Fungal endophytes from the tundra to the tropics: leaves, seeds, and a global mosaic hypothesis

- ▶ ELIZABETH ARNOLD, UNIVERSITY OF ARIZONA

The little things that really run the world: lessons from long-term plant-microbiome experiments in the field

- ▶ ERIC GRIFFIN, NEW MEXICO HIGHLANDS UNIVERSITY

Can metabolomics reveal the chemical-defense niches thought to generate and maintain tree diversity in tropical forests?

- ▶ BRIAN SEDIO, UNIVERSITY OF TEXAS AT AUSTIN

Diversification of ergot alkaloids and heritable fungal symbionts in morning glories

- ▶ KEITH CLAY, TULANE UNIVERSITY

//// 10:50am **BREAK** | 10 minutes

 11:00am – 12:30pm **Live Discussion SESSION 3**
speakers and questions from audience

.....
12:30pm – 2:00pm **BREAK**
.....

 **AFTERNOON SESSION MODERATOR:**
LAETITIA WILKINS, MAX PLANCK INSTITUTE FOR MARINE MICROBIOLOGY

 2:00pm **SESSION 4 | Community Composition, Assembly, and Function: Implications for Restoration and Remediation**
Prerecorded lightning talks | 6 minutes each

Connecting fungal endophyte community assembly to function in tropical trees

- ▶ NATALIE CHRISTIAN, UNIVERSITY OF LOUISVILLE

Phages and bacteria in coral reef holobiont interactions

- ▶ MARK LITTLE, SAN DIEGO STATE UNIVERSITY

THURSDAY MARCH 25

AFTERNOON SESSION 4 CONTINUED

Tropical forest soil microbes, carbon and climate warming

▶ ANDREW NOTTINGHAM, UNIVERSITY OF LEEDS

Assembly of soil microbial communities in lowland tropical forests

▶ KRISTIN SALTONSTALL, SMITHSONIAN TROPICAL RESEARCH INSTITUTE

Are microbes responsible for decreasing marine biodiversity?

A case study of coastal deoxygenation in tropical marine sediments

▶ NOELLE LUCEY, SMITHSONIAN TROPICAL RESEARCH INSTITUTE

Using probiotics as a treatment for stony coral tissue loss disease

▶ BLAKE USHIJIMA, UNIVERSITY OF NORTH CAROLINA, WILMINGTON

 2:50pm **BREAK** | 10 minutes

 3:00pm – 4:30pm **Live Discussion SESSION 4**
speakers and questions from audience

----- DAY 2 WRAP UP AND NEXT STEPS -----



Photo courtesy of Phyllis D. Coley

SPEAKERS AND ABSTRACTS

WEDNESDAY MARCH 24

PLENARY TALK

Seeing the forest for the microbes: how important are plant-microbe interactions to the maintenance of forest biodiversity?

► JOSEPH LAMANNA

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Academic Affiliation:

Dept. of Biological Sciences, Marquette University

ABSTRACT

For hundreds of years, ecologists have been fascinated with widespread patterns in plant species diversity across latitudes and elevations. Mounting evidence indicates that interactions between plants and their microbial associates (including both mutualists and pathogens) are important regulators of plant populations, plant species diversity, and the relative abundance of plant species in communities. However, substantial debate remains about the role that plant-microbe interactions might play in determining larger-scale patterns of biodiversity. In this talk, the current state of this field is briefly reviewed and synthesized, and fundamental gaps are identified that need further study. Future studies are encouraged that test specific mechanisms by which different types of plant-microbe interactions (e.g. different functional groups of mycorrhizae, pathogens, etc.) influence plant populations and diversity maintenance. Replicated experiments across a variety of different tropical and temperate forests will be most helpful to disentangling the influence of plant-microbe interactions on global biodiversity patterns.

Useful literature:

- Jia, S., Wang, X., Yuan, Z., Lin, F., Ye, J., Lin, G., ... & Bagchi, R. (2020). Tree species traits affect which natural enemies drive the Janzen-Connell effect in a temperate forest. *Nature communications*, 11(1), 1-9. Web: <https://www.nature.com/articles/s41467-019-14140-y>
- Liang, M., Shi, L., Burslem, D. F., Johnson, D., Fang, M., Zhang, X., & Yu, S. 2021. Soil fungal networks moderate density-dependent survival and growth of seedlings. *New Phytologist*. Web: <https://nph.onlinelibrary.wiley.com/doi/10.1111/nph.17237>
- LaManna, J. A., S. A. Mangan, J. A. Myers. 2021. Conspecific negative density dependence and why its study should not be abandoned. *Ecosphere*. 12(1):e03322. 10.1002/ecs2.3322. Web: <https://esajournals.onlinelibrary.wiley.com/doi/full/10.1002/ecs2.3322>
- Kandlikar, G. S., Johnson, C. A., Yan, X., Kraft, N. J., & Levine, J. M. 2019. Winning and losing with microbes: how microbially mediated fitness differences influence plant diversity. *Ecology letters*, 22(8), 1178-1191. Web: <https://onlinelibrary.wiley.com/doi/full/10.1111/ele.13280>
- Ke, P. J., & Wan, J. (2020). Effects of soil microbes on plant competition: a perspective from modern coexistence theory. *Ecological Monographs*, 90(1), e01391. Web: <https://esajournals.onlinelibrary.wiley.com/doi/abs/10.1002/ecm.1391>
- Johnson, D. J., Clay, K., & Phillips, R. P. 2018. Mycorrhizal associations and the spatial structure of an old-growth forest community. *Oecologia*, 186(1), 195-204. Web: <https://link.springer.com/article/10.1007/s00442-017-3987-0>

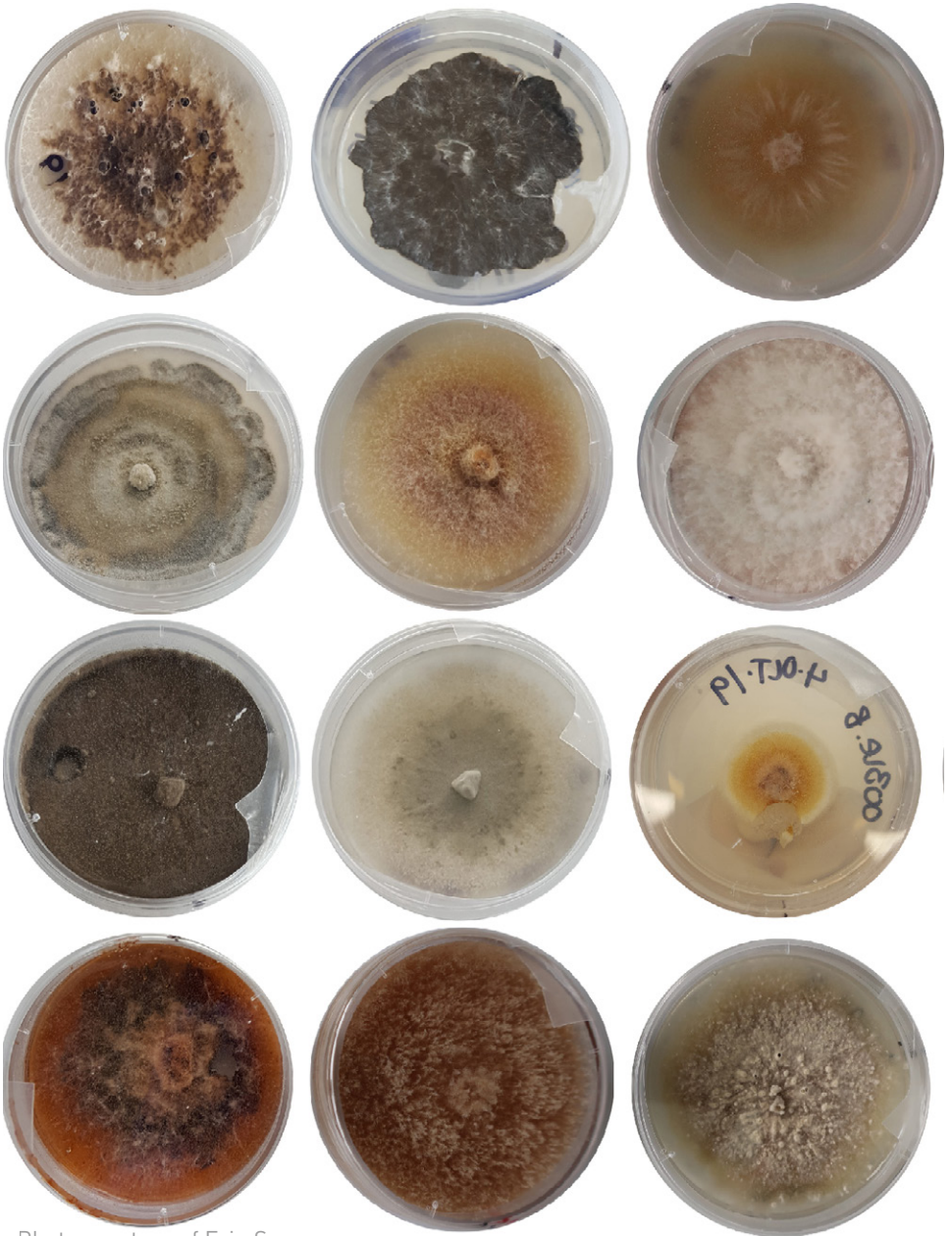


Photo courtesy of Erin Spear

SESSION 1

The Evolutionary Ecology of Host Immune Systems:
the Interface/Playground for Hosts and their Microbiomes

Ecological and evolutionary interactions with enemies shapes diversity and divergence of defenses in a genus of rainforest trees

► PHYLLIS D. COLEY

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Academic Affiliation:
University of Utah

ABSTRACT

Ecological and evolutionary interactions of plants with enemies may drive new adaptations and new species. We see evidence for this with *Inga* (Fabaceae), a common and speciose rainforest tree and the insect herbivores that feed on it. *Inga* has evolved a battery of defense classes, including physical defenses such as hairs, mutualisms with ants, phenological escape of vulnerable young leaves and secondary metabolites. A typical leaf invests 50% DW in >200 defensive metabolites. All classes are independent, leading to an enormous diversity of defensive profiles across *Inga*. As a consequence, herbivores are extremely specialized. The high local diversity of rainforest trees is enforced by Conspecific Negative Density Dependence, with nearby neighbors being different in defenses, but not in resource acquisition traits. Additionally, the species of *Inga* co-occurring at a single site (eg BCI) are over-dispersed with respect to chemistry. Thus, specialist herbivores are prohibiting any one *Inga* species from dominating at the scale of meters as well as kilometers. There is no phylogenetic signal for defenses, suggesting that herbivores are driving rapid, divergent evolution of defenses. More effective escape from enemies may involve large changes in chemistry rather than variation on a theme. For example, one evolutionary mechanism could be through changes in gene regulation, allowing sister species to switch from investment in phenolics to saponins. Related herbivores choose hosts with similar defensive traits rather than similar ancestry. These results do not support reciprocal coevolution, instead herbivores are tracking defenses, feeding on hosts for which they have appropriate preadaptations.

Useful literature:

- Kursar, T.A., K.G. Dexter, J. Lokvam, R.T. Pennington, J.E. Richardson, M.G. Weber, E. Murakami, C. Drake, R. McGregor and P.D. Coley. 2009. The evolution of anti-herbivore defenses and their contribution to species coexistence in the tropical tree genus *Inga*. Proceedings of the National Academy of Sciences 106:18073-18078.
- Coley, P.D. and T.A. Kursar. 2014. Is the high diversity in tropical forests driven by the interactions between plants and their pests? Science 343: 35-36.
- Endara, M.-J., P.D. Coley, G. Ghabash, J.A. Nicholls, K.G. Dexter, D.A. Donoso, G. N. Stone, R.T. Pennington and T.A. Kursar. 2017. Coevolutionary arms race versus host defense chase in a tropical herbivore-plant system. Proceedings of the National Academy of Sciences 114:E7499-7505. doi: 10.1073/pnas.1707727114.
- Coley, P.D., M.-J. Endara, and T.A. Kursar. 2018. Consequences of interspecific variation in defenses and herbivore host choice for the ecology and evolution of *Inga*, a speciose rainforest tree. Oecologia 187:361-376. doi: 10.1007/s00442-018-4080-z.
- Endara, M.-J., Nichols, J.A., Coley, P.D., Forrister, D.L., Younkin, G.C., Dexter, K.G., Kidner, C.A., Pennington, R.T., Stone, G.N. and T.A. Kursar. 2018. Tracking of host defenses and phylogeny during the radiation of neotropical *Inga*-feeding sawflies (Hymenoptera; Argidae). Frontiers in Plant Science 9:1237. doi: 10.3389/fpls.2018.01237.
- Forrister, D.L., Endara, M.-J., Younkin, G.C., Coley, P.D., and T.A. Kursar. 2019. Herbivores as drivers of negative density dependence in tropical forest saplings. Science 363:1213-1216. doi: 10.1126/science.aau9460.

Plant immune pathways and the genetics affecting disease resistance and microbiome assembly

► LUIS C. MEJÍA

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Academic Affiliation:

Center for Biodiversity and Drug Discovery, INDICASAT-AIP, Panama

ABSTRACT

I will discuss the defensive pathways which characterize how most higher plants interact with microorganisms. Much of the molecular and genetic basis for these pathways comes from studies of *Arabidopsis* and a few crop plants. I will give examples from my own work with collaborators on *Theobroma cacao* (the source of chocolate) and *Coffea arabica* (the source of coffee) on how plant immune pathways are induced by dominant species composing the microbiome, the role of host genetics and plant organ on microbiome assembly. We have characterized microbial communities (microbiomes including both pathogens and mutualists) for a range of cultivars of both of these host plants that have been grown under a variety of agricultural settings. We have also characterized how host physiology and genetic expression respond to many of these microbial symbionts. Finally, we have also determined how the genetic expression of some of these symbionts responds to interactions with their hosts. Understanding the factors that affect plant microbiome assembly and their temporal dynamics promises to be of value for plant protection against diseases in agricultural settings.

Useful literature:

- Christian, N., Herre, E.A., Mejia, L.C., Clay, K., 2017. Exposure to the leaf litter microbiome of healthy adults protects seedlings from pathogen damage. *Proc Biol Sci* 284, 20170641. <https://doi.org/10.1098/rspb.2017.0641>
- Cregger, M.A., Veach, A.M., Yang, Z.K., Crouch, M.J., Vilgalys, R., Tuskan, G.A., Schadt, C.W., 2018. The *Populus* holobiont: dissecting the effects of plant niches and genotype on the microbiome. *Microbiome* 6, 31. <https://doi.org/10.1186/s40168-018-0413-8>
- Mejía, L.C., Herre, E.A., Sparks, J.P., Winter, K., García, M.N., Van Bael, S.A., Stitt, J., Shi, Z., Zhang, Y., Gultinan, M.J., Maximova, S.N., 2014. Pervasive effects of a dominant foliar endophytic fungus on host genetic and phenotypic expression in a tropical tree. *Frontiers in Microbiology* 5, 479. <https://doi.org/10.3389/fmicb.2014.00479>
- Mejía, L.C., Rojas, E.I., Maynard, Z., Bael, S.V., Arnold, A.E., Hebban, P., Samuels, G.J., Robbins, N., Herre, E.A., 2008. Endophytic fungi as biocontrol agents of *Theobroma cacao* pathogens. *Biological Control* 46, 4–14. <https://doi.org/10.1016/j.biocontrol.2008.01.012>
- Teixeira, P.J.P., Colaianni, N.R., Fitzpatrick, C.R., Dangl, J.L., 2019. Beyond pathogens: microbiota interactions with the plant immune system. *Current Opinion in Microbiology* 49, 7–17. <https://doi.org/10.1016/j.mib.2019.08.003>
- Wagner, M.R., Lundberg, D.S., del Rio, T.G., Tringe, S.G., Dangl, J.L., Mitchell-Olds, T., 2016. Host genotype and age shape the leaf and root microbiomes of a wild perennial plant. *Nature Communications* 7, 12151. <https://doi.org/10.1038/ncomms12151>

Investigating interactions between the *Pocillopora* coral innate immune system and coral-associated bacteria communities

► MICHAEL CONNELLY

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ABSTRACT

Reef-building corals are complex holobionts that consist of a coral host and associated microbes including symbiotic algae, bacteria, viruses and micro-eukaryotes whose interactions are mediated by the coral innate immune system. Corals in the genus *Pocillopora* have emerged as model species for the study of coral evolution, symbiosis and immunity because of their hardiness, persistent associations with numerous endosymbiotic microbes, and the diversity of innate immune factors (including pattern recognition receptors, signaling pathways and defense mechanisms) present in the *P. damicornis* genome. To investigate interactions between *Pocillopora* corals' complex immune repertoire and coral-associated bacteria communities, replicate fragments of *P. damicornis* and *P. acuta* corals from southern Taiwan were subjected to separate experimental treatments with bacterial lipopolysaccharide (LPS) and broad-spectrum antibiotics. LPS exposure stimulated *Pocillopora* coral immunity and caused upregulation of Toll-like receptors (TLRs), immune transcription factors, and pore-forming toxins such as perforin-2 but did not alter bacteria community composition. Antibiotics treatments significantly decreased *Pocillopora* bacteria community diversity and dramatically changed both coral host and *Cladocopium* algal symbiont gene expression, suggesting disruptions in the metabolic exchanges among symbiotic partners. Altogether, these results identify novel genes and pathways involved in *Pocillopora* coral-symbiont-bacteria interactions and highlight the utility of antibiotics treatments as an experimental tool to manipulate coral-associated bacteria communities.

Useful literature:

- Traylor-Knowles, N., & Connelly, M. T. (2017). What Is Currently Known About the Effects of Climate Change on the Coral Immune Response. *Current Climate Change Reports*, 3, 252–260. doi: 10.1007/s40641-017-0077-7
- Connelly, M. T., McRae, C. J., Liu, P., & Traylor-Knowles, N. (2020). Lipopolysaccharide treatment stimulates *Pocillopora* coral genotype-specific immune responses but does not alter coral-associated bacteria communities. *Developmental and Comparative Immunology*, 109(April), 103717. doi: 10.1016/j.dci.2020.103717
- Walters, B. M., Connelly, M. T., Young, B., & Traylor-Knowles, N. (2020). The Complicated Evolutionary -Diversification of the Mpeg-1/Perforin-2 Family in Cnidarians. *Frontiers in Immunology*, 11(August), 1–5. doi:10.3389/fimmu.2020.01690

When and why do insects need microbiomes for immune function?

► TOBIN J. HAMMER

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University of Texas at Austin

ABSTRACT

The immune system's *raison d'être* is to manage microbes, but could microbes themselves be important contributors to immune function? Support for this possibility is accumulating, adding to the ever-expanding pile of host processes that seem to benefit from microbial symbionts (the microbiome). Drawing on insect examples, I argue that the situation is more complex, and interesting, than how it is often portrayed. There are indeed plenty of insects whose microbiome provides its host with novel immunological capabilities—e.g., unique toxic metabolites that ward off pathogens. But in others, apparent microbiome benefits are more likely to be the outcome of evolved dependency. In this scenario, symbionts may never have actually provided any useful services, but hosts have become “addicted” to their presence, such that the immune system now malfunctions in their absence. And finally, there are many insects which altogether lack microbial symbionts, implying that a resident microbiome is not strictly necessary to build and operate a functioning immune system. I will discuss how these different forms of immunity-microbiome interactions might extend to non-insect hosts, and to other aspects of host biology, such as development and behavior.

Useful literature:

- McFall-Ngai M. 2007 Care for the community. *Nature* 445, 153. (doi:10.1038/445153a)
- Sullivan W. 2017 *Wolbachia*, bottled water, and the dark side of symbiosis. *Molecular Biology of the Cell* 28, 2343–2346. (doi:10.1091/mbc.E17-02-0132)
- Hammer TJ, Sanders JG, Fierer N. 2019 Not all animals need a microbiome. *FEMS Microbiol. Lett.* 366, fnz117. (doi:10.1093/femsle/fnz117)
- Flórez LV, Scherlach K, Gaube P, Ross C, Sitte E, Hermes C, Rodrigues A, Hertweck C, Kaltenpoth M. 2017 Antibiotic-producing symbionts dynamically transition between plant pathogenicity and insect-defensive mutualism. *Nature Communications* 8, 15172. (doi:10.1038/ncomms15172)
- Login FH, Balmant S, Vallier A, Vincent-Monégat C, Vigneron A, Weiss-Gayet M, Rochat D, Heddi A. 2011 Antimicrobial peptides keep insect endosymbionts under control. *Science* 334, 362–5. (doi:10.1126/science.1209728)

Tiers of defense of multicellular host taxa

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Department of Ecology & Evolutionary Biology
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ABSTRACT

Multicellular organisms fight pathogens and curate symbionts via a tiered suite of defenses. Structural barriers such as bark, cuticle, and skin keep a large fraction of microbes at bay; microbes that breach those barriers are subject to innate immune scrutiny that is highly conserved across multicellular taxa. Yet induced innate responses can be slower than microbial replication, especially at high inoculating doses. Adaptive immune defenses (best described in vertebrates) match the speed and diversity of microbes. Alas, the famed plasticity of B and T cells arguably leads to a détente with microbes. I will outline how such multi-tiered defenses apply across host taxa.

Useful literature:

- Beutler, B. 2004. Inferences, questions and possibilities in toll-like receptor signalling. *Nature* 430: 257-63.
- Kagan, J. C. 2017. Lipopolysaccharide detection across the kingdoms of life. *Trends Immunol* 38: 696-704.
- Ost, K. S. & J. L. Round. 2018. Communication Between the Microbiota and Mammalian Immunity. *Annu Rev Microbiol* 72: 399-422.
- Wertheim, B. 2015. Genomic basis of evolutionary change: evolving immunity. *Front Genet* 6:222.

The sponge holobiont from the host perspective

► LUCIA PITA

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Academic Affiliation:

GEOMAR Helmholtz Center for Ocean Research Kiel

ABSTRACT

The mechanisms of host-microbe interactions remain elusive but hold the key to understand the health of marine organisms and their susceptibility to disease. Now, the rapid changes in our world are threatening the delicate balance of host-microbe intimate associations in marine organisms. Sponges (phylum Porifera) feed on seawater bacteria by filtering thousands of liters of water per day; yet, they harbor complex species-specific microbial communities. Sponge microbiology has developed in last decade, but we know little about the host perspective. From the host side, we put the focus on sponge immunity as the guardian of animal homeostasis and animal-microbe communications. The first sponge genome, published in 2010, revealed that sponges harbor a diverse repertoire of immune receptors that can potentially detect a diverse array of signals, but the genetic basis of sponge immunity and how sponges sense their environment remains understudied. We performed independent experiments to address the response of sponges to microbes by ways of RNA-seq. We found that sponges express a high diverse array of immune receptors. SRCRs and GPCRs are emerging as key sensors in sponges. The response to microbes was further characterized by the activation of apoptotic pathways, genes related with extracellular matrix and vesicular-mediated transport, and the down-regulation of serine threonine protein kinases and lipid metabolism. We observed that the density of the microbiome (i.e., whether the mesohyl of the sponge is packed with microbes or rather colonize for few microbial cells) affects sponge immune response, in terms of number of genes involved and their changes in expression. Thus, we proposed that the dense microbiome was sending conflicting signals to silence host immune response, but also affect which genes are constitutively-expressed. In a recent study we observed that individuals of the sponge *Halichondria panicea* express a unique repertoire of immune receptors. Thus, we proposed that microbial density, host genotype, and host life history interact in determining the response of the holobiont to environmental stressors.

Useful literature:

- Jahn, M. T., Arkhipova, K., Markert, S. M., Stigloher, C., Lachnit, T., Pita, L., et al. (2019). A Phage Protein Aids Bacterial Symbionts in Eukaryote Immune Evasion. *Cell Host Microbe* 26, 542-550.e5. doi:10.1016/j.chom.2019.08.019.
- Pita, L., Hoepfner, M. P., Ribes, M., and Hentschel, U. (2018a). Differential expression of immune receptors in two marine sponges upon exposure to microbial-associated molecular patterns. *Sci. Rep.* 8, 16081. doi:10.1038/s41598-018-34330-w.
- Pita, L., Rix, L., Slaby, B. M., Franke, A., and Hentschel, U. (2018b). The sponge holobiont in a changing ocean: from microbes to ecosystems. *Microbiome* 6, 46. doi:10.1186/s40168-018-0428-1.
- Pita, L., Turon, X., López-Legentil, S., and Erwin, P. M. (2013). Host rules: spatial stability of bacterial communities associated with marine sponges (*Ircinia* spp.) in the Western Mediterranean Sea. *FEMS Microbiol. Ecol.* 86, 268- 276. doi:10.1111/1574-6941.12159.



Photo courtesy of STRI

SESSION 2

Spatial and Temporal Scale in the Function and
Physiology of Host-Microbial Interactions

400 million years of symbiosis: Marine lucinid clams and the symbionts that feed them

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Academic Affiliation:
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ABSTRACT

No organism evolved or lives in isolation, even in the year 2020. Virtually every living organism, including humans, relies on symbiotic microbial partners that provide a range of health benefits including synthesizing food and vitamins, protecting against pathogens, and detoxifying the environment. These symbiotic partnerships evolved in a complex environmental context, but our understanding of how the environment drives the function and evolution of host-microbe interactions is still in its infancy. In the marine environment, 'extreme' or challenging habitats are characterized by symbioses between animals and the microbes that underpin their survival. One ubiquitous example is lucinid clams, which burrow in sandy coastal sediments, a challenging habitat for animals due to the complete lack of oxygen, and abundance of the toxin sulfide. However, they have teamed up with bacterial symbionts that use this toxic sulfide to power primary production, turning toxins into food for their hosts. These partnerships are so successful, the animal hosts have diversified into one of the most species-rich animal families in the oceans today, and have dispersed to a range of coastal and deep-sea habitats worldwide. Thanks to their reliance on environmental energy sources, and the natural 'simplicity' of this symbiosis between one host and one prominent bacterial symbiont species, they are ideal for understanding how environments shape microbiomes at the molecular level. The Group in Vienna works to understand the genomic innovations that underpin the ecological and evolutionary success of these symbioses from seagrass meadows to the deep sea.

Useful literature:

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Exploring the microenvironmental landscape of aquatic symbioses

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ABSTRACT

Aquatic symbiosis research becomes increasingly dominated by molecular studies that can provide very detailed insight to microbial diversity and potential metabolic interactions between microbes, symbionts and hosts. Such approaches are powerful but are often performed with larger samples with little understanding of underlying system heterogeneity and the actual landscape of physico-chemical microenvironments, wherein such interactions take place. The microenvironmental dynamics under natural and stress conditions in different holobiont compartments and their connectivity remain poorly investigated, in part due to technical challenges and missing methodology to map and align the physicochemical microenvironment with the complex structural landscape of coral holobionts. Measuring and accounting for spatial heterogeneity at very small scales, is a prerequisite for more reliable inference of the ecological mechanisms structuring microbial and microbe-host interactions in aquatic symbioses, and this is a key research interest of my research group. Over the years, we have developed and applied sensing techniques based on microsensors and functional imaging approaches that have provided novel insight to the microenvironmental landscape of various aquatic photosymbioses (foraminifera, ascidians, corals). In my presentation, I will give an overview and examples of such studies – with a focus on the coral holobiont.

Useful literature:

- Wangpraseurt, D., Wentzel, C., Jacques, S. L., Wagner, M., and Kühl, M. (2017) In vivo imaging of coral tissue and skeleton with optical coherence tomography. *Journal of Royal Society Interface* 14: 20161003. <https://doi.org/10.1098/rsif.2016.1003>
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3D bioprinted coral host microenvironments

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ABSTRACT

3D bioprinting is a rapidly evolving technique that has revolutionized regenerative medicine via the development of living, functional tissues and organ models. Here, I demonstrate a new 3D bioprinting platform for applications on reef-building corals. The coral-inspired biomaterials are capable of cultivating a range of microalgae including Symbiodiniaceae in a controlled physio-chemical microhabitat. The hybrid living photosynthetic biomaterials are produced with micron-scale resolution and mimic morphological features of living coral tissue and the underlying skeleton, including their optical and mechanical properties. The programmable synthetic microenvironment thus allows for replicating both structural and functional traits of the coral-algal symbiosis. This work defines a new class of bionic materials capable of interacting with living organisms, that can be exploited for novel ecophysiological studies on the coral-algal photosymbiosis as well as disruptive approaches for coral reef conservation.

Useful literature:

- Wangpraseurt D, You S, Azam F, Hildebrand M, Gaidarenko O, Jacucci G, Kuhl M, Smith AS, Davey MP, Deheyn DD, Chen S, Vignolini S. 2019 Bionic 3D printed corals *Nature Communications* 11, 1748
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- Wangpraseurt D, Larkum AWD, Franklin J, Szabo M, Ralph PJ and Kühl M. 2014. Lateral light transfer ensures efficient resource distribution in symbiont-bearing corals. *Journal of Experimental Biology* 217, 489-498
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Multi-host pathogens and the maintenance of forest diversity

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ABSTRACT

Phytopathogens are believed to be key to the coexistence of plant species, yet few studies have identified the pathogens or characterized their interactions with specific plants. I will describe some of the pathogens attacking tree seedlings in Panama's lowland forests, observed variability among tree species in pathogen susceptibility, and the relationship between disease susceptibility and plant habitat associations. Multi-host pathogens may contribute to the maintenance of local and regional forest diversity by effective specialization and/or by the reinforcement of resource partitioning, thereby limiting the spatial distributions of host species. Given the prevalence of multi-host pathogens in natural plant communities, these potential mechanisms represent key knowledge gaps.

Useful literature:

- Augspurger CK, Wilkinson HT. 2007. Host specificity of pathogenic *Pythium* species: Implications for tree species diversity. *Biotropica* 39: 702–708.
- Barrett LG, Kniskern JM, Bodenhausen N, Zhang W, Bergelson J. 2009. Continuum of specificity and virulence in plant host–pathogen interactions: causes and consequences. *New Phytologist* 183: 513–529.
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A continental divide? Contrasting apparent benefits of ectomycorrhizal fungi in neotropical and paleotropical forests

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ABSTRACT

Tropical forests are broadly characterized as occupied by tree species that form arbuscular mycorrhizal (AM) associations. Nonetheless, ectomycorrhizal (EM) tree species dominate large expanses of forest in both the neo- and paleotropics. These include montane oak and walnut forests of Central America, *Dicymbe* forests of Guyana, *Gilbertiodendron* forests of the Congo basin, and dipterocarp forests of SE Asia. The proposed potential benefits provided by EM associations differ between these regions. In SE Asia, where dipterocarp forests dominate on phosphorus-poor soils, EM must be effective in providing phosphorus (P) to their hosts, relative to AM neighbors. In neotropical forests, EM are thought to enhance nitrogen (N) nutrition, and to promote monodominance by reducing inorganic nitrogen availability to AM neighbors. As a consequence of soil N impoverishment, neotropical EM forests are also associated with extensive soil organic matter accumulation. A second potential benefit associated with EM is a reduction of the strength of pathogen-driven negative density-dependence. This is thought to arise because the EM hyphal sheath that surrounds root tips provides a barrier to pathogen entry. While there is evidence for protective effects in temperate North American and sub-tropical Asian forests our work in Panama shows that EM associations are insufficient to overcome negative plant-soil feedbacks that reduce seedling growth performance in EM forests. Future comparative work to understand the success of EM tree species should take advantage of the contrasting environmental contexts and phylogenetic composition of EM tree species in neo- and paleotropical forests, and focus on characterizing functional gene and functional trait composition of EM fungi in addition to their taxonomic dissimilarities.

Useful literature:

- Corrales, A., Mangan, S.A., Turner, B.L. and Dalling, J.W., 2016. An ectomycorrhizal nitrogen economy facilitates monodominance in a neotropical forest. *Ecology Letters*, 19(4), pp.383-392.
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Interactions of root inhabiting fungi determine contrasting patterns of dominance and diversity among tropical ectmycorrhizal and arbuscular mycorrhizal trees

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ABSTRACT

Many subtropical and tropical forests are dominated by trees that form ectomycorrhizal (EM) root associations, whilst simultaneously displaying a high diversity of arbuscular mycorrhizal (AM) trees. For example, on the 50-ha ForestGEO plot at Danum Valley in Sabah, Malaysia, EM trees represent 42.6% of total basal area (stems ≥ 1 cm dbh), but only 6.8% of all species. A similar dominance of EM trees occurs in forests across South and Southeast Asia. Tropical forests dominated by EM species also occur sporadically in Africa and the neotropics, indicating a strong influence of biogeographical setting. EM root associations are generally thought to enhance the uptake of organic N for trees and seedlings in temperate and neotropical forests. However, our experiments also showed that that EM enabled seedlings to respond to organic as well as inorganic P sources. Conversely, sympatric AM trees were unable to utilize the organic P. EM root associations also appear to suppress root pathogens, which are the pervasive drivers of negative conspecific density dependence and the maintenance of high diversity in many temperate and tropical tree communities. Positive plant-soil feedbacks (PSFs) has been proposed to explain the local dominance by EM trees. Consistent with these predictions, our analyses of spatial patterns of tree seedling survival over 10 years in a subtropical forest in southern China showed positive PSFs for EM species and contrasting patterns of negative PSFs for AM species. The abundance of likely pathogens was four-fold greater in microbial communities extracted from the root systems of AM than EM tree seedlings. Our field experiments suggest that the presence of EM with hyphal connections to external mycelium increased seedling survival, whereas survival of AM seedlings was unaffected by access to external mycelium. Similarly, the net effect of PSFs on growth switched from negative to positive in the presence of hyphal connections for EM species, but was consistently negative for AM species irrespective of hyphal connections. These demographic and experimental results support the hypothesis that hyphal connections protect EM tree species from root pathogens and promote positive PSFs, while AM species within the same community do not receive an equivalent benefit from their mycorrhizal associates and display negative PSFs. Further research is required to determine the factors that set the upper limit of EM dominance, and to understand why EM dominance is comparatively rare in lowland tropical environments outside Asia.

Useful literature:

- Laliberté, E., Lambers, H., Burgess, T. I. & Wright, S. J. (2015) Phosphorus limitation, soil-borne pathogens and the coexistence of plant species in hyperdiverse forests and shrublands. *New Phytologist*, 206, 507–521.
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- Liu, X., Burslem, D.F.R.P., Taylor, J.D., Taylor, A.F.S., Khoo, E., Majalap-Lee, N., Helgason, Y. & Johnson, D. (2018) Partitioning of soil phosphorus among arbuscular and ectomycorrhizal trees in tropical and subtropical forests. *Ecology Letters*, 21, 713–723. doi.org/10.1111/ele.12939.
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A microbiological view of the causes and consequences of coral decline

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ABSTRACT

This talk will discuss scientific efforts from our lab to understand how microbes and viruses influence the health of coral hosts and reef ecosystems. I will present methods and data on what microbes and viruses are found in the coral tree of life, show time-series and experimental data on the dynamics of coral microbiomes and viromes, and discuss new ecological and genomic data about the critical role and importance of a novel bacterial parasite in US coral reef restoration projects.

Useful literature:

- Baker LJ, Reich HG, Kitchen SA, Klings JG, Koch HR, Baums IB, Muller E, Vega Thurber R. The coral symbiont *Candidatus Aquarickettsia* is variably abundant in threatened Caribbean acroporids and transmitted horizontally (submitted ISME J) BioRxiv: <https://doi.org/10.1101/2021.01.28.428674>
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- Klings JG, Rosales SM, McMinds R, Shaver EC, Shantz AA, Peters E, Eitel M, Wörheide G, Sharpe KH, Burkepille DE, Silliman B, Vega Thurber R+. Phylogenetic, genomic, and biogeographic characterization of a novel and ubiquitous marine invertebrate-associated Rickettsiales parasite, *Candidatus Aquarickettsia rohweri*, gen. nov., sp. nov. (2019) *International Society for Microbial Ecology Journal* 13, 2938–2953 <https://doi.org/10.1038/s41396-019-0482-0>
- Klings JG, Maher RL, Muller E, Vega Thurber R. (2020) Parasitic ‘*Candidatus Aquarickettsia rohweri*’ is a marker of disease susceptibility in *Acropora cervicornis* but is lost during thermal stress (2020) *Environmental Microbiology* doi: [10.1111/1462-2920.15245](https://doi.org/10.1111/1462-2920.15245)
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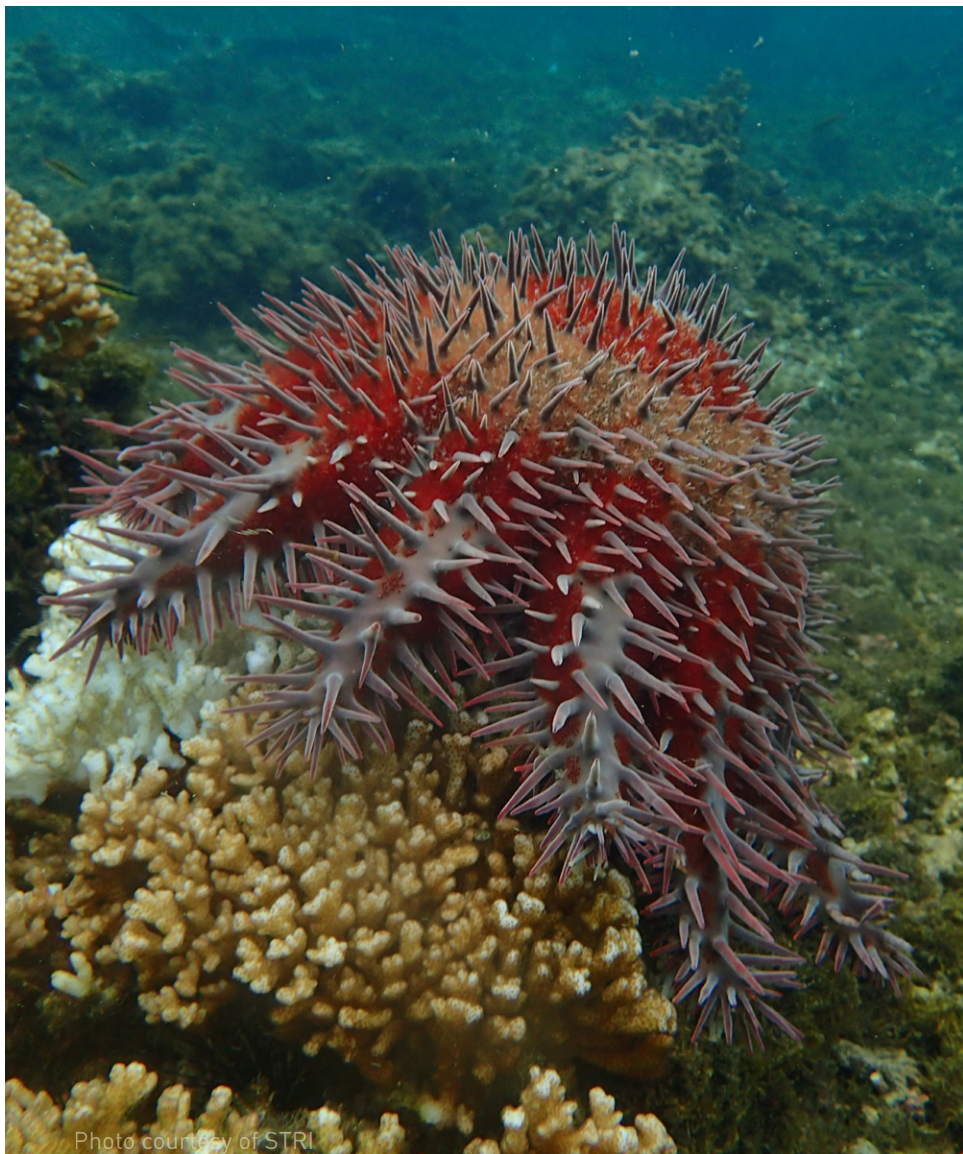


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SPEAKERS AND ABSTRACTS

THURSDAY MARCH 25

PLENARY TALK

Microbial Symbioses and the Future of Coral Reefs

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ABSTRACT

Coral reef symbioses rule coral reef ecosystems, and many of these symbioses involve microbes. Coral reefs are also in trouble, and again, microbes are often part of the problem. In some cases, this has to do with the destabilization of beneficial microbial symbioses, and in other cases it has to do with increases in microbial pathogens.

STRI has a long history research in this area: Peter Glynn documented the first mass bleaching of coral reefs in the Eastern Pacific, due to the destabilization of coral-microalgal symbiosis from high temperatures. Haris Lessios documented the massive die-off of sea urchins due to a still unidentified microbial pathogen that swept through the Caribbean, which ultimately resulted in the death of many corals from algal overgrowth. I, together with Rob Rowan and Forest Rohwer highlighted the diversity and complexity of microbial associations with corals - between species, between individuals, and within individual corals - including the role of this diversity in understanding patterns of coral bleaching. This work was all done now decades ago, using methods that are unimaginably primitive by today's standards. But they were successful because of a combination of opportunism, prepared minds, long-term data sets from Panamanian reefs, and a bit of luck facilitated by being on the reefs on a regular basis, something that characterizes STRI research to this day.

Now however, reefs around the world lie in ruins, and a more focused approach to addressing the problems they face is called for. Fortunately, the molecular and analytic methods available today allow us to not only document events and patterns, but understand their functional and mechanistic basis. And increasingly, the goal of understanding is no longer enough – we urgently need practical solutions to prevent more coral death. Today I will talk about two questions of particular importance in this regard: 1) Can beneficial microbial symbioses be made more resilient to stress caused by global change? 2) Can pathogenic microbes be brought under better control? I will close with a discussion of the challenge of taking solutions suggested by targeted research to regional and ecosystem scales.

Useful literature:

- Buerger P et al. 2020. Heat-evolved microalgal symbionts increase coral bleaching tolerance. *Sci. Adv.* 6: eaba2498.
- Knowlton, N. 2021. Ocean optimism: Moving beyond the obituaries in marine conservation. *Ann. Rev. Mar. Sci.* 13: 479-499.
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- Van Oppen MJH, Oakeshott JG. 2020. A breakthrough in understanding the molecular basis of coral heat tolerance. *PNAS* 117: 28546-28548.
- Vega Thurber R, et al. 2020. Deciphering coral disease dynamics: Integrating host, microbiome, and the changing environment. *Front. Ecol. Evol.* 8: 575927



Photo courtesy of STRI

SESSION 3

Evolutionary Ecology of Microbial Symbioses

The formation of the Isthmus of Panama: a natural experiment in marine host-microbe ecology and evolution

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ABSTRACT

Within the vast and dazzling biological diversity that inhabits the world's oceans, it would be challenging to find a eukaryotic organism that does not live in association with microbial partners. Nevertheless, we still have a poor understanding of the identity and functional role(s) of key members of microbiomes in the vast majority of marine hosts, and our knowledge of how microbes and hosts co-evolve remains limited. What is also unclear is how dynamic interactions between hosts and the immense standing pool of microbial genetic variation will affect how well marine ecosystems can adjust to ongoing environmental changes.

I will talk about how we can address some of these big questions by intensifying long-term research on “natural experiments” where ecological and evolutionary contexts have been well-documented. The closure of the Isthmus of Panama - a time-calibrated geological event where decades of taxonomical, ecological and evolutionary research can be leveraged - presents an unparalleled opportunity. It generated a unique natural Darwinian evolutionary experiment in the sea, by creating two oceans with strikingly different geophysical characteristics. Today's Caribbean and Tropical Eastern Pacific marine ecosystems of Panama and Central America are home to hundreds of sister species, representing all major taxonomic groups, that diverged on separate evolutionary trajectories. Hosts adapted to the strongly contrasting environments on opposite sides of the Isthmus, and presumably their associated microbiomes did so too. I will show how we take advantage of the numerous species pairs of fish, crustaceans and clams for which well-calibrated phylogenetic data is available to understand changes that occurred to their associated microbiomes. I will also talk about ongoing research investigating mechanisms that organisms use to cope with drastic annual fluctuations in temperature, pH, oxygen, salinity, and nutrients, due to intense seasonal upwelling in the Tropical Eastern Pacific.

Useful literature:

- Clever F, Sourisse JM, Orezuisi RF, Eisen JA, Rodriguez Guerra ED, Scott JJ, Wilkins GE, Altieri AH, McMillan WO, Leray M. 2020. The gut microbiome stability of a butterflyfish is disrupted on severely degraded Caribbean coral reefs. *bioRxiv*
- Wilkins LGE**, Leray M**, Yuen B, Peixoto R, Pereira TJ, Bik HM, Coil DA, Duffy JE, Herre EA, Lessios H, Lucey N, Mejia LC, O’dea A, Rasher DB, Sharp K, Sogin EM, Thacker RW, Vega Thurber R, Wcislo WT, Wilbanks EG, Eisen JA. 2019. Host-associated microbiomes drive structure and function of marine ecosystems. *PLoS Biology* 17, e3000533
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Examining the natural and anthropogenic drivers affecting host-parasite interactions in marine systems

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ABSTRACT

Parasitism is a complex, antagonistic relationship between two organisms, where one benefits and the other is harmed. In the Marine Disease Ecology Laboratory at SERC, we conduct research at the intersection of disease and parasite ecology, examining multi-parasite and multi-host systems across many aquatic habitats and geographic regions. We examine patterns and causes of marine parasite diversity, the host and habitat specificity of parasites, the ecology of multi-host systems, and the genomic and genetic population diversity of different species and strains of marine parasites. This research incorporates a wide range of parasite and host phyla, and examines the role of environmental reservoirs in the ecology and epidemiology of marine disease.

Useful literature:

- SA Gignoux-Wolfsohn, M Newcomb, GM Ruiz, & KM Pagenkopp Lohan (2020) Temperature and time of day drive release of *Perkinsus marinus* from infected oysters. *Parasitology*. Online preview.
- KM Pagenkopp Lohan, R DiMaria, D Martin, C Ross, & GM Ruiz (2020) Examining the diversity and habitat association of *Labyrinthulasp.* in Florida coastal waters with targeted metabarcoding. *Diseases of Aquatic Organisms*. 137: 145-157.
- KM Pagenkopp Lohan, GM Ruiz, & ME Torchin (2020) Chapter 7: Invasions can alter marine disease dynamics. For *Marine Disease Ecology*. Eds: DC Behringer, BR Silliman, KD Lafferty. Pgs. 115-138.
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- KM Pagenkopp Lohan, RC Fleischer, KJ Carney, KK Holzer, & GM Ruiz (2017) Molecular characterization of protistan species and communities in ships' ballast water across three U.S. coasts. *Diversity and Distributions*. 23: 680-691.

Fungal endophytes from the tundra to the tropics: leaves, seeds, and a global mosaic hypothesis

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ABSTRACT

Fungal symbionts complement, extend, and manipulate plant phenotypes in all biotic communities. From polar deserts to tropical rainforests, the fungi that inhabit photosynthetic tissues of plants (such as leaves) and reproductive propagules (such as seeds) often live between cells, with the apoplastic space thus representing a tremendous ‘endosphere’ of biological and functional diversity at a global scale. Alignment of data sets from diverse plant lineages and environments worldwide increasingly shows that endophyte assemblages are often distinctive in a given host and given location, typically with a strong signature of climate that may act on fungi, hosts, and their emergent traits together. This talk will describe the resulting global mosaic of biodiversity, function, and evolutionary diversification that spans small to large scales and is aligned with functional importance in a rapidly changing world.

Useful literature:

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The little things that really run the world: lessons from long-term plant-microbiome experiments in the field

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ABSTRACT

The plant microbiome, or the fungi and bacteria found on and inside plant hosts, comprise a cryptic ecosystem component and yet are critical drivers of plant performance, trophic interactions, and entire plant community dynamics. I use long-term field experiments to assess the diversity, distribution, and impacts of plant-associated microbes in temperate and tropical forests and temperate grasslands. Moreover, I am interested in the factors that drive microbiome composition among co-occurring plant species in these biomes. Our results demonstrate that plant-associated bacteria and fungi, under different circumstances (e.g., soil nutrient availability, host species, plant diversity, disturbance regime), substantially impact host performance (e.g., growth, leaf production) across spatial scales as well as additional trophic levels (e.g., herbivores). Contrary to popular belief, we have found that host species identity is not a primary filter shaping bacterial endophyte communities in the tropics; moreover, temperate tree diversity and fungal endophyte diversity are negatively correlated. Moving forward, explicit tests of temperate versus tropical biomes are needed, in addition to simultaneous assessments of both bacterial and fungal communities. We are currently assessing how leaf chemistry drives/is driven by microbes and how these patterns are important to additional trophic levels in temperate and tropical forests. Ultimately, microbes may be the critical pivot point which drives entire ecosystem dynamics in terrestrial biomes.

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Can metabolomics reveal the chemical-defense niches thought to generate and maintain tree diversity in tropical forests?

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ABSTRACT

Much of our understanding of the mechanisms by which biotic interactions shape communities has been constrained by the methods available to study the diverse chemistry that defines relationships between organisms, particularly plants and their insect herbivores and microbial pathogens. However, chemical ecology is on the cusp of a revolution, thanks to developments in mass spectrometry bioinformatics that make it possible to identify and compare the structures of unknown metabolites at scales necessary for the study of chemical community ecology. Here, I illustrate the potential for mass spectrometry metabolomics to enable unprecedented tests of seminal hypotheses that propose a fundamental role for plant chemical defenses against herbivores and pathogens in the evolutionary origins and ecological coexistence of plant species diversity by examining variation in community-wide metabolomic richness and interspecific disparity over large-scale climatic gradients and latitude. I compare chemical richness, similarity, and phylogenetic signal in eight forest plots in Canada, the United States, and Panama that represent 29.9 C variation in mean annual temperature (MAT), 2171 mm variation in mean annual precipitation (MAP), and from 10 to 315 free-standing woody plant species. Among these forests, metabolomic richness increases and interspecific similarity of co-occurring species decreases with MAT and MAP, consistent with predictions that biotic interactions result in greater chemical divergence in warmer and wetter climates. To leverage these metabolomic data to test fundamental hypotheses in ecology and evolution, I suggest we will need to integrate metabolomics with microbial ecology, pursue assay methods used in natural products chemistry to assess function, and take advantage of big-data efforts in community ecology, such as the Smithsonian Forest Global Earth Observatory.

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Diversification of ergot alkaloids and heritable fungal symbionts in morning glories

with co-authors Wesley T. Beaulieu, Daniel G. Panaccione, Quynh N. Quach, Richard E. Miller, Katy L. Smoot, Donald Windsor and Kristin Saltonstall

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ABSTRACT

Heritable microorganisms play critical roles in life cycles of many organisms but their prevalence and functional roles are unknown for most plant families. Bioactive ergot alkaloids (EAs) produced by heritable *Periglandula* fungi have been reported in some morning glories (Convolvulaceae), similar to the presence of ergot alkaloids in grasses infected with related fungi in the family Clavicipitaceae. EAs have been of longstanding scientific and cultural interest given their toxic effects on humans and other animals, their psychoactive properties, and their medical applications. Here we show that EAs are concentrated primarily in four morning glory clades that exhibit major differences in alkaloid profiles and larger seed size, a key plant life history trait, than species lacking EAs. Further, we found a phylogenetically-independent, positive correlation between seed size and EA concentrations in symbiotic species. Our findings suggest that heritable symbiosis has proliferated and diversified among particular clades by vertical transmission through host seeds combined with host speciation, and that EAs are particularly beneficial to species with larger seeds, which represent a larger investment by maternal plants. Our results are consistent with the hypothesis of defensive symbiosis where bioactive EAs from *Periglandula* symbionts protect seeds and seedlings from predators and pathogens, and provide a framework for exploring the role of microbial chemistry that could be applied to other plant-microbe interactions.

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Photo courtesy of Andrew Nottingham

SESSION 4

Community Composition, Assembly, and Function:
Implications for Restoration and Remediation

Connecting fungal endophyte community assembly to function in tropical trees

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ABSTRACT

Traditional culture-based approaches coupled with recent advances in sequencing technologies have uncovered diverse communities of fungal endophytes associated with leaves. However, a major challenge in the areas of microbiome ecology and plant–fungal interactions is connecting processes and outcomes of community assembly to functional effects in hosts. I will discuss a series of manipulative studies conducted on foliar endophytic fungal communities associated with tropical trees. Together, these studies work to untangle not only the processes that drive the formation of host-specific suites of endophytic fungi, but also to understand how those endophytic communities then feed back in ways that are ultimately beneficial for both host and endophyte.

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Phages and bacteria in coral reef holobiont interactions

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ABSTRACT

Direct competition between corals and macroalgae is one of the major processes associated with coral reef ecosystem phase shifts. I will discuss viral, bacterial, and metabolomic findings from our studies on coral-algal interactions in situ using multi-omics techniques. The multi-omic approaches used to analyze corals, algae, and their interaction zones, revealed an emergent microbiome and metabolome at the competitive interface. Furthermore, machine learning analyses were shown to predict competition outcomes (e.g., whether a coral wins/loses against its algal competitor). Epifluorescence microscopy of microbes and viruses in these holobiont interactions was used to determine their abundances, which provided insight into the underlying mechanisms at play, where turf algae exhibit higher microbial loads and lower levels of lytic phages. In addition, I will present our study on the three-dimensional molecular cartography of the endangered reef-building coral, *Orbicella faveolata*. Here, we revealed findings on holobiont microbial diversity, microbial gene expression, and biochemistry in a spatially resolved framework using three-dimensional imaging.

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Tropical forest soil microbes, carbon and climate warming

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ABSTRACT

Climate warming is predicted to stimulate microbial activity resulting in the breakdown of soil organic matter, increasing the flux of carbon from soils into the atmosphere and contributing a potentially large positive climate-feedback. However, our understanding of this process is limited by a lack of information on how microbial communities 'adapt' to temperature change across scales in space and time. The uncertainty is greatest for tropical forests, which are the most productive terrestrial ecosystem and contain a third of global soil carbon, and where warming in the coming century will result in average temperatures under which no closed canopy forest exists today. Using tropical forest soil warming experiments I demonstrate that warming destabilises soil organic matter and at the same time alters the structure and metabolism of microbial communities: diversity declines, community growth and carbon-use becomes warm adapted and enzymatic activity increases.

Together these results illustrate a relationship between the thermal responses of microbial communities and the carbon balance of tropical forest soils. However, to more fully understand the impact of warming on the tropical forest carbon balance and biota, major questions remain unresolved. How can we reconcile responses to short-term experimental warming with gradual decadal warming at landscape-scales? Is the relationship between microbial growth adaptation and carbon loss causative and does it arise through the response of specific microbial taxa? How can we characterise these microbial responses in climate models? How will warming affect plant-microbial interactions, with consequences for the productivity and diversity of tropical forests? Can we use this knowledge to better manage the tropical soil microbiome for carbon sequestration? This talk will summarise these results and point towards future studies to better understand how soil microbial communities will affect the carbon balance and biota of tropical forests in a warmer world.

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Assembly of soil microbial communities in lowland tropical forests

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ABSTRACT

Today's tropical landscapes are typically mosaics of remnant patches of mature forests, regrowing secondary forests of different ages, plantations, crop land, and pastures. In many tropical regions, secondary forests now cover more area than mature forests and are often an integral part of agricultural land use systems. The process of forest succession has been widely studied from the perspective of the vegetation, but much less is known about belowground processes and the role that individual microbes play in enhancing or arresting plant succession and conserving ecosystem services and biodiversity. I will discuss ongoing projects looking at large scale patterns in belowground microbial diversity across various land uses in Panama as well as in the experimental plantations of the Agua Salud project. These results can form a baseline for future work looking at plant-soil interactions, microbial responses to landscape change, and the sustainable conservation of ecosystem services and biodiversity.

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Are microbes responsible for decreasing marine biodiversity? A case study of coastal deoxygenation in tropical marine sediments

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ABSTRACT

Climate change is disproportionately impacting coastal marine ecosystems through complex interactive multiple stressors. Microbes are without a doubt important in these coastal systems, yet the microbial ecology of many marine systems is still poorly understood. Our research aims to address pressing questions regarding which microbial assemblages are correlated to broad-scale ecosystem shifts in coastal habitats. We measured environmental oxygen, temperature, and pH weekly over the course of a year at four shallow sites (~20 m) along a natural ~15 km gradient in a Caribbean Bay. In addition to environmental parameters, we collected weekly sediment samples and determined the abundance and diversity of both the macrofauna and microbial communities (16S rRNA) throughout the year. At sites with severe deoxygenation (compared to more normoxic sites), we find a strong relationship between reduced macrofaunal abundance and diversity, as well as significant differences in microbial community composition. Using an integrative time-series approach we identify specific oxygen thresholds that appear to underpin changes in both macro- and micro- benthic diversity. These results hint at potential microbial drivers involved in benthic community changes, however a more complete understanding of the functional role of microorganisms in these systems requires a metagenomic approach.

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Using probiotics as a treatment for stony coral tissue loss disease

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ABSTRACT

The Florida Reef Tract and greater Caribbean is currently experiencing a widespread mortality event that is affecting at least 20 different species of coral. The mortalities are attributed to a mysterious disease termed stony coral tissue loss disease (SCTLD). Although the cause of SCTLD is unknown, pathogenic bacteria are believed to be involved with lesion progression. The current treatment for SCTLD is a paste mixed with the antibiotic amoxicillin, a common medication in human and veterinary medicine. However, among concerns of contributing to antibiotic resistance and a lack of prophylactic utility, this has prompted a search for alternative treatments. One such alternative is the use of beneficial microorganisms (probiotics). After screening isolates from corals more resistant to SCTLD, one isolate, *Pseudoalteromonas* sp. Mch1-7, was observed to have broad-spectrum antibacterial activity. When cultures of Mch1-7 were inoculated into coral with signs of SCTLD, disease progression was slowed or stopped in a majority of the coral fragments in the laboratory. Additionally, when healthy corals were pre-treated with Mch1-7, they appeared to be resistant to disease transmission. After rounds of safety testing and a comprehensive characterization of the strain, field trials have begun with Mch1-7 along some reefs in Florida. Currently, this probiotic is administered using a weighted bag for whole-colony treatment and a novel paste medium that can be applied directly to SCTLD lesions. This strain represents the first bacterium to be tested as a potential probiotic in a reef system and, if effective, an additional treatment for SCTLD.

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