Smithsonian
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The Isthmus of Panama for the study of microbial symbiosis:

WHAT CAN WE LEARN FROM COMPARATIVE ANALYSIS OF HOST-ASSOCIATED MICROBIOMES ACROSS TWO OCEANS?

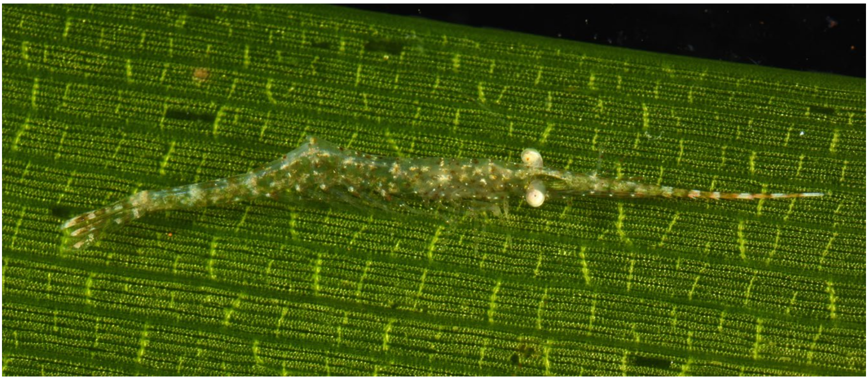
DECEMBER 2019
Smithsonian Tropical Research Institute | Panamá

Workshop funding generously provided, in part, by the Smithsonian Office of the Provost's *One Smithsonian Symposia Program* and the Gordon and Betty Moore Foundation.

This workshop aims to summarize the remarkable opportunities that the Isthmus of Panama presents for understanding the evolution of microbial symbiosis in the sea. Marine organisms and their microbial symbionts that were once able to move freely in a nutrient-rich sea gradually became physically isolated when the Isthmus formed and finally closed ~3 million years ago. The land mass progressively blocked oceanic currents causing the Caribbean to become oligotrophic while the Eastern Pacific remained rich in nutrients. Animal hosts and their associated microbiome followed separate evolutionary trajectories and adapted to contrasting environments. Today's Caribbean and Eastern Pacific marine ecosystems of Panama and Central America are home to hundreds of sister species from all major taxonomic groups that emerged through transisthmian vicariance. Much of the marine research at STRI in the last 50 years has taken advantage of these parallel events of divergence (replicated evolution) to understand evolutionary mechanisms, behaviors and physiological processes that drive reproductive isolation and adaptation in marine animals. With the support of the Gordon and Betty Moore Foundation, STRI is now expanding this research to the microbial symbionts.

During last year's workshop (3-8 December 2018, Bocas del Toro) we discussed the importance of microbial symbiosis for the functioning of ocean ecosystems and we listed questions that could be answered by expanding the phylogenetic and ecological breath of host-microbiome studies. The outcome was summarized in a perspective manuscript currently in early publication in PloS Biology (expected formal publication November 21). We encourage all workshop participants to read this document click here in advance.

This year, we will elaborate on how and why the Isthmus could help understand general principles of host-microbiome evolution and adaptation in the sea, and the intricacies of host-microbe interactions. We will discuss the benefits and limitations of taxonomic groups known to include transisthmian sister taxa for the study of symbiosis (e.g., sponges, fish, snapping shrimps, lucinid clams, gutless worm), and we will outline the questions that each taxon could help answer. The goal is to establish a roadmap for how to take full advantage of this evolutionary experiment and design inter-institutional project on focal groups.



Shrimp on a seagrass blade. Photo by Matthieu Leray

ATTENDEES

For a list of attendees with institution, area of study and contact information please click here.

In addition, we will be joined by Friederike Clever and Marina De León, STRI graduate students who are assisting in workshop planning and execution.

Lucinid Clam. Photo by Laetitia Wilkins

SPEAKERS AND ABSTRACTS

Insights into host-microbe specificity, interactions and co-evolution from marine animals

▸ AMY APPRILL

Academic Affiliation:
Woods Hole Oceanographic Institution

ABSTRACT

Microbial partnerships with marine animals occur throughout all biomes and depths of the ocean, but our understanding of these relationships and their importance for host function, adaptation and evolution is still minimal. Marine mammals provide a unique system to address outstanding questions in host-microbial associations due to their unique evolutionary history, diverse animal morphologies and lifestyles and close connections with marine food webs and biogeochemical cycles. In this talk, I will share work from my lab that examines the microbial communities associated with the skin, respiratory blow and gastrointestinal tract of large whales. I will present new knowledge about the simplicity and specificity of these relationships, which are maintained across ocean basins, as well as the potential role of the whale-microbe associations in larger ocean processes. Additionally, I will present preliminary data suggesting host-microbiome co-evolution among diverse lineages of wild sampled marine mammals.

Ubiquitous but overlooked: the ecological and evolutionary importance of nematode-microbe associations

▸ HOLLY BIK

Academic Affiliation:
University of Georgia, USA

ABSTRACT

Microbial associates of nematode worms are critically understudied compared to their potentially immense global importance. Nematodes are the most abundant invertebrates in marine sediments (exhibiting densities of 100,000-84 million nematodes per m^2), and patterns of abundance and biomass are strongly linked to that of prokaryotic assemblages. Many nematode species are known to maintain associations with sulfur-utilizing Gammaproteobacteria, either comprising a dense coating of ectosymbionts (Stilbonematidae nematodes) or tightly packed endosymbionts maintained within a vestigial nematode gut tract (Astomonema spp.). Although most nematode symbioses have been described from tropical marine sediments, recent work suggests that nematode-microbial associations can be commonly found across many shallow water and deep-sea ecosystems. Furthermore, novel symbioses are being routinely discovered on new branches of the Nematode Tree of Life (e.g. predatory nematodes in the family Oncholaimidae) and evidence from *C. elegans* and other freshwater nematodes indicates that many microbial associates are host-specific and can confer strong evolutionary benefits in terms of pathogen resistance and tolerance to environmental stress (e.g. bacterial strains from the genera *Pedobacter* and *Ochrobactrum*). Nematode symbioses also appear to play an important but unacknowledged role in global biogeochemical cycling—for example, ectosymbionts of *Laxus* onestis are capable of nitrogen fixation. Current phylogenies indicate multiple independent origins for known nematode-microbial symbioses; although bacterial symbionts are monophyletic and closely related, the nematode host species represent divergent and diverse molecular clades. Thus, nematode-microbial associations offer an ideal model system to test longstanding hypotheses in ecology and evolutionary biology.

The role of microorganisms in the nutrition of marine herbivorous fish: why mechanism is important

▸ KENDALL CLEMENTS

Academic Affiliation:
Auckland University, New Zealand

ABSTRACT

Herbivorous fishes are considered critical to ecosystem processes on coral reefs. However, the photoautotroph assemblage that constitutes potential foods for these fishes is phylogenetically diverse and biochemically disparate. Fish taxa differ in their capacity to harvest, digest and assimilate these resources, and specialise to varying degrees. The literature to date has been dominated by plant-based approaches, where herbivores are defined in terms of plant removal. In contrast, animal-based approaches focus on how photoautotroph resources satisfy the nutritional demands of herbivores. This talk will discuss the types of photoautotroph resources present on coral reefs, how these are processed by the major fish taxa involved, and how these resources are partitioned by different fish taxa. Like terrestrial herbivorous vertebrates, herbivorous fishes lie along a spectrum from those that pass material through the gut rapidly and assimilate only easily digestible macronutrient components (rate maximisers) to those that employ symbiotic relationships with gut microbes to digest their food, a strategy that involves lengthy gut retention time and more complete digestion of foods (yield maximisers). Parrotfishes are the dominant group of rate maximisers on coral reefs, targeting protein-rich microscopic photoautotrophs such as cyanobacteria that require little digestion. Kyphosid chubs represent the other extreme of this nutritional spectrum, as yield maximisers with a symbiotic hindgut microbiome that ferments refractory carbohydrate in macroalgae into metabolically useful short-chain fatty acids. The talk will discuss nutrition in herbivorous reef fishes and argue that an animal-based approach involving nutritional mechanisms is key to developing an understanding of herbivory on coral reefs.

The Population Biology of Oomycetes in the Tropics

▸ KIRK BRODERS

Academic Affiliation:
Smithsonian Tropical Research Institute - Panama

ABSTRACT

Oomycete biology and diversity in the tropics can be described as a scientific mystery. There is a general consensus in the Oomycete community as well as among fungal taxonomists that tropical regions are significantly undersampled. Global species diversity for Oomycetes is estimated at ca. 20,000 yet only a little over 1,000 species are known to date, with knowledge of tropical species far behind that of temperate species. This is in great contrast to true Fungi where ca. 75,000 species are known. Our preliminary surveys, along with data from collaborators, suggest that lowland tropical forests are hotspots of Oomycete diversity and abundance. *Phytophthora* and *Pythium* species are among the most notorious Oomycete plant pathogens because they can have wide host ranges and appear capable of thriving in diverse ecosystems and have been shown to play a role in driving patterns of negative density dependence from some tropical tree species. However, we still have a very limited understanding of the ecology, epidemiology and population genetics of these potentially important pathogens. This talk will summarize the current state of tropical oomycete disease ecology and propose a structure for future research into this group of organisms.

Ecology of a keystone pathogen and its role in transforming North Atlantic coastal ecosystems

▸ EMMETT DUFFY

Academic Affiliation:
Marine Global Earth Observatory (MarineGEO)

ABSTRACT

Plant-microbial interactions are known to affect ecosystem Keystone species have strong community impacts disproportionate to their biomass. Pathogens are the ultimate keystone species as they have almost no biomass but can transform entire ecosystems. Perhaps the most consequential interactions in nature are pathogen infections of foundation species that define ecosystems. Understanding and managing such interactions requires marrying long-separate traditions of classical ecology and microbiology. Eelgrass (Zostera marina) is the foundation of coastal ecosystems across the northern hemisphere, supporting fisheries and storing blue carbon. Eelgrass collapsed throughout the North Atlantic in the 1930s due to an outbreak of Eelgrass Wasting Disease (the slime mold Labyrinthula zosterae). "Laby" is now known to be endemic in some populations that show no symptoms, while others decline with pathogenic disease. What tips the balance between a benign commensal and a virulent pathogen? We are seeking answers in a holistic study of interactions among climate, microbiome, associated animals, and eelgrass phenotypic plasticity in mediating eelgrass wasting disease and its landscape-scale consequences from San Diego to Alaska.

The research leverages MarineGEO's growing global network and co-development of standard interoperable protocols for marine research, including a state-of-the-art computer app developed by Cornell colleagues to identify wasting disease using artificial intelligence. Integration with the recently published eelgrass genome promises fertile ground for using the eelgrass community as a model system for integrating ecology from molecule to seascape and informing management under global change.

Case studies of Rice and seagrass interacting with their microbiomes to affect their environment

▸ JONATHAN EISEN

Academic Affiliation:
University of California Davis, USA

ABSTRACT

TBC

Anvi’o: an open-source, community-driven software platform for high-resolution microbial ‘omics

▸ A. MURAT EREN

Academic Affiliation:
University of Chicago

ABSTRACT

With the advent of sequencing, microbiology has rapidly become a data-enabled field. This transformation led to remarkable discoveries; but it came with a price. Heavy reliance on computation despite limited educational resources for training in bioinformatics have confined microbial ‘omics investigations for the vast majority of microbiologists to ‘what is doable’ given the existing tools, rather than ‘what is possible’ given the new ‘omics opportunities. We developed anvi’o to address this bottleneck. Anvi’o combines multiple aspects of today’s cutting-edge analysis strategies for genomics, metagenomics, metatranscriptomics, pangenomics, phylogenomics, and microbial population genetics and offers interactive interfaces for complex data visualizations and exploratory analyses. Modular design principles behind anvi’o not only allows microbiologists to work with some of the most complex environmental sequencing datasets with high levels of control over their workflows, but also help programmers to use its internal data structures through accessible application programmer interfaces. With its online tutorials that exceed 120,000 words, anvi’o is committed to empower microbiologists against complex stream of data.

Common interactions with reef fishes can alter coral microbiomes

▸ LEILA EZZAT

Academic Affiliation:
University of California, Santa Barbara

ABSTRACT

Coral microbiomes are sensitive to multiple environmental and biotic stressors that can lead to dysbiosis and mortality. Although the processes contributing to shifts in coral microbial communities remain unclear, a number of potential mechanisms have been identified. For instance, several reef fishes are suspected to act as microbial vectors through corallivory, as well as via fecal enrichment of bacterial opportunists. We therefore used a combination of mesocosm experiments and field-based approaches to investigate whether i) fecal deposition by surgeonfish or ii) parrotfish corallivory can alter *Porites lobata* microbial communities and to identify the potentially relevant processes (e.g. transmission) that may contribute to these changes. Our 48h-surgeonfish experiment demonstrated that fecal deposition by *Ctenochaetus striatus* increased alpha diversity and induced a compositional shift towards greater abundance of potential opportunistic bacteria (e.g. Rhodobacteraceae,Verrucomicrobiaceae, Flavobacteriaceae, Vibrionaceae, Fusobacteriaceae), with some of these taxa also found in fish feces. Increased abundances of bacterial opportunists were even more pronounced when feces was combined with mechanical wounding, indicating that impacts to the coral microbiome may be exacerbated when stressors interact. Our parrotfish corallivory experiment demonstrated that feeding by *Chlorurus spilurus* also increased bacterial alpha diversity and altered community composition of *P. lobata* corals. This included blooms of potential beneficial coral symbionts (e.g. Ruegeria), as well as opportunistic taxa (e.g. Flammeovirgaceae). Many of these taxa were detectable only in *C. spilurus* mouths, not on corals, before predation. Our findings suggest that surgeonfish fecal deposition and parrotfish corallivory may represent novel routes of bacterial transmission and/or enrichment within reef-building corals. Both could impact coral health and may be critical for understanding and predicting coral disease dynamics as reefs further degrade.

Using microbiome research in conservation biology

▸ **ROB FLEISCHER**

Academic Affiliation:
Center for Conservation Genomics, Smithsonian Conservation Biology Institute, USA

ABSTRACT

Understanding microbial diversity and its interactions with hosts and host environments can be useful for developing conservation strategies and mitigation. At the Smithsonian Conservation Biology Institute, we conduct research aimed at saving species and the habitats in which they live. Our conservation research programs have developed significant microbiome laboratory and analytical tools to help achieve these goals. We currently conduct a wide range of mostly collaborative microbiome research. Areas of research and projects include: 1) Understanding how microbes interact with pathogens in amphibian, mammalian and avian disease systems. We present an overview of some ongoing SCBI studies of microbiome interactions with chytrid fungus infection in Plethodon salamanders, Panamanian golden frogs and hellbenders. 2) Assessing how microbiomes interact with diet and general animal health in captive and wild mammal and bird populations. These include SCBI studies of red and maned wolves, primates, cheetahs, pandas, honeyguides, and rhinos. 3) Comparing soil microbial diversity in shade versus sun coffee farms in central America, to see if patterns of diversity match those of other taxa. And, 4) using microbiome analysis to identify and apply "biomarkers" for ecological assessments. For example, our use of fecal microbial analysis to determine whether rat consumption of native birds represents predation, scavenging, or both.

Pathobiomes of oysters and corals are strongly influenced by location

▸ SARAH GIGNOUX-WOLFSOHN

Academic Affiliation:
Smithsonian Environmental Research Center, Edgewater, USA

ABSTRACT

In this presentation, I will highlight previously published research characterizing the pathobiomes of both oysters and corals collected from multiple sites along both coasts of Panama. I will also discuss how the macro communities that these organisms live in can influence their microbial communities. Finally, I will discuss future directions and expansions of this work into how we can manipulate location and host community to influence microbial ecosystem and host health.

Factors affecting Symbiont Transmission, Community Assembly, and the Resulting Effects on Hosts: Implications of Three Case Studies of Mutualisms in Panama

▸ EDWARD ALLEN HERRE

Academic Affiliation:
Smithsonian Tropical Research Institute -
Panama

ABSTRACT

Comparative studies of figs (*Ficus*) and their many associates suggest that vertical transmission (direct from mother to offspring) of symbionts promotes benign or mutually beneficial interactions to form and be maintained over evolutionary time scales. Experimental studies strongly support the proposition that given a predominance of horizontal transfer of symbionts, host sanctions (e.g., preferential host allocation of resources to more productive strains or species of symbionts) is often necessary to prevent exploitation of the host, promote beneficial interactions, and maintain the stability of the mutualism. The combination of structured sampling and experimental studies in Arbuscular Mycorrhizal Fungi (AMF) and Foliar Endophytic Fungi (FEF) show that these symbionts can benefit their host either through direct effects (e.g., producing defensive chemicals that the host is otherwise incapable of producing) or, interestingly, through indirect effects (e.g., stimulating the activities of the host defensive pathways). It appears that these benefits in augmented pathogen resistance or nutrient uptake also come with some clear costs. It also appears that AMF and FEF can be employed as natural biocontrol agents, but that an understanding of the ecology and physiological basis of the symbionts' interactions with the host are needed to do this effectively.

Diversity of partners in the legume-rhizobial mutualism and its importance for ecosystem function

▸ KIM KOMASTU

Academic Affiliation:
Smithsonian Environmental Research Center, USA

ABSTRACT

The mutualism between plants in the Fabaceae (legumes) and their rhizobial partners is the basis for the majority of biological nitrogen fixation on the planet. Therefore, in depth understanding of the drivers of this mutualism is key to understanding large biospheric processes. While there has been a substantial amount of research examining the abiotic factors that influence N-fixation, much less is known about the role of diversity of both legumes and rhizobia in determining the functioning of the mutualism. I will present evidence related to the current state of knowledge on the roles of rhizobial diversity impacting N-fixation at the level of a legume individual, legume diversity impacting N-fixation at the ecosystem level, and the interactions between legume and rhizobial diversity that may underpin these effects.

Worms! Worms everywhere! - Symbiotic nematodes in shallow marine waters

▸ NIKOLAUS TOBIAS LEISCH

Academic Affiliation:
Smithsonian Tropical Research Institute -
Max Planck Institute for Marine Microbiology, Bremen,
Germany

ABSTRACT

Nematodes occur worldwide in every habitat and are the most successful animal phylum on this planet. Similarly, symbiotic nematodes, which live in close association with bacteria, are highly abundant in marine sediments. One worldwide occurring group, the Stilbonematinae have a characteristic coat of ectosymbionts. Using single-worm-based metagenomics, we generated a robust phylogenetic framework but also highlight the difficulties of primer based barcoding approaches. The symbionts belong to the clade of Ca. Thiosymbion and these Gammaproteobacteria use sulfur-oxidation to fix carbon, generate biomass and feed their host. The symbionts have adapted their morphology and their cell cycle to the symbiotic lifestyle, challenging many established paradigms of bacterial cell biology. Furthermore, the symbionts arrangement on the worms' surface is so specific, that we propose to use it as an informative characteristic to identify the host genus. While the members of the genus Astomonema also live in symbiosis with closely related Ca. Thiosymbion bacteria, the symbiont reside within the hosts' tissue and the host has no more mouth or digestive tract. Often considered a rare member of the meiofauna, we have recently identified shallowwater habitats where Astomonema is highly abundant, allowing for the first time a detailed analysis of the host morphology, phylogeny and the genomic potential of the symbiont.

The binary nature of both symbioses, with one host and one symbiont make these systems ideal for advancing our understanding of host-symbiont interactions. The difference of association with closely related members of the Ca. Thiosymbion clade, as ectosymbionts in the case of stilbonematid nematodes and as endosymbionts in Astomonema, allow us to further explore the ecological niches and evolutionary adaptations of ecto- vs. endosymbionts.

Specificity of microbial symbioses can drive patterns of diversity at higher levels

▸ MELISSA MCCORMICK

Academic Affiliation:
Smithsonian Environmental Research Center, USA

ABSTRACT

Symbiotic associations, such as mycorrhizae, are critical, but often cryptic, drivers of biodiversity patterns. Because they are ubiquitous and key to acquiring nutrients, such symbioses are expected to drive patterns of species distribution, rarity, and evolution. Orchids are the most diverse plant group on Earth, and all rely on associations with mycorrhizal fungi to grow. The Republic of Palau is home to ~100 orchid species, at least 30 of which are endemic. Leveraging the new Palau ForestGeo plot, we compared the specificity of mycorrhizal associations in widespread (on many islands beyond Palau) and endemic orchids and in abundant and rare (within Palau) orchids. We also compared orchid abundance to the distribution of their mycorrhizal fungi in substrates. We found that endemic orchids had mostly evolved to associate with specific fungi, while widespread orchids associated with diverse fungi. Abundant and rare orchids had similar levels of mycorrhizal specificity, but abundant orchids associated with fungi that were common, while rare orchids were those that associated with uncommon fungi. Combined with our work on eastern US orchids, this points to a strong role for symbiotic associations in governing plant distribution, abundance, and population ecology.

Climate Homeostasis Arising From Plant-Microbe Interactions

▸ **PAT MEGONIGAL**

Academic Affiliation:
Smithsonian Environmental Research Center, USA

ABSTRACT

Plant sinks and microbial sources dominate the greenhouse gas budget of Earth's atmosphere and can moderate or exacerbate human-caused climate perturbations. I will discuss examples of plant-microbe interactions that tend to stabilize the greenhouse gas balance of the atmosphere such that any change in the amount of carbon dioxide removed by plants is at least partially compensated by microbes that return the carbon as carbon dioxide or methane. These interactions are driven the stoichiometry of living biomass and reflect the fact that plants and microbes are dependent on one another for metabolic energy, nutrients, and other resources. The net effects of these interactions are homeostatic feedbacks that tend to stabilize climate.

400 Million Years of Symbiosis: Ecology and Evolution of the Ancient Partnerships between Marine Lucinid Clams and Sulfur-Oxidizing

▸ JILLIAN PETERSEN

Academic Affiliation:
University of Vienna

ABSTRACT

Marine lucinid clams are thought to have lived in symbiosis with chemosynthetic, sulfur-oxidizing bacteria since the Silurian, before the age of the dinosaurs. These symbiotic partners interact intimately, with a massive population of symbiotic bacteria inhabiting the animal's gill cells. They also interact intimately with their surrounding environments; lucinids and their bacterial symbionts can promote the growth of endangered seagrasses, and contribute to the productivity of commercial fisheries. We use a suite of methods from isotope tracer incubations to molecular analyses of holobiont gene expression to reveal how animal-microbe interactions underpin ecosystem health, and to understand the function and evolution of these interactions in their natural environmental context.

The effects of phylogeny, habitat and adult diet on the milk microbiome”

▸ MICHAEL L. POWER

Academic Affiliation:
Smithsonian Conservation Biology Institute, USA

ABSTRACT

Lactation is an ancient, fundamental adaptation of the mammalian lineage that provides mothers with a biochemical signaling mechanism through which they affect the growth and development of their offspring. Although the nutritional importance of milk is well established, milk provides more than food. Milk contains immune factors, growth factors, hormones, and other bioactive molecules. Recent evidence suggests that the microorganisms in mother’s milk may be another guiding mechanism. The milk microbiome may serve to educate the developing infant’s immune system and be one mechanism by which the neonate’s immune system becomes tolerant of maternal commensal microbes. Previous research in primate species have indicated that milk microbial communities are distinguishable between species. The current research examines milks from more than 40 species across all four super orders of mammals to assess the effects of phylogeny and adult diet on a species’ milk microbiome. Preliminary data on eight species, seven terrestrial and the marine mammal Orcinus orca, indicate that marine and terrestrial species may have radically different milk microbiomes. I will be presenting the results from the complete sample in the study, focusing on comparing the 12 species of marine mammals included in the study to the terrestrial species.

Land use as a driver of change in microbial communities

▸ KRISTIN SALTONSTALL

Academic Affiliation:
Smithsonian Tropical Research Institute, Panama

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, yet little is known about belowground processes and the role that individual microbes play in enhancing or arresting plant succession and conserving ecosystem services and biodiversity. Even less is known about how land use can impact microbial communities in the many streams, both permanent and ephemeral, that often intersect these landscapes. I will discuss ongoing projects looking at large scale patterns in belowground and aquatic microbial diversity across various land uses in the experimental watersheds of the STRI Agua Salud project. These results can form a baseline for future work looking at plant-soil interactions, microbial responses to landscape change, water quality, and the sustainable conservation of ecosystem services and biodiversity.

Seagrasses excrete sugars to their rhizosphere making them the sweet spots in the sea

▸ EMILIA MARGARET SOGIN

Academic Affiliation:
**Max Planck Institute for Marine Microbiology,
Bremen, Germany**

ABSTRACT

Seagrasses are one of the most efficient natural sinks of carbon dioxide (CO2) on Earth. Despite covering less than 0.1 % of coastal regions, they have the capacity to bury up to 10 % of marine organic matter and can bury the same amount of carbon 35 times faster than tropical rainforests. On land, the soil's ability to sequestrate carbon is intimately linked to microbial metabolism. Despite the growing attention to the link between plant production, microbial communities, and the carbon cycle in terrestrial ecosystems, these processes remain enigmatic in the sea. Here, we show that seagrasses excrete organic sugars, namely in the form of sucrose, into their rhizospheres. Surprisingly, the microbial communities living underneath meadows do not fully use this sugar stock in their metabolism. Instead, sucrose piles up in the sediments to mM concentrations underneath multiple types of seagrass meadows. Sediment incubation experiments show that microbial communities living underneath a meadow use sucrose at low metabolic rates. Our metagenomic analyses revealed that the distinct community of microorganisms occurring underneath meadows is limited in their ability to degrade simple sugars, which allows these compounds to persist in the environment over relatively long periods of time. Our findings reveal how seagrasses form blue carbon stocks despite the relatively small area they occupy. Unfortunately, anthropogenic disturbances are threatening the long-term persistence of seagrass meadows. Given that these sediments contain a large stock of sugars that heterotopic bacteria can degrade, it is even more important to protect these ecosystems from degradation.

The Smithsonian Marine Station at Fort Pierce

▸ BLAKE USHIJIMA

Academic Affiliation:
Smithsonian National Museum of Natural History, Fort Pierce Marine Station, USA

ABSTRACT

The Smithsonian Marine Station (SMS) is locate in Fort Pierce, FL and focuses on a wide array of research topics. Research ranges from benthic ecology, invertebrate development, coral physiology, natural products chemistry, marine disease ecology, and microbial pathogenesis. The infrastructure of the SMS is equipped to handle experiments with live specimens, various wet labs, flow-through systems, ocean seawater reservoirs, near and off-shore vessels, and aquarium systems. However, the SMS has the capabilities to handle more laboratory-based work with a chemistry, histology, molecular biology, and microbiology laboratory along with advanced equipment such as a flow cytometer and confocal microscope. Microbiome research as the SMS delves into a variety of different topics, which includes the investigations of fouling biofilms, algae phylogeny, microbes associated with coral recruitment, the bacterial pathogens associated with a coral disease outbreak, and microbiome manipulation (probiotics) to treat coral diseases.

The pathogenesis of stony coral tissue loss disease and the development of probiotic treatments

▸ **BLAKE USHIJIMA**

Academic Affiliation:
Smithsonian National Museum of Natural History, Fort Pierce Marine Station, USA

ABSTRACT

An outbreak of stony coral tissue loss disease (SCTLD) is currently devastating the reefs in Florida and parts of the Caribbean. First observed in 2014 around Miami-Dade County, SCTLD has spread through the Florida Reef Tract, the Yucatán Peninsula, Jamaica, and the U.S. Virgin Islands. At least 20 different coral species are affected, which results in tissue loss and mortality of the entire coral colony. Disease transmission can occur between different coral species, which occurs through the water column. Pathogenic bacteria are important for disease progression, but the identity of the etiological agents is unknown. Currently, antibiotics or chlorine powder embedded in marine pastes are the main treatments for SCTLD, however, these do not provide lasting protection to colonies or cannot be used for healthy colonies. Therefore, beneficial bacteria (probiotics) isolated from disease-resistant coral colonies are being tested as an alternative treatment. A library of over 1,200 isolates displaying antibacterial activity have been cultured from healthy corals. One of these isolates, McH1-7, was able to stop or slow disease progression in 75% of diseased fragments exposed to the probiotic (n=16). However, McH1-7 was able to completely prevent disease transmission when healthy fragments were pre-treated with this probiotic prior to exposure to SCTLD (n=12). McH1-7 was discovered to produce the antibiotic korormicin, which is specific to Gram-negative marine bacteria, as well as the antimicrobials marinocine and tetrabromopyrrole. Currently, there are additional potential probiotics that are being tested along with combinational treatments with multiple strains. Additionally, field trials, with McH1-7 acting as the prototype strain, are being planned to refine deployment of probiotic treatments on Florida corals.

Avian gut microbiomes and host health

▸ **ELIN VIDEVALL**

Academic Affiliation:
Center for Conservation Genomics, Smithsonian Conservation Biology Institute, USA

ABSTRACT

The gut microbiomes of avian hosts have been shown to substantially vary between species and across ecological contexts. This pattern is partly due to differences in host phylogeny and diet, though different studies are using different methods to measure the gut microbiota of birds which will influence the results. My talk will touch upon on aspects we have learned from studying avian gut microbiomes and how birds can help us better understand how microbes may influence vertebrate host fitness and health.

The useful context provided by Terrestrial Census Plots, Log Term Monitoring of Plant populations, and water and fertilizer manipulation plots

▸ JOE WRIGHT

Academic Affiliation:
Smithsonian Tropical Research Institute, Panama

ABSTRACT

One of the distinguishing characteristics of the Smithsonian Tropical Research Institute in Panama is the commitment to and continued support of long term (decades) collection of a variety of types of data that relate to tropical forest species composition, function, and dynamics. In addition to a 50-hectare plot on BCI where all individual woody plants above 1 Cm dbh have been tagged, located and repeatedly censused, we have access to similar information for seed rain, seedling establishment and long-term survival. We have established plots where plant nutrients of known fundamental importance (e.g., N, P, K) have been experimentally manipulated, and the effects of those manipulations can be assessed on plant functions. We possess in depth knowledge of the relative abundances, geographical distributions, and traits of the flora (life histories, physiological properties such as photosynthesis and water relationships, defense syndromes, and, increasingly, secondary chemistry). We are now in a position to add detailed knowledge of the microbial

Eastern Pacific

Snapping shrimps. Photos by Arthur Anker

Caribbean

Snapping shrimps. Photos by Arthur Anker

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