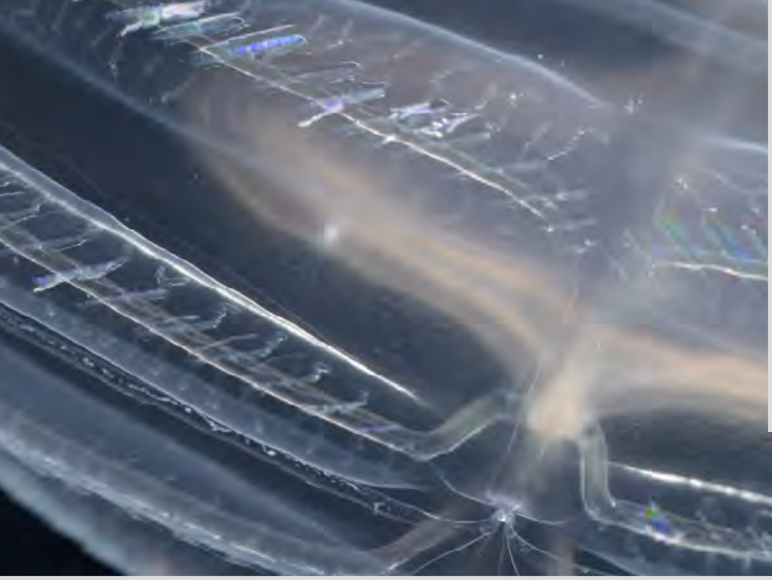
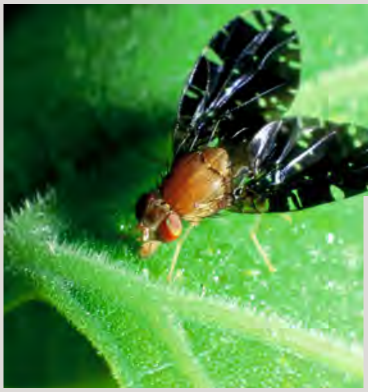
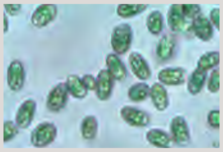
Dimensions of Biodiversity

NATIONAL SCIENCE FOUNDATION







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2010-2015 PROJECTS

Introduction 4
Project Abstracts 2015 8
Project Updates 2014 30
Project Updates 2013 42
Project Updates 2012 56
Project Updates 2011 72
Project Updates 2010 88

IMAGE CREDIT

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FIELD SITES

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- Dominican Republic
- Ecuador
- Finland
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- French Guiana
- French Polynesia
- Germany
- Iceland
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- Madagascar
- Malaysia
- Mexico
- Norway
- Palau
- Panama
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- South Africa
- Suriname
- Spain
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- Switzerland
- Tahiti
- Taiwan
- Thailand
- Trinidad
- United States
- United Kingdom
- Venezuela
- Labrador Sea
- North Atlantic Ocean
- North Pacific Ocean

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INTERNATIONAL PARTNERS

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- Brazil (FAPESP)

ACKNOWLEDGMENTS

Many NSF staff members, too numerous to mention individually, assisted in the development and implementation of the Dimensions of Biodiversity competitions that resulted in the projects described herein. We thank and congratulate the Dimensions of Biodiversity investigators for their creativity and achievements in the research and coordination activities that these projects represent.

We thank Mina Ta and Matthew Pepper for their graphic design contribution to the abstract booklet. Finally we are grateful to AAAS Science and Technology Policy Fellows Drs. Sara Chun, Sean M. Watts, Karen Alroy, and Rachel S. Meyer who were most helpful in the strategic planning for the Dimensions of Biodiversity program and the production of this abstract booklet.

About the Program

The Dimensions of Biodiversity program is now in its sixth year of research support to characterize the least-well-known aspects of the diversity of life on Earth. The National Science Foundation (NSF) funded 10 new projects in fiscal year 2015 bringing the total number of funded projects to 77.

The majority of the planet's biological diversity has yet to be explored. With estimates hovering around 12 million existing global species, and with only about 15% of those described to date, there is a bounty of exciting discovery to be made that can have major impacts on human wellbeing, technology, food security, and the health of planet Earth.

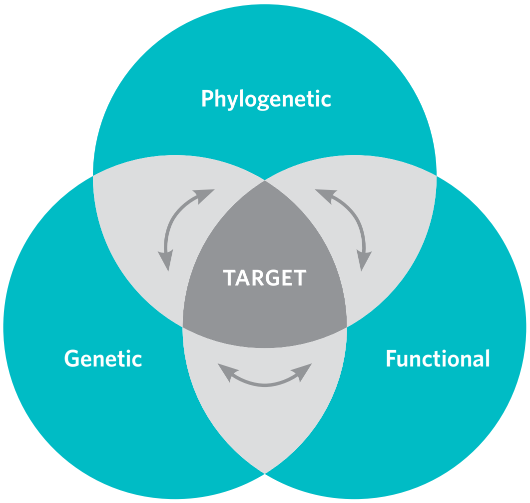
Beyond taxonomic investigation of the planet's species, **genetic** diversity within even a single species can be vast. The tremendous variation among domestic dog breeds illustrates this: genetic diversity of populations can express major differences in appearance, behavior, lifespan, and metabolic physiological adaptations to radically different environments. The Dimensions of Biodiversity program is a platform for exploration of species and population-level diversity, recognizing that genetic diversity are best understood in a **phylogenetic** context to reveal how biodiversity is shaped over time. For instance, researchers using phylogeny can ask: *Why* have some species endured time while others did not? *What* interactions, conditions, or events provided opportunities for diversification? And of peak interest is *how* do genetic distances that separate species in phylogeny relate to the different roles, appearances, life histories, and behaviors we observe? Despite centuries of study, we still have much to learn about the origin, maintenance, and function of diversity.

The **functional** roles of all these aspects of diversity are hardly understood. Dimensions researchers are making the connections from genetic diversity to gene function, and from

> *This year's Dimensions of Biodiversity investigators join an international and multidisciplinary network of scientists who, through cutting-edge and integrative approaches, are transforming our understanding of biodiversity.*
>
> **James Olds**
> Assistant Director
> NSF Biological Sciences Directorate

STREAMS OF ACTIVITY	**2020 GOALS**
Research	An integrated understanding of the key but unknown dimensions of biodiversity on Earth
Cyberinfrastructure	Informatics and infrastructure that support accessible, interoperable information capability for Dimensions of Biodiversity
Collections	Digitization of collections and enhanced physical infrastructure to link to cyberinfrastructure and leverage the enormous investments of the past
Workforce	A diverse, interdisciplinary, globally-engaged, scientific workforce capable of transforming and communicating our understanding of biodiversity on Earth
Synthesis	Scientific analyses and syntheses that generate and disseminate useful information for scientists, educators and decision makers

APPROACH → Planning & partnering → Base lining & synchronizing → Assessing progress → Aligning investments with emerging priorities



> *Understanding the diversity of life on land and in the sea is critical as our environment changes. This year's Dimensions of Biodiversity projects include important but poorly known branches of animals and microorganisms in understudied regions of the oceans.*
>
> **Roger Wakimoto**
> Assistant Director
> NSF Geosciences Directorate

the expression of traits to their effects on our environment. Many are assessing the impacts of diversity on ecosystems over time. And many are pioneering studies that help close the loop: what impact does the feedback from those environmental functions have on species and communities? The projects supported through the Dimensions of Biodiversity program have applied *creative integration* of phylogenetic, genetic, and functional studies to ask grand questions about life on Earth that single-discipline studies cannot approach.

Addressing the substantial knowledge gaps in our understanding of biodiversity requires new thinking and a *coordinated* effort among several sub-disciplines of biology. The Dimensions of Biodiversity program is actively developing the workforce and partnerships necessary for the unique human- and cyber-infrastructure challenges of an *interdisciplinary network* of researchers. Dimensions previously partnered with NASA to fund projects that use remote sensing technologies to expand biodiversity investigations across broad spatial and temporal scales. Current international partnerships with the National Natural Science Foundation of China (NSFC) and The São Paulo Research Foundation (FAPESP) support the exchange of students and scientists, joint research projects, and university partnerships. Through these developments and intellectual partnerships, this 10-year Dimensions of Biodiversity program is redefining the way we understand the evolutionary and ecological significance of biodiversity in today's changing environment, and in the deep geologic past.

	PARTNERS	PROJECTS	OTHER NSF	GEO/OCE SHIP COSTS	GEO/OCE SCIENCE	BIO	NASA (N)	US TOTAL	CHINA (C)	BRAZIL (B)
FY 2010		16		$2.9M	$9.3M	$18.9M		$31.1M	¥750k	
FY 2011		12	$6.5M	$1.5M	$2.5M	$17.5M		$28.0M	¥610k	
FY 2012	C, B, N	14	$3.2M	$168K	$2M	$22.8M	$720k	$29M	¥6M	R$2.8M
FY 2013	C, B, N	13			$1M	$21.7M	$2.5M	$25.2M	¥3M	R$2.7M
FY 2014	C, B	12			$1M	$22.5M		$23.5M	¥3M	R$3.1M
FY 2015	C, B	10		$3.6M	$2.5M	$17.7M		$23.8M	¥3M	
FY 2016	C, B								Up to ¥3M	Up to $2M

Dimensions of Biodiversity
Broader Impacts

CITIZEN SCIENCE

Through dimensions projects are connected with...

- Taxonomic Thesaurus
- Soil Experimental Treatments
- Biodiversity Gradients
- New Image Analysis Techniques
- Remote Sensing
- Herbaria
- Fungal Ecologists
- Climate Gradients
- Vascular Plants
- Terrestrial Mammals
- R Programming
- Intertidal Zone
- Symbiotic Organisms
- Carbon Monitoring
- Early Career Scientists
- Decision Makers
- Environmental Engineering

DATABASE CURATION

Through dimensions projects are connected with...

- Undergraduate Research
- Single Cell Genomics
- Flowering Plants
- Climate Change Scenarios
- Arabian Sea
- Soil Organic Matter
- Oxygen Minimum Zone
- Arthropod Diversity
- Adaptive Radiation
- Coral Reefs
- Extreme Weather Events
- Extinction Risk
- The New York Botanical Garden
- Deep Subsurface
- Barro Colorado Island
- Parallel Sequencing

UNDERGRADUATE AND GRADUATE EDUCATION

Through dimensions projects are connected with...

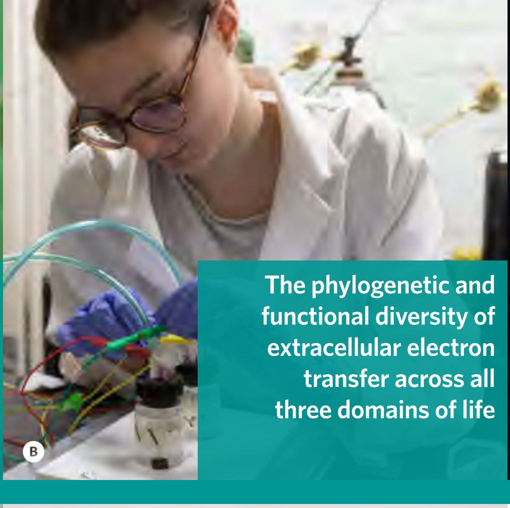
- Nutrient Ratios
- Plant Pathogens
- Oxygen Minimum Zone
- Herbaria
- Isotope Ratios
- Copepods
- Genomics
- Dry Valleys
- Subtropical Indian Ocean
- Deep Shale
- Phytoplankton Diversity
- Microbiome
- Extinction Risk
- Science Festivals

K-12 EDUCATION

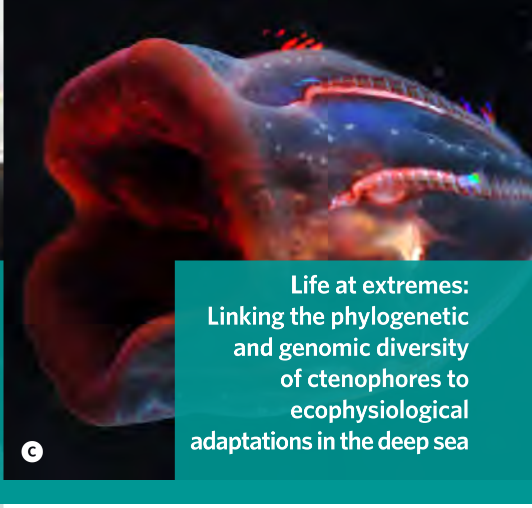
Through dimensions projects are connected with...

- Community Engagement
- Color Pattern Divergence
- Avian malaria
- Nitrogen Cycling
- Elevation ranges
- Coastal Ecosystems
- Microbial Sciences
- Trophic Interactions
- Drought Tolerance
- Adaptive Radiation
- Weather Station Data
- Plant Mating Systems
- Soil Organic Matter
- Wild Nightshades
- Genetic Architecture
- The Pacific Northwest

Diversification dynamics of multitrophic interactions in tropical communities

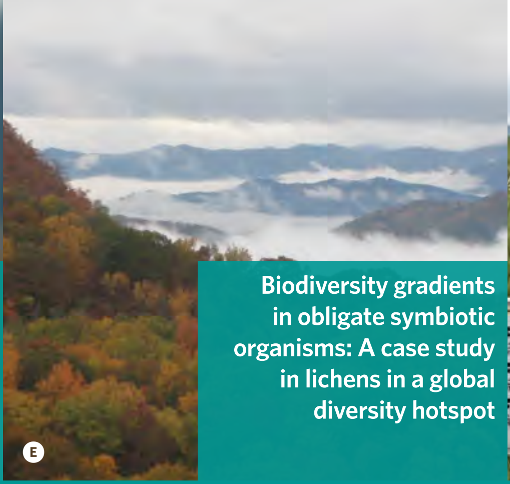


The phylogenetic and functional diversity of extracellular electron transfer across all three domains of life



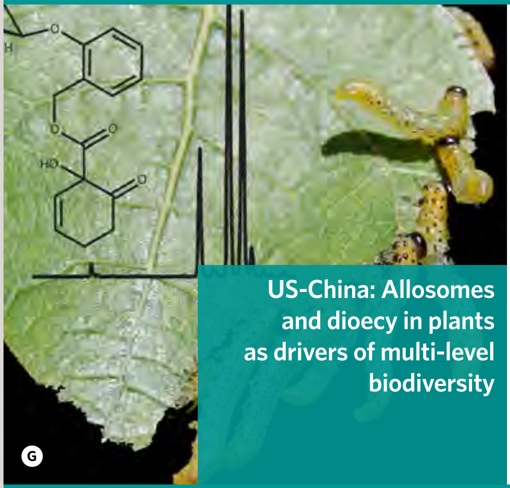
Life at extremes: Linking the phylogenetic and genomic diversity of ctenophores to ecophysiological adaptations in the deep sea

The evolution of pollination syndrome diversity in *Penstemon*

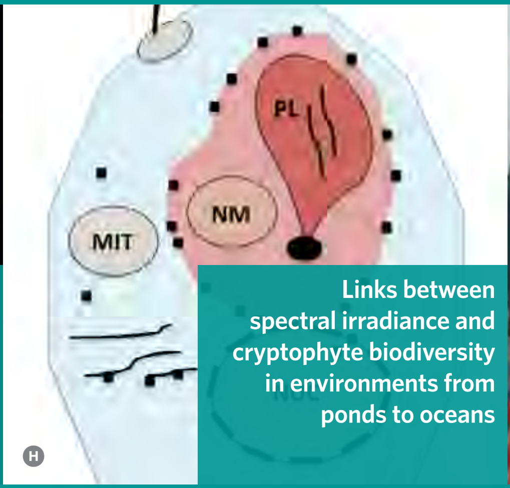


Biodiversity gradients in obligate symbiotic organisms: A case study in lichens in a global diversity hotspot

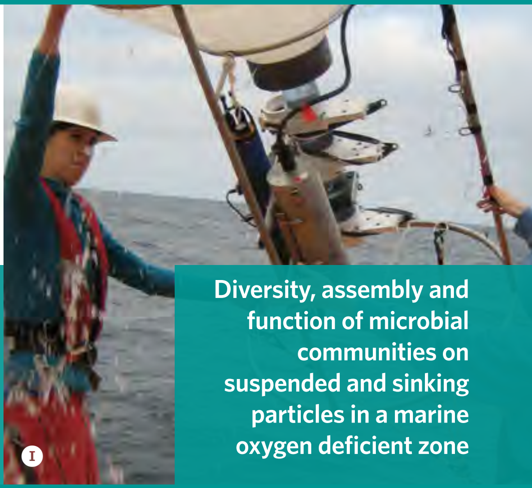
Community genomic drivers of moss microbiome assembly and function in rapidly changing Alaskan ecosystems



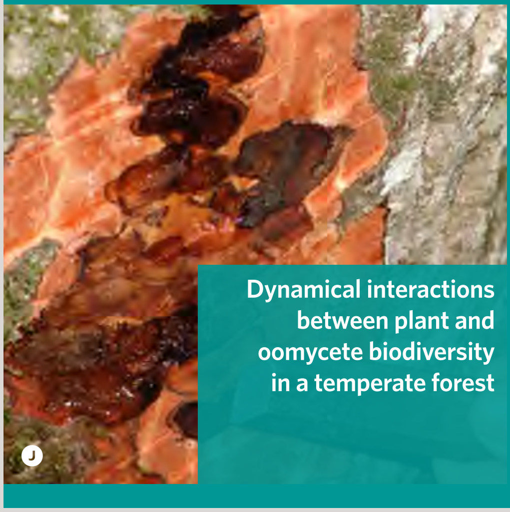
US-China: Allosomes and dioecy in plants as drivers of multi-level biodiversity



Links between spectral irradiance and cryptophyte biodiversity in environments from ponds to oceans



Diversity, assembly and function of microbial communities on suspended and sinking particles in a marine oxygen deficient zone



Dynamical interactions between plant and oomycete biodiversity in a temperate forest

2015
abstracts

IMAGE CREDIT

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Proj. 1 / 10

Diversification dynamics of multitrophic interactions in tropical communities

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This project focuses on a species-rich tropical community of plants (Cucurbitaceae), tropical plant-feeding insects, and their predators (parasitic wasps), and tests the hypothesis that highly specific lethal interactions between herbivores and predators may explain patterns of diversity and diversification.

In the biodiverse tropics, many ecologically important species interactions remain poorly understood, such as bi-directional lethal interactions between predator and prey. This project has a goal of solving the basis of the patterns of diversity seen in three realms: the predators, their herbivore prey, and the plants the prey feed on. The team focuses on recently described fruit flies in the genus *Blepharoneura* as the herbivores, which are parasitized by a diverse group of braconid wasp (*Bellopius)* that express extraordinary specificity. Each wasp species parasitizes and kills a specific fly species. In turn, many of the different fruit fly species each feed on a different single species of plant within the pumpkin family (Cucurbitaceae), although some species can escape to other host plants. These interacting phenomena may drive the evolution of "cryptic species" (different species that look alike) and drive diversification of microbes that provide the virulence mechanism that kills or defends. A holistic understanding of these complex ecological and biogeographic patterns can illuminate forces that generate and maintain tropical diversity where species-specific interactions are rampant.

The team predicts that in insect lineages with weak virulence mechanisms (highly vulnerable to parasitoids or to hosts' defenses), selection favors host-shifts to "enemy-free-space", that is, shifts to different host plants or host insects. Then, if the parasitic wasp moves to a different Cucurbitaceae species, the wasp is likely to encounter a new vulnerable fly that has recently shifted to the plant. Therefore, the highly vulnerable fly-lineages are predicted to show very high rates of recent diversification. Condon and colleagues predict strongly defensive, resistant wasps or flies would not shift host plants as much, and would have lower diversification rates. A large sample set is required to better be able to detect emerging patterns: the team has over 8000 reared fly specimens, 15% of which have been parasitized, yielding at least 100 fly species and 40 parasitic wasp species.The team will increase their sample of specimens with planned collection trips to Colombia, Ecuador, French Guiana, Panama, Peru, and Suriname.

This project will use methods designed to detect and analyze mechanisms associated with "hard selection" (life or death), and will reveal fine-scale patterns of genetic divergence that are not associated with selection using multiple high-resolution population genetic approaches. Condon and colleagues will uncover ancient patterns of divergence in order to grasp how evolutionary rates change as function changes, and will identify mechanisms of host-detection and defense (functional diversity) through lab and field experiments that quantify immune responses and the ability of third-party mediated defense (e.g., the microbiota) to act. Both phylogenies and field experiments will be combined to test hypotheses about mechanisms generating and controlling diversity in plants, flies, wasps and microbes on ancient, recent, and contemporary timescales.

Panoramic view of Brownsberg Nature Park, Suriname, on the Guianan Shield, an area rich in species that occur nowhere else in the world.

CREDIT: MATTHEW L. LEWIS

Lethal parasitic wasps (called parasitoids) search for immature flies hidden within the flowers.

CREDIT: ILLUSTRATION BY TAINA LITWAK, SYSTEMATIC ENTOMOLOGY LABORATORY, USDA

Parasitic wasp on a male flower of *Gurania costaricensis*, which is host to at least two species of *Blepharoneura.*

CREDIT: MATTHEW L. LEWIS

Cornell College undergraduates and a Peruvian graduate student extract DNA and will analyze sequences to discover the diversity of insects reared from flowers collected in the tropics.

CREDIT: MARTY CONDON

Students visit the electron microscopy facility at the University of Georgia where the team is looking for microbes that may play a role in lethal interactions between wasps and flies.

CREDIT: MARTY CONDON

Clippers on long aluminum poles are used to harvest flowers of rainforest vines growing at least 12m above the forest floor.

CREDIT: MARTY CONDON

Unique among flies, *Blepharoneura* feed on plant surfaces where they may acquire microbes affecting diversification. The Condon lab has over 8000 fly specimens.

CREDIT: MARTY CONDON

Proj. 2 / 10

The phylogenetic and functional diversity of extracellular electron transfer across all three domains of life

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Life harnesses energy primarily through the transfer of electrons within cells. However, some microorganisms harness energy by passing electrons to the outside of the cell in a process called extracellular electron transfer (EET). This project seeks to identify and characterize the full diversity of EET microbes and the mechanisms they use to transfer energy.

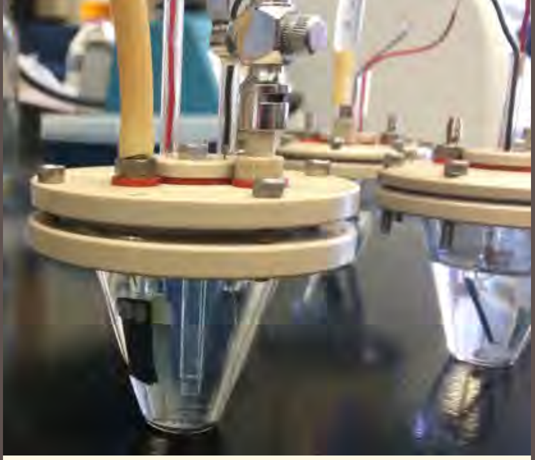
All living cells, from microorganisms to animal cells, primarily generate energy by passing electrons among chemical compounds brought into the cell, to make energy molecules for cellular maintenance and growth. However, microbes—bacteria, archaea and single celled eukaryotes—also have the capacity to extend their cellular physiology beyond the limits of their cell and use insoluble substrates for growth and reproduction in a process called extracellular electron transfer (EET). Learning of these microbes' capabilities has fundamentally changed our perceptions of cellular life, as EET employs electrical charge to extend the influence of cellular metabolism to beyond the cell membrane. While these microbes are potentially ubiquitous, and likely have a pronounced influence on global biogeochemical cycles as well as promising benefits to industrial energy production, our understanding of their diversity is in its infancy.

The overarching goal of this project is to comprehensively assess the genetic diversity and metabolic activity of microbes that use EET across all three domains of life (bacteria, archaea and eukarya) and investigate the roles these organisms play in the health of the biosphere. To achieve this, Girguis and colleagues will conduct the first broad, systematic assessment of microorganisms capable of EET in natural habitats and then use these results to identify 20 "representative" communities that will become the focus of genomic, transcriptomic, and biogeochemical analyses. They will characterize phylogenetic diversity via a 96-channel bioelectrochemical screening system that uses chambers to cultivate microbes across a range of temperatures from 2 °C to 50 °C. They will also learn the biophysical attributes of cultivated but uncharacterized microbes commonly found on electroactive surfaces. The researchers will characterize the metabolic rates of these EET microbes and make predictions about where such communities might occur in natural and industrial settings. Ultimately, this project will reveal the extent of organisms capable of EET within the Tree of Life, the materials used for the process, and the importance of these organisms in the global ecosystem. Another aim of the project is focused on developing a community-accessible robust data archives. These efforts will provide, for the first time, a comprehensive dataset linking phylogenetic data (16S, 18S) with functional potential (genomics), physiological poise (transcriptomics) and metabolic activity (geochemical measurements) that has many applications to our field and beyond.

As part of this research effort, Girguis and colleagues will develop an interactive museum exhibit that documents and describes EET and other microbes, a new educational curriculum that engages middle school students in the research, and a pedagogical training and lab exchange program that affords students and postdocs an opportunity to conduct interdisciplinary research. These programs will be coordinated by the Harvard Museum of Natural History, and will incorporate external evaluations to assess the extent to which these programs achieve their learning goals.

Harvard undergraduates building microbial fuel cells, devices that can foster the growth of electroactive microbes (i.e. microbes that are capable of extracellular electron transfer).

CREDIT: PETER GIRGUIS



Many bioreactors used for growing microorganisms with electrodes.

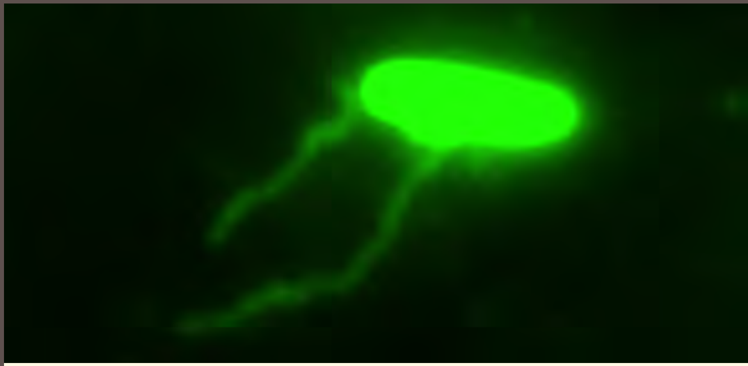
CREDIT: DANIEL BOND

USC undergraduate student, Sarah French, testing extracellular electron transfer of microbes isolated from Death Valley, CA.

CREDIT: A. B. HULFACHOR

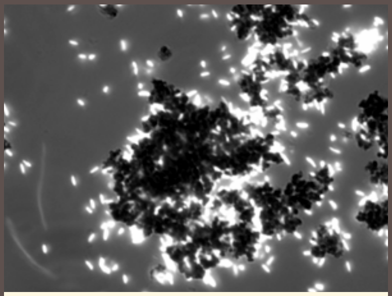
Microbes capable of producing electricity are ubiquitous in the seafloor, and scientists have been developing systems that harness that electricity to power sensors.

CREDIT: MONTEREY BAY AQUARIUM RESEARCH INSTITUTE (MBARI) AND PETER GIRGUIS



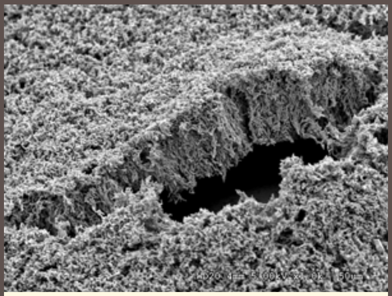
The metal-reducing bacterium, *Shewanella oneidensis*, produces bacterial nanowires (shown here) that mediate extracellular electron transfer to external surfaces.

CREDIT: MOHAMED EL-NAGGAR



The bacterium *Shewanella oneidensis*, labeled with green fluorescent protein, grown using an insoluble mineral (manganese oxide) as an electron acceptor.

CREDIT: ORIANNA BRETSCHGER



The bacterium *Geobacter sulfurreducens* grown using an electrode — a process that requires extracellular electron transfer.

CREDIT: ORIANNA BRETSCHGER

Bacteria, archaea and single cell eukaryotes are extremely important to industrial applications including wastewater treatment. The picture shows a large-scale microbial fuel cell installation treating swine waste at the Escondido high school agriculture center.

CREDIT: ORIANNA BRETSCHGER

Proj. 3 / 10

Life at extremes: Linking the phylogenetic and genomic diversity of ctenophores to ecophysiological adaptations in the deep sea

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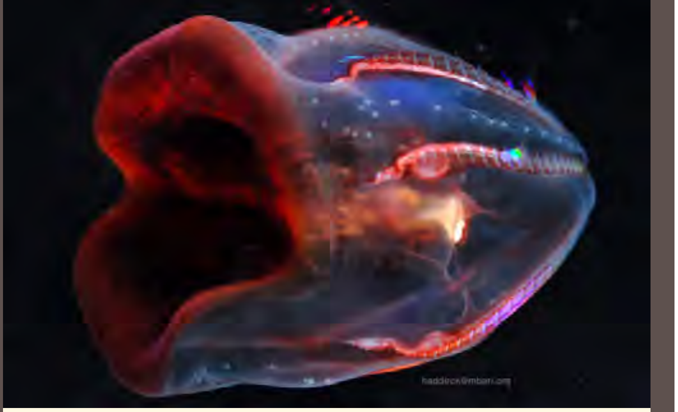
DEEPC: Diversity, Evolution, and EcoPhysiology of Ctenophores. This project is investigating the genomic and physiological diversity that allow comb jellies to survive in the deep sea.

More than 90 percent of the inhabitable space on Earth is in the ocean below 200 meters, making it by far the largest habitat on the planet, yet life there is largely a mystery to science. Over evolutionary time, many marine animal lineages have made extraordinary habitat transitions to and from the deep sea. This habitat is tremendously different from the shallow ocean in many respects, including light, temperature, stability, food availability, pH, oxygen content, and hydrostatic pressure. Despite the exceptional adaptive challenges required to transition between deep and shallow marine environments, relatively little is understood about the genetic and physiological changes that accompany these extraordinary evolutionary events. This project aims to address key questions about these changes and transform our understanding of the forces that shape biodiversity in our oceans.

The fundamental goal of this project is to understand evolution and diversification in the phylum Ctenophora (phylogenetic diversity) using cutting edge molecular analyses (genetic diversity) and the deep-sea habitat as the generating force of novel adaptations (functional diversity). Many thousand specimens will be collected using advanced methods (blue-water SCUBA in surface waters and remotely operated vehicles in the deep sea), in order to generate complementary physiological and genomic data across the full phylogenetic and functional diversity of ctenophores. The group will examine the exact genetic events that underlie physiological tolerances and adaptations to the high hydrostatic pressures in the deep sea.

This project will sample the diversity of the phylum Ctenophora across a range of habitats from shallow tropical waters to the temperate bathypelagic zone; measure physiological capabilities and sequence transcriptomes; screen transcriptomes with novel algorithms to identify genes involved in depth adaptation and to recognize convergent signals in a comparative phylogenetic framework; express proteins and characterize them in vitro to confirm how their phenotypic diversity arises from the genetic diversity. For example, some cnetophores from boreal waters can have faster axonal responses and swimming capability than many tropical species; this project will determine the molecular pathways related to these special physiological traits.

Some of the primary merits include the following: training the next generation of students to initiate a comprehensive view of the many kinds of diversity; revealing the genetic mechanisms for important evolutionary events, including routes for deep-sea adaptation, diversification in the face of extreme constraints, and even the origins of animal life; developing and distributing novel tools and methods that will be transferable to integrated studies of other habitats, including other aquatic habitats and terrestrial systems; populating public databases with metabolic and genomic data from difficult-to-access organisms, allowing others to perform meta-analyses and test their own hypotheses related to deep-sea and planktonic diversity; Producing the first synthesis of the overall taxonomic diversity and phylogenetic relationships of this important group of animals.



Deep sea ctenophore *Bathyctena chuni*, showing its large mouth and the dark red pigmentation typical of deep-sea species.

CREDIT: STEVEN HADDOCK

Detail of shallow-water ctenophore (comb jelly) *Ocyropsis maculate* showing the characteristic comb rows used for locomotion, and the sensing organ used for balancing.

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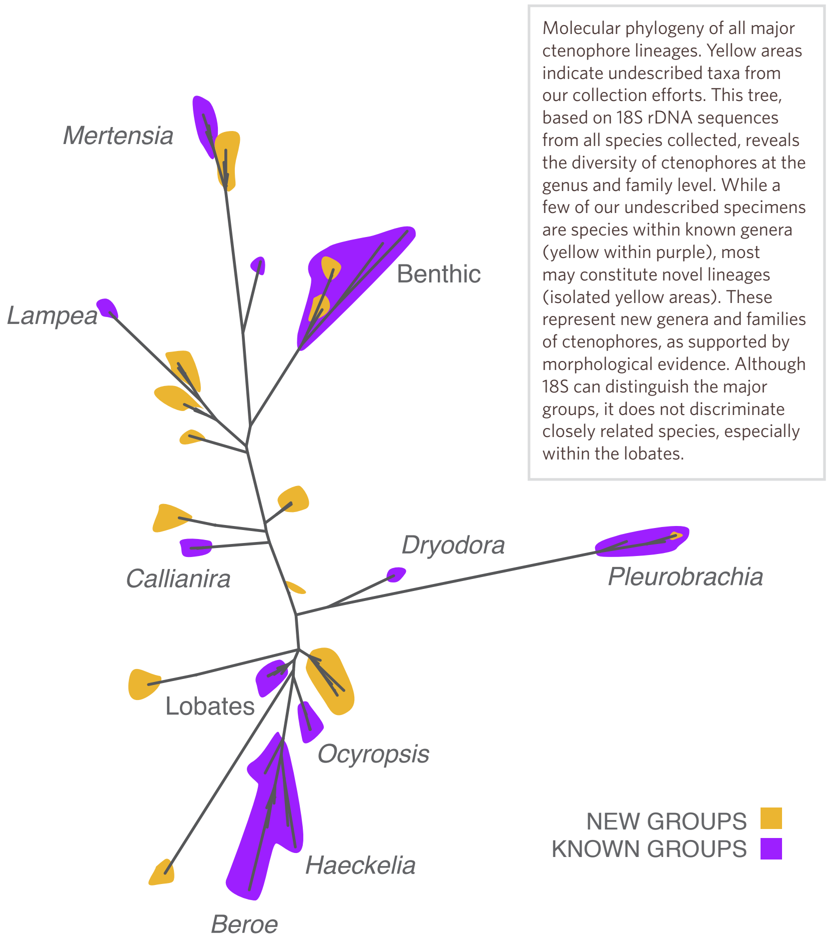

Molecular phylogeny of all major ctenophore lineages. Yellow areas indicate undescribed taxa from our collection efforts. This tree, based on 18S rDNA sequences from all species collected, reveals the diversity of ctenophores at the genus and family level. While a few of our undescribed specimens are species within known genera (yellow within purple), most may constitute novel lineages (isolated yellow areas). These represent new genera and families of ctenophores, as supported by morphological evidence. Although 18S can distinguish the major groups, it does not discriminate closely related species, especially within the lobates.

Project logo for Diversity, Evolution and Eco-Physiology of Ctenophores.

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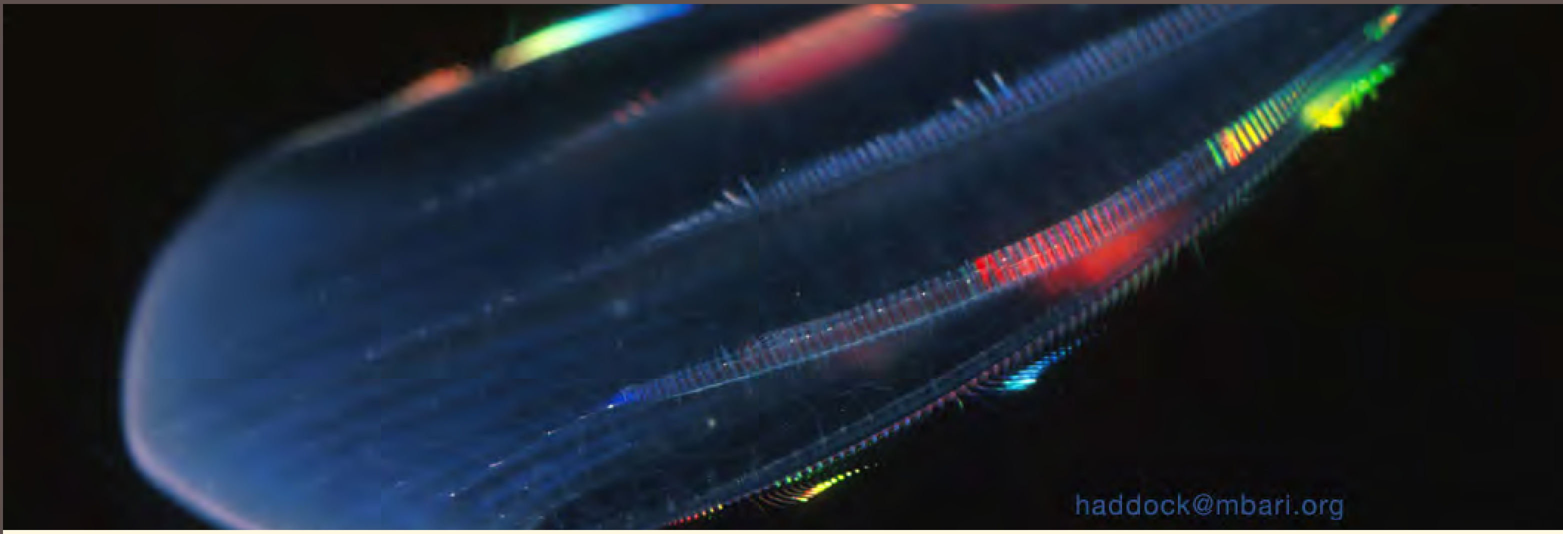

Ctenophore *Beroe forskalii* with the rainbows caused by diffraction of white light through its many comb plates (swimming paddles).

CREDIT: STEVEN HADDOCK

Proj. 4 / 10

The evolution of pollination syndrome diversity in *Penstemon*

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Floral diversity in terrestrial communities often reflects divergent pollination modes (e.g. bees, hummingbirds, butterflies, wind). This research examines ecological and genetic processes that may shape patterns of pollination syndrome diversity in the largest flowering plant genus endemic to North America.

Flowers exhibit a wide array of trait diversity, including color, morphology, nectar and scent production. Within this diversity, however, are organizing principles. Many species exhibit specific pollination syndromes – combinations of floral traits typically associated with pollination by specific agents (e.g. bees, hummingbirds, butterflies, bats, generalist insects, or wind). Evolutionary transitions among these syndromes have occurred frequently during the diversification of flowering plants, and in any contemporary terrestrial community, floral diversity can be measured as the number and relative abundance of different pollination syndromes.

Understanding this floral diversity requires integrated knowledge of the ecological and genetic processes that influence evolutionary shifts among pollination syndromes. For example, do functional interactions between flowers and pollinators favor the evolution of certain pollination syndromes from a particular starting point over others? Do the types of genetic mutations that underlie certain pollination syndrome floral traits constrain the subsequent evolution of novel syndromes? To answer these sorts of questions, the research team will study pollination syndrome diversification in *Penstemon* – the largest flowering plant genus endemic to North America containing over 280 species, with species adapted primarily to either bee or hummingbird pollination.

The research team will integrate field experiments with macroevolutionary modeling and state-of-the-art genomic methods to explore the processes that shape pollination syndrome evolution. The researchers will develop a phylogenetically-based model that predicts the expected equilibrium frequencies for bee and hummingbird pollination syndromes within *Penstemon*. This model will allow the researchers to determine if the expected equilibrium has been reached, and whether some shifts in pollination syndrome are more common than others. Their preliminary findings suggest that transitions from bee to hummingbird pollination are much more common in *Penstemon* than the reverse. The team will determine if evolutionary shifts from hummingbird to bee pollination are rare because of constraining functional interactions between pollinators and floral traits, or because the types of genetic mutations that underlie hummingbird adaptation constrain the subsequent evolution of bee adapted flowers. Ultimately, the evolutionary patterns and ecological/genetic processes identified through this research can be extended to better understand the forces that shape trait diversity across the tree of life.

Developing *Penstemon* as a model system will allow researchers to address ecological and evolutionary questions beyond those of floral trait evolution. This project will provide important tools for those interested in expanding *Penstemon* research; these include a clearer understanding of species relationships, sequenced genomes for two species, high-density genetic maps for those species, and protocols for studying gene function such as virus-induced gene silencing. This cross-disciplinary project will engage high school and college students at the interface of evolution, genetics, genomics, and ecology through independent projects pursued in the lab, in the field and in structured classroom settings.

Penstemon eatonii being visited by Anna's hummingbird in Pinal County, Arizona. *P. eatonii* displays the stereotypical hummingbird-adapted *Penstemon* floral type: red flowers that are long and narrow, producing copious amounts of dilute nectar.

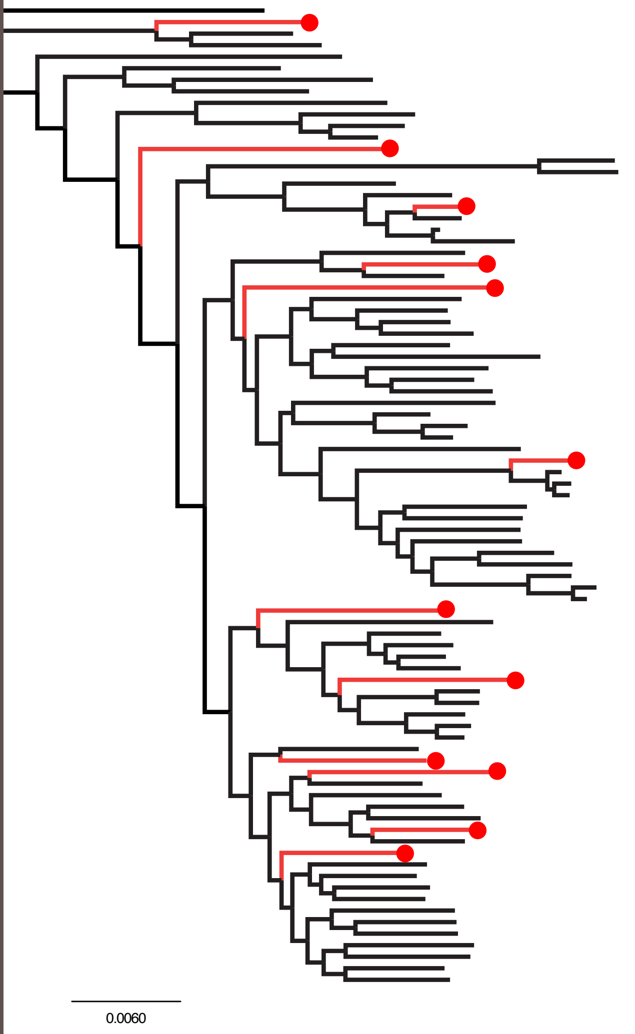
CREDIT: CAROLYN WESSINGER

Penstemon patens displays a typical bee-adapted *Penstemon* floral type: bluish-purple flowers that are wide enough to admit bee visitors.

CREDIT: CAROLYN WESSINGER

The center of *Penstemon* diversity is in the intermountain west of North America. *P. utahensis*, a hummingbird-adapted species, grows on the roadside in Clark County, NV.

CREDIT: CAROLYN WESSINGER



A preliminary maximum likelihood phylogeny of 85 *Penstemon* taxa representing 77 species based on reduced genomic data. Red dots indicate hummingbird pollination-adapted taxa, remaining taxa are primarily bee pollination-adapted. Shifts from bee to hummingbird adaptation are common, but reversals are not detected.

CREDIT: CAROLYN WESSINGER

Demonstration that virus-induced gene silencing works in *P. grandiflorus*, indicated by leaf photobleaching from knock-down of *PDS*. This technique will help characterize function of candidate genes underlying floral syndrome differences in *Penstemon*.

CREDIT: CAROLYN WESSINGER

Penstemon neomexicanus (left) and *P. barbatus* (right) are two closely related species adapted to pollination by bees and hummingbirds, respectively. The research team is contributing genetic and genomic resources for these species including genome sequences, mapping populations, and hybrid introgression lines.

CREDIT: CAROLYN WESSINGER

Proj. 5 / 10

Biodiversity gradients in obligate symbiotic organisms: A case study in lichens in a global diversity hotspot

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Diversity and distributions of obligate symbiotic organisms: lichens as a model system for deconstructing biotic and abiotic factors that drive major patterns in macroecology and macroevolution.

Obligate symbioses are relationships between two or more species that depend entirely on each other for growth and survival. Such symbioses characterize some of the most common and ecologically important relationships on Earth, ranging from human gut bacteria and diseases, to corals and specialized plant-pollinator relationships. Many of these obligate symbioses are imperiled by unprecedented rates of environmental change and permanent biodiversity losses. This project aims to transform understanding of factors that impact diversity and distributions of obligate symbiotic biodiversity through investigation of lichens as a model system in a unique natural laboratory and global lichen diversity hotspot: the southern Appalachian Mountains, where the team will conduct large-scale field inventories. Lichens, symbionts of two or more algae (photobiont) and fungi (mycobiont), are hubs of trophic interactions, and can be considered microcosms actually hosting many more unique lineages of fungi, bacteria, and specialist invertebrates. This project will explore both biotic and abiotic drivers of biodiversity across multiple dimensions and will include metagenomic analyses of those microcosms.

Through field and genomic inventories of lichens in a biodiversity hotspot, this project will generate and investigate data from symbiotic biodiversity initiated from a single information source: a unique museum voucher. Across local, regional, and landscape scales, inventories will yield site-specific metrics for phylogenetic (including taxonomic) and functional diversity together with site-specific metrics for a mostly unexplored genetic dimension—potential of diversity—that quantifies the availability of compatible symbiont propagules in the environment. Studies have supported the distant travel of propagules in dust, making lichens an ideal system to study macroecological processes.

Analyses of these metrics in light of biotic and abiotic variables will enable assessment of factors that impact overall dimensions of biodiversity. These analyses will also permit understanding of interactions among dimensions, for example, whether phylogenetic, functional, and genetic dimensions are positively correlated and predicted by the same sets of variables, or in what contexts other types of correlations exist. Additionally, deconstructing constraints on individual partners of the symbiosis and quantifying feedbacks between/among them will make possible full analysis (i.e., including biotic constraints) of the factors that impact diversity and distribution of the symbiotic organism as a whole.

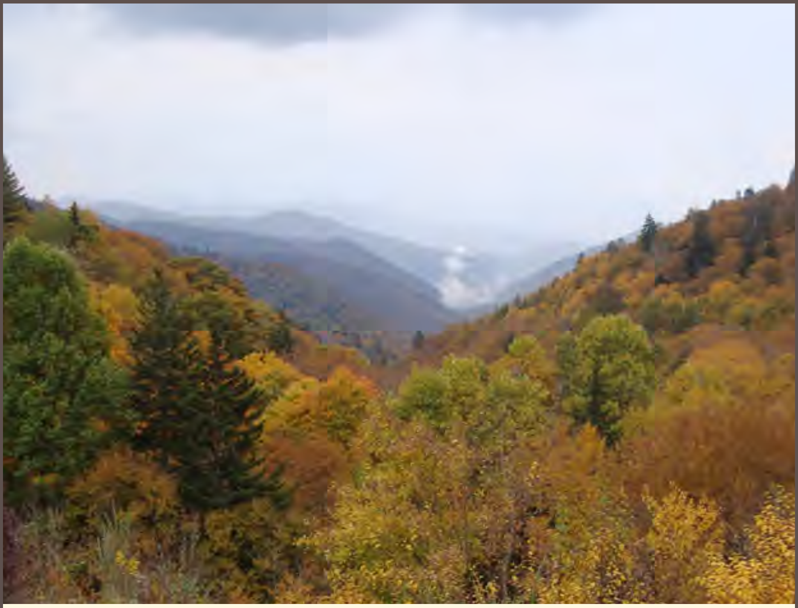
Broader impacts of this research will improve scientific literacy, expand awareness of symbiotic biodiversity, build capacity in U.S. lichenology, broaden collaborations between scientists and land managers, and establish new ‘big data’ resources for a diverse audience of researchers and educators. Finally, this project will advance conservation of an ecologically important group of understudied organisms in a premier biodiversity hotspot.

Lobaria pulmonaria: An ecologically important foliose lichen indicative of high quality habitats in eastern North America (Voucher Specimen: Erin Tripp 4994 [NY Herbarium]).

CREDIT: JAMES LENDEMER

Student researcher Heather Stone installs a forest experiment to trap lichen propagules, to document early stages of lichen colonization. Field supplies: cheese cloth, lab tape, and microscope slides soaked in various media to cultivate mycobiont and photobiont.

CREDIT: ERIN TRIPP



Great Smoky Mountains National Park contains more species of lichens than any other national park in the United States. Also the most visited national park in the country, the park staff faces a delicate balancing act between facilitating tourism and protecting the park's natural heritage by minimizing human impacts.

CREDIT: MOLLY STEVENS

Anaptychia palmulata: A foliose lichen of the southern Appalachian Mountains (Voucher Specimen: James Lendemer 33129 [NY Herbarium]).

CREDIT: ERIN TRIPP

James Lendemer, working in laboratory to identify field collections at the Southern Appalachian Highlands Learning Center (aka 'Purchase Knob'), Great Smoky Mountains National Park.

CREDIT: ERIN TRIPP

Early stages of lichen development: obligate symbiotic organisms often must successfully find partners in nature at a young stage.

CREDIT: VANESSA DÍAZ

The Appalachian Highlands Science Learning Center at Purchase Knob is a high altitude educational facility in the heart of the southern Appalachians. Each year, staff members Paul Super, Susan Sachs, and associated personnel host upwards of 5,000 visiting scholars, teachers, and volunteers with the common goal of expanding knowledge.

CREDIT: MOLLY STEVENS

Proj. 6 / 10

Community genomic drivers of moss microbiome assembly and function in rapidly changing Alaskan ecosystems

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This team plans to model the role of bryophyte genetic and phylogenetic variation in driving the assembly and function of their associated microbial community, and model the interactions between these dimensions of biodiversity that influence Arctic and boreal ecosystem processes.

Understanding ecological and evolutionary interactions between microbes and hosts are critical for predicting the response of ecosystem function to rapidly changing climate. This research tackles this problem using the nitrogen-fixing microbes associated with the closely related feather mosses *Hylocomium splendens* and P*leurozium schreberi*, two of the most widespread plant species in boreal forest and arctic tundra ecosystems. *H. splendens* and *P. schreberi* are key players in high-latitude carbon and nitrogen cycles because they associate with nitrogen-fixing microbes, providing most of the inputs of this limiting nutrient. The high northern latitudes are warming more rapidly than anywhere else on earth, making these biomes ideal for evaluating how climate change will impact the assembly and function of key ecosystems components.

The first aim of this research is to characterize how the diversity of microbes varies across moss species in order to estimate the degree of niche conservatism in moss-microbe associations. They will do this by measuring growth and testing fixation for 10 common moss species. The next phase will involve sampling along a 20 patches on a latitudinal gradient in Alaska in order to model genotype specific interactions between two keystone moss species, their microbiomes, photosynthetic rate, and biological nitrogen fixation, an ecosystem process that is a critical determinant of soil fertility and plant productivity. They will use an enclosed nitrogen isotope tracer test to estimate species-specific fixation rates, and analyze the microbial community of each sample as well as isolate moss DNA for genetic analysis (genotype-by-sequencing). After the tests, in the final phase, the results of this model will be tested using reciprocal transplants and warming experiments. These tests and surveys should resolve the roles of host phylogeny and environmental conditions in structuring communities, and elucidate how the different community compositions function.

Although it is clear that microbes are critical components of living systems at all levels of biological organization, the long-term role of the interdependencies between host genotype and host-associated microbes in the generation and maintenance of biodiversity are poorly understood. This work will associate microbiome assembly and function to host-plant genetic variants that themselves have dynamic responses to changing environmental conditions. This project will leverage the resources now developed for model system mosses and microbes and the environmentally well-characterized LTER sites to answer fundamental questions relevant to coupled carbon and nitrogen cycles in changing high latitude terrestrial ecosystems using predictive models followed by experimental model verification.

The project team is dedicated to broadening participation in science and will be focusing on recruiting undergraduates from underserved populations. They will be incorporating the results of the ongoing research into their courses for richer authentic research experiences for students. Videos will be made as part of the Florida Museum of Natural History’s Explore Research program, shared online and to secondary school teachers at a workshop. The PIs will also make themselves available to the public for questions, and will distribute their research and educational tools to their scientific societies.

Adam Payton prepares sequencing libraries to genotype mosses.

CREDIT: STUART MCDANIEL

Graduate students conducting field surveys on a manipulative experiment at the Eight Mile Lake site in Healy, Alaska, to understand how biogeochemical processes will be affected by future climate.

CREDIT: VERITY SALMON

Communities of *P. schreberi, H. splendens,* and *Polytrichum sp.*, along with associated lichens and vascular plants, cover large areas of the boreal forest understory.

CREDIT: MICHELLE MACK

A field technician at the Eight Mile Lake manipulative experiment places open-top chambers to warm the air around tundra vegetation.

CREDIT: VERITY SALMON

An undergraduate from NAU collects individual *P. schreberi* stems for genetic analysis near Fairbanks, Alaska.

CREDIT: SAMANTHA MILLER

Proj. 7 / 10

US-China: Allosomes and dioecy in plants as drivers of multi-level biodiversity

(CO-FUNDED WITH NSFC)

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This research aims to understand how sex-specific differences in poplars and willows influence chromosomal evolution and the biodiversity of their associated insect communities in the U.S. and China, where these plants often play a dominant role in ecosystems.

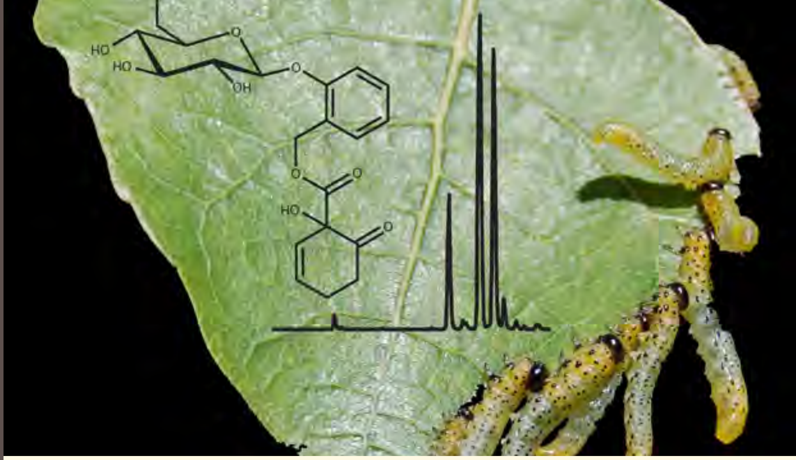
Only seven percent of plant species have separate male and female individuals (termed dioecy), and like animals, male and female plants may also exhibit differences in growth rates or the production of chemicals used to attract and/or deter insects. The goals of this research are to provide an integrated understanding of how the evolution of the genes controlling sex determination is influenced by the ecology of insect defense across the Salicaceae, a diverse family of plants that includes poplars (genus *Populus*) and willows (genus *Salix*). Poplars and willows are particularly well suited to addressing these questions because all species are dioecious, and the movement and characteristics of the genomic region controlling sex determination is quite dynamic. This team's studies will investigate how the sex determination region has been moving around the genome. Preliminary evidence suggests that clues may come from insects that eat these plants, and from the responses of male and female plants to those insects. They hypothesize that defense genes are beneficial to only one sex, so they migrate to genomic regions of sex determination and influence changes in the genomic locations of the sex determination region.

Their approach combines genomics tools and biodiversity sampling from the two main centers of poplar and willow biodiversity: China and the U.S. They will develop a robust phylogenetic model for the relationships among poplar and willow species, which will provide a historical framework for understanding transitions and evolution in the sex determination regions. Using novel genomic mapping techniques, the chromosomal locations of the sex determination regions will be determined for 16 new poplar and willow species to better estimate the rate at which these regions are evolving. Biodiversity of insects will be determined across genders and species, and correlated with defense and pollinator attraction chemistry. They will also be determining the genomic locations of the genes influencing defense and pollinator attractiveness, thereby identifying likely candidates influencing the evolution of sex determination. Finally, computational bioinformatic techniques will be developed to probe how these defense and attractiveness genes have influenced the past evolution of the sex determination regions.

This China-US collaboration will provide cross disciplinary and cross-cultural training opportunities for over 15 graduate students and 5 postdoctoral scholars, and the data will be incorporated into course exercises for teaching in the Chinese and US institutions. Dozens of undergraduates from diverse backgrounds will be provided training in genomics and functional ecology through direct contributions to data collection and analysis, or through access to the data for research immersion experiences. Finally, the team will lead K-12 teacher training workshops targeted at under-represented groups in rural Texas to encourage teaching of the foundational theories of biodiversity.

Poplars and willows are important components of ecosystems in both the US and China. Pictured is one of the northernmost populations of trees in North America at Ivishak Hot Springs in Alaska's Arctic National Wildlife Refuge. These small stands of trees support populations of large mammals and rare Arctic birds.

CREDIT: AMY BREEN



Sawfly larvae feeding on a Populus species leaf. The chemical structure represents salicortin, one of the most common defensive compounds in the foliage of poplars and willows. The graph shows a typical chromatogram from a liquid chromatography analysis of similar compounds.

CREDIT: KENNETH KEEFOVER-RING

Cornell University doctoral candidates Craig Carlson and Fred Gouker work with technician Lauren Ferragut to collect male and female catkins from a segregating F2 family of *Salix purpurea* and freeze them in liquid nitrogen for later RNA extraction and gene expression analysis.

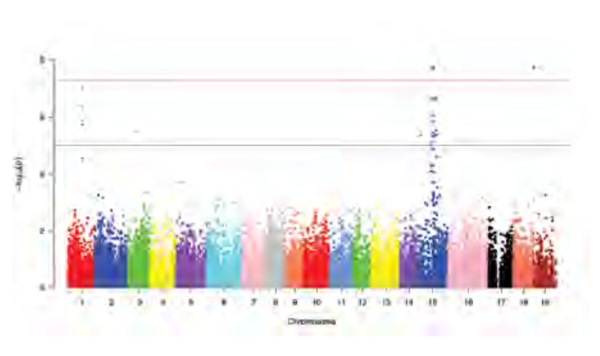
CREDIT: LAWRENCE SMART

Catkins of the female genotype 94006, chosen as the reference genome of *Salix purpurea.* Droplets of nectar on these female flowers are foods and attractants for native bees that pollinate the species.

CREDIT: LAWRENCE SMART

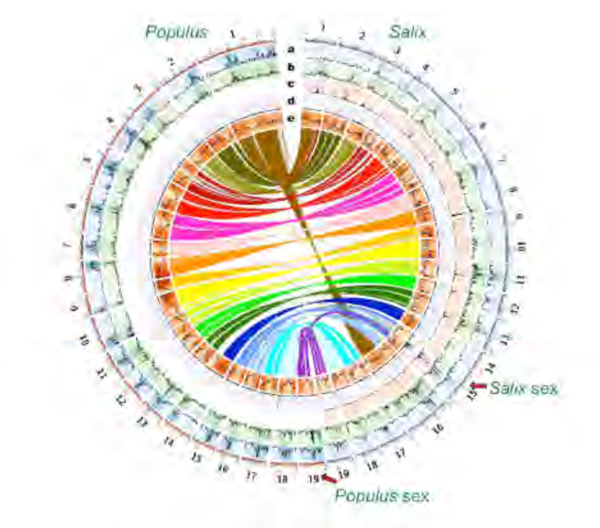
Abundant production of pollen by the male cultivar *Salix dasyclados* 'India'. This project will identify the genomic regions involved in determining male or female sex in willows and poplars.

CREDIT: LAWRENCE SMART



Manhattan plot showing location for main sex determination locus in *Salix purpurea*. This was determined using genetic association analysis with 78,423 single nucleotide polymorphisms and 72 unrelated individuals, mostly collected in New York and Pennsylvania.

CREDIT: STEPHEN DIFAZIO



Comparison of chromosomes from the *Populus trichocarpa* (left) and *Salix purpurea* (right) genomes. There is a high overall conservation of gene order (shown by colored lines connecting orthologous genes), except in the sex determination regions (red arrows).

CREDIT: STEPHEN DIFAZIO

Proj. 8 / 10

Links between spectral irradiance and cryptophyte biodiversity in environments from ponds to oceans

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(1542555)

Cryptophytes are microscopic algae found in aquatic ecosystems. This project examines how color of the underwater light field influences the molecular evolution of cryptophyte light-capture genes, the spectral efficiency of their light absorption, and the taxonomic diversification and ecological distribution of cryptophyte species in nature.

Photosynthesis by microscopic algae fuels life in many aquatic ecosystems. The color of light available for photosynthesis varies among environments, and resident microalgae must have photosynthetic pigments that are tuned to absorbing the colors of light available to them. In this project, the researchers focus on the cryptophytes, a relatively uncharacterized group of microalgae that are abundant in aquatic habitats ranging from small ponds to oceans. Cryptophytes use phycobilin pigments to capture light energy; these pigments allow cryptophytes to photosynthesize in light environments that are poorly exploited by other types of algae. Their central question is: How do functional, genetic, and phylogenetic diversity interact in the ecological diversification of cryptophytes with respect to light environment? We will conduct an integrative research program on the biodiversity of cryptophytes to understand how environmental variation in spectral irradiance (light color) is associated with the physiological diversity of light capture in cryptophytes in the context of their historical diversification.

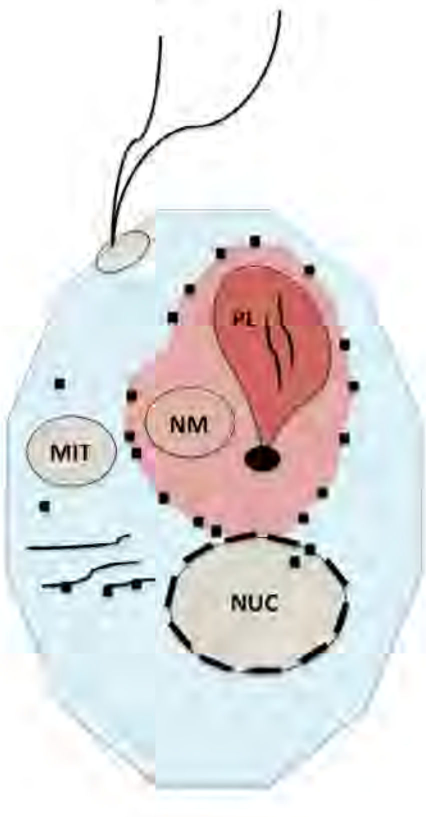
This work integrates several components: (1) Field sampling in water bodies ranging from small ponds to oceans to identify the specific light environments in which strains live, to determine the pigments that cryptophytes produce in those habitats, and to identify novel species; (2) Phenotypic studies to determine how variation in spectral irradiance influences light capture, photosynthesis, and growth of diverse taxa. These will also determine spectral absorption of phycobilins in strains throughout the cryptophyta; (3) Construction of a well-supported phylogeny based on sequencing nucleomorph genomes of ~200 strains; (4) Analyses of molecular evolution of key light capture genes, in particular those that encode the alpha and beta subunits of the cryptophyte phycobiliproteins, and those involved in the phycobilin synthesis pathway; (5) Experimental evolution to test the ability of diverse strains of cryptophytes to evolve into new light niches; (6) Experimental transcriptomics to identify the functional responses of diverse strains to variation in spectral irradiance; and (7) Phylogenetically-informed tests of the associations between habitat, molecular evolution, organismal performance, and spectral absorbance.

Ultimately, this work should be a transformative contribution to the understanding of the diversification of photosynthesis and the role of diversification in the ecological distribution of cryptophytes. An understanding of these issues is important to predicting how changes in land-use and potentially changes in climate will affect aquatic productivity.

This project will provide training for a post-doc, 2-4 graduate students, and 10 undergraduates. Through a partnership with Morris College and other University of South Carolina programs, underrepresented minorities will be recruited into summer fellowships. Novel cryptophyte strains will be deposited in living culture collections for use by other researchers.

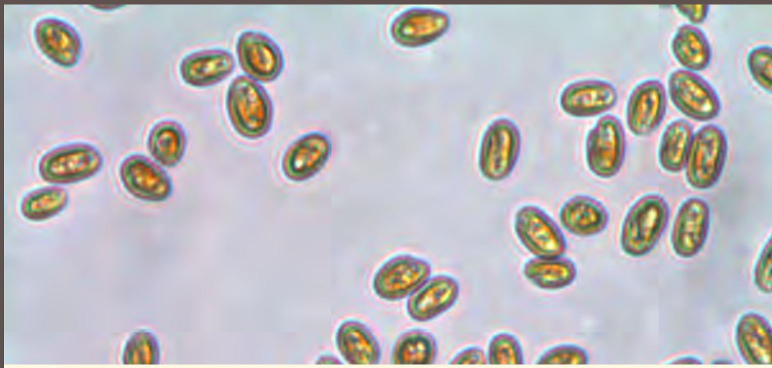
Batch cultures of cryptophytes (from left to right) *Guillardia theta, Chroomonas mesostigmatica, Rhodomonas salina, Proteomonas sulcata, Cryptomonas ovata,* and *Chroomonas sp.* showing the diversity in pigmentation among species.

CREDIT: TAMMI L. RICHARDSON



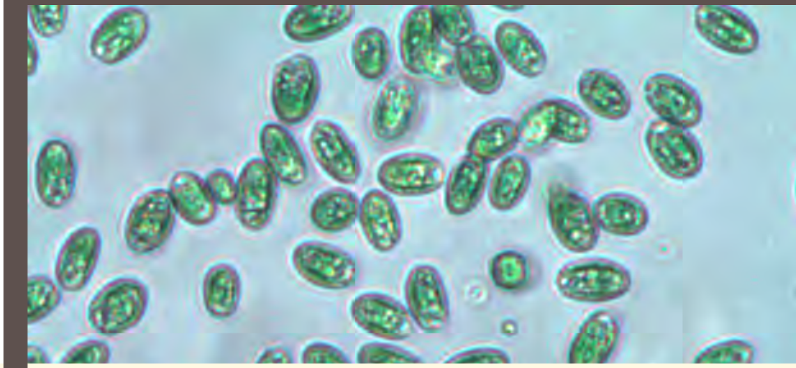
Sketch of a generic cryptophyte, showing the plasmid (PL), nucleus (NUC), nucleomorph (NM) and mitochondrion (MIT); each of which contains a separate genome.

CREDIT: TAMMI L. RICHARDSON



Cells of *Rhodomonas salina* under light microscopy, 40x. Individual cell length is approximately 10 micrometers.

CREDIT: STEVEN LITAKER



Cells of *Chroomonas sp.* under light microscopy, 40x. Individual cell length is approximately 20 micrometers.

CREDIT: STEVEN LITAKER

Proj. 9 / 10

Diversity, assembly and function of microbial communities on suspended and sinking particles in a marine oxygen deficient zone

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(1542240)

This project aims to improve our understanding of nitrogen cycling in an understudied marine microbial system, which can improve predictions for modeling oxygen availability and ocean productivity under future climate scenarios.

Marine Oxygen Deficient Zones (ODZs) are complex environments harboring rich microbial diversity. Free-living bacteria may bind to particles that will influence their flux in the system—keeping them suspended or sinking them. Understanding these systems is important because a large proportion (30-50%) of nitrogen is lost in ODZs, despite their rarity in the ocean. This study aims to study the phylogenetic and metabolic diversity, as well as the operational networks of these microbes that influence the loss of Nitrogen.

The approach will be to assay both phylogenetic (16S rRNA tag sequencing) and functional genetic diversity (genomics) on sinking particles collected using large-volume sediment traps. Phylogenetic and genomic studies will be intimately tied to measurements of activity - who is doing key biogeochemical transformations (proteomics) and what are the in situ rates at which they are doing them (using novel incubation systems). Data will then be used to model how diversity and corresponding function change on a range of time and space scales, from the sinking of a single particle to seasonal cycles. To understand the relationship of community diversity and function on suspended and sinking particles, a series of three cruises to the Eastern Tropical North Pacific ODZ are proposed.

Phylogenetic diversity will be studied in multiple scales to understand community structure and function of microbial species: they will be evaluated on a taxonomic, genomic, and genetic scale, in which important proteins that act on nitrogen are cataloged. Proteomics work will functionally characterize the affinity of proteins to transform nitrogen. By using all the data together, predictions across a range of time and space scales will be made about how climate fluctuations impact diversity and nitrogen availability, which potentially leads to drastic environmental effects.

The team of Oceanography graduate students and postdocs involved in the project will be training University of Washington Masters in Science for Science Teachers, who can jointly bring authentic research to K-8 classrooms. In addition, middle school students and undergraduates from underserved communities will participate in the project research.

Many areas in the ocean are oxygen deficient, which leads microbes to convert nitrogen in the water into N2 gas. This process leaves the ocean depleted of nitrogen that is an element essential to sustain marine food webs. Climate change is predicted to exacerbate this problem. Many microbes operate in consortia in this N reduction process.

CREDIT: YK, SHUTTERSTOCK

Researchers sample the oxygen deficient zone for marine bacteria and phytoplankton at different ocean depths.

CREDIT: GABRIELLE ROCAP

Office of Naval Research ship R/V Thomas G. Thompson is used to collect marine samples with the Rocap research team aboard. A variety of teachers and students are actively involved in the collection efforts.

CREDIT: GABRIELLE ROCAP

Proj. 10 / 10

Dynamical interactions between plant and oomycete biodiversity in a temperate forest

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USDA-ARS
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This project will examine the role of native oomycete plant pathogens in maintaining plant species diversity in an old growth forest in the Pacific Northwest. This information will improve management of natural ecosystems and diseases that occur within them.

Understanding the mechanisms that maintain plant biodiversity in forests and other natural ecosystems is a fundamental challenge in ecology. While the impact of invasive pathogens and pests on ecosystems can be dramatic, the functions of pathogens and pests that are native members of ecosystems are less well understood. For example, do pathogens and pests promote biodiversity by limiting the most dominant species? Alternatively, do species achieve dominance through evolution of higher levels of resistance or tolerance to endemic pathogens? Environmental microbes, including oomycetes and other pathogens, are highly adaptable. Some have evolved to colonize a narrow range of hosts, while others have evolved to colonize very wide ranges of hosts. However, the mechanisms of adaptation by environmental microbes such as oomycetes and the importance of microbial adaptation for the ecosystem services they provide are largely unknown.

This project focuses on the role of native oomycete pathogens in maintaining plant species diversity in an old growth forest in the Pacific Northwest, focusing on the Wind River Forest Dynamics Plot in southern Washington State, which is affiliated with the Smithsonian ForestGEO network. Oomycetes, or water molds, are highly destructive fungus-like plant pathogens, best known for causing the Irish potato famine in the 1850's. Though well known as agricultural pathogens, oomycetes are native to and abundant in many forest ecosystems. However, little is known about the potentially influential ecological roles that oomycete pathogens play in these ecosystems. In order to address these questions, this project will examine three dimensions of oomycete-plant interactions at the Wind River site: (i) a census of the oomycete species present in the Wind River forest, (ii) the ability of each oomycete species to attack or limit major and minor plant species in the forest, and (iii) the genetic and genomic mechanisms oomycetes use to adapt to different plant hosts. A particular focus will be on the role of endemic broad host range oomycetes, and how their interactions with dominant and less abundant host plants may differ. By integrating all this information, a better understanding will be developed of the roles of oomycetes and other pathogens in this and other natural ecosystems. This understanding will improve management of natural ecosystems and the diseases that occur within them.

Much of the field and microbiological research will be conducted by undergraduate researchers. Classes at their home institutions and summer workshops at the Wind River site will introduce the tools and concepts of molecular ecology, including genomics, big data, bioinformatics and ecoinformatics. Graduate students and postdoctoral fellows will play lead roles in the research, gaining experience in project management and mentoring as well in transdisciplinary ecology.

Undergraduate researchers will conduct much of the forest research. Here, a senior biology major from Lewis & Clark College measuring seedlings and forest regeneration.

CREDIT: ALLISON SIMLER

Sudden oak death symptoms on tanoak caused by the oomycete *Phytophthora ramorum.*

CREDIT: NIKLAUS GRÜNWALD

Four images from different parts of the Wind River Forest Dynamics Plot (http://wfdp.org) illustrate defining characteristics of this wet, temperate, old-growth ecosystem. The forest is composed of large-diameter canopy trees with abundant and diverse shrubs, ferns, and herbs.

CREDIT: JAMES LUTZ

Undergraduate researchers will conduct much of the forest research. Here, Brent Bordon, University of Washington undergraduate, walks through the WFDP to measure dendrometers in April 2013.

CREDIT: JAMES LUTZ

A

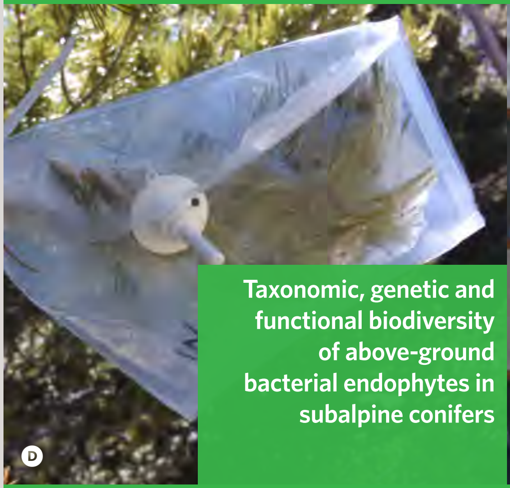
The macroalgal microbiome in space and time—maintaining primary producers in the Atlantic Rocky Intertidal Zone

B

Discovering genomic and developmental mechanisms that underlie sensory innovations critical to adaptive diversification

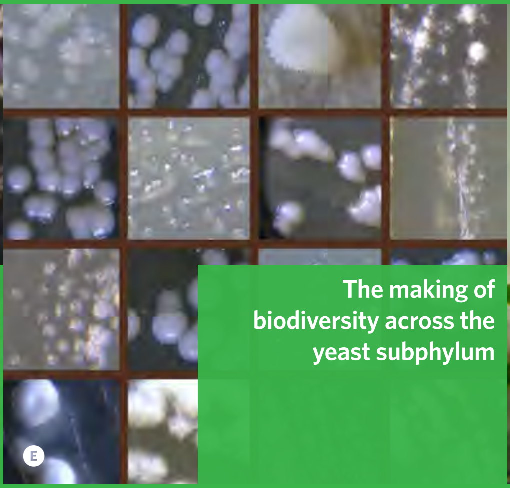
C

US-BIOTA-São Paulo: Chemically mediated multi-trophic interaction diversity across tropical gradients



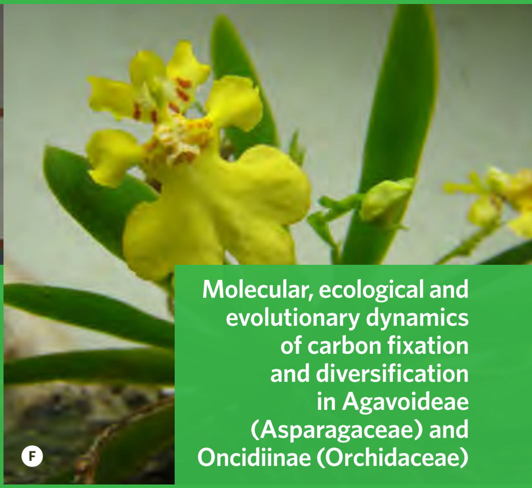
D

Taxonomic, genetic and functional biodiversity of above-ground bacterial endophytes in subalpine conifers



E

The making of biodiversity across the yeast subphylum

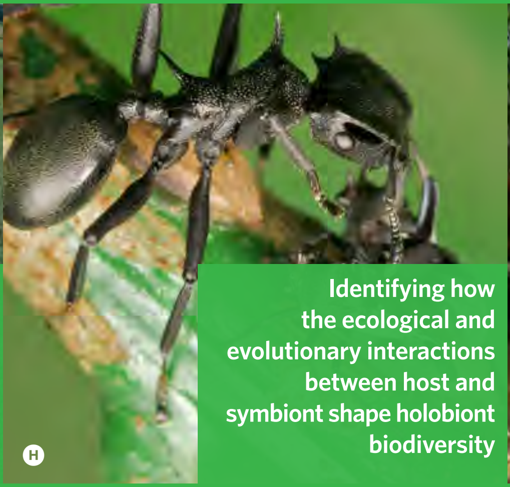


F

Molecular, ecological and evolutionary dynamics of carbon fixation and diversification in Agavoideae (Asparagaceae) and Oncidiinae (Orchidaceae)

G

Collaborative Research: Microbial seed banks: processes and patterns of dormancy-driven biodiversity

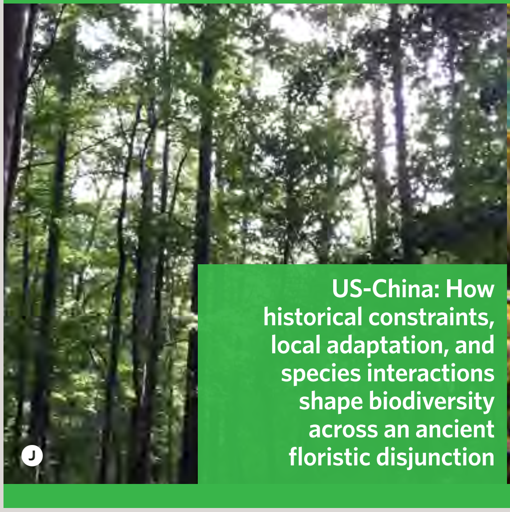


H

Identifying how the ecological and evolutionary interactions between host and symbiont shape holobiont biodiversity

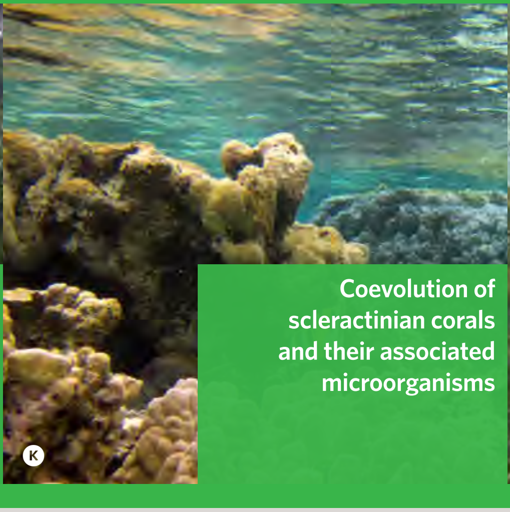
I

US-BIOTA-São Paulo: Integrating dimensions of microbial biodiversity across land use change in tropical forests



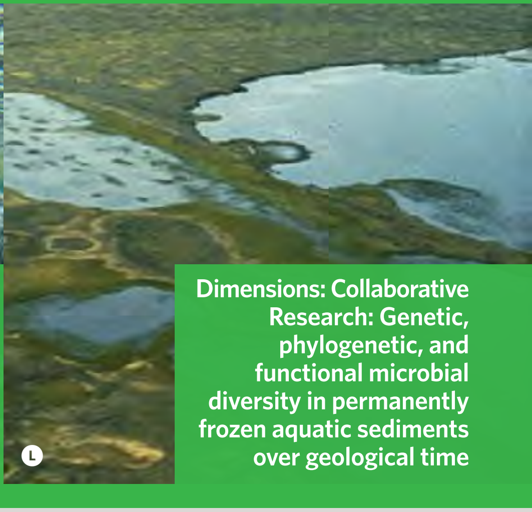
J

US-China: How historical constraints, local adaptation, and species interactions shape biodiversity across an ancient floristic disjunction



K

Coevolution of scleractinian corals and their associated microorganisms



L

Dimensions: Collaborative Research: Genetic, phylogenetic, and functional microbial diversity in permanently frozen aquatic sediments over geological time

2014 updates

IMAGE CREDIT

Ⓐ Susan H. Brawley
Ⓑ Laurel R. Yohe
Ⓒ Lee Dyer
Ⓓ Andrew Moyes
Ⓔ Dana A. Opulente & Amanda B. Hulfachor
Ⓕ Katia Silvera
Ⓖ Kurt Stepnitz
Ⓗ Jon G. Sanders
Ⓘ Klaus Nüsslein
Ⓙ Pam Soltis
Ⓚ Ryan McMinds & Jerome Payet
Ⓛ E.M. Rivkina

Proj. 1 / 12

The macroalgal microbiome in space and time—maintaining primary producers in the Atlantic Rocky Intertidal Zone

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This research examines the genetic, taxonomic, and functional aspects of the bacteria associated with several macroalgae that are prominent structural "bioengineers" of the intertidal food web.

Update

The team used common garden experiments to develop methodology to recover and evaluate microbiomes from sampling sites that are both near and far from a laboratory. Three rounds of sampling at the primary field site in Maine were completed (winter, summer, fall 2015) and the first set of trans-Atlantic samples (Greenland to North Carolina in the northwestern Atlantic; Bödo (Norway) to Cadiz (Spain) in the northeastern Atlantic) was made in summer of the two-mid-zoned species *Fucus vesiculosus* and *Porphyra umbilicalis*. Microhabitat environmental profiles were measured during the periods of the collections. DNA extractions/sequencing are underway, and microhabitat data are being analyzed. Functional work will be guided by the biodiversity data.

Proj. 2 / 12

Discovering genomic and developmental mechanisms that underlie sensory innovations critical to adaptive diversification

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Elizabeth Dumont
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This international research team connects the evolution of sensory genes, developmental regulation, and morphological structures to the ecological and taxonomic diversity of New World noctilionoid bats, which exhibit a range of distinctive sensory adaptations, including multiple forms of echolocation, vision, and a variety of repertoires for volatile and pheromone olfaction.

Update

Dávalos and colleagues launched their research with a planning meeting at the 2014 North American Bat Research Society meeting. The team then conducted fieldwork in Puerto Rico, the Dominican Republic, Belize, and Peru. With these new field collections, they have produced 38 sensory transcriptomes from 20 species, as well as developmental series from ecologically divergent bat lineages, and multiple detailed soft-tissue scans of sensory organs. The project is vastly expanding resources for understanding the complex morphological structures that enable multiple sensory specializations in the compact space available in the bat skull. They have also recruited three undergraduate students and supported three REU-PUI summer students.

Publications

Dahan, R.A., et al. (2015) Amino acid transporter expansions associated with the evolution of obligate endosymbiosis in sap-feeding insects (Hemiptera: sternorrhyncha). *BMC Evol Biol* 15: 52.

Yohe, L.R., et al. (2015) Bayesian hierarchical models suggest oldest known plant-visiting bat was omnivorous. *Biol Lett* 11: doi: 10.1098/rsbl.2015.0501.

US-BIOTA-São Paulo: Chemically mediated multi-trophic interaction diversity across tropical gradients

(CO-FUNDED WITH FAPESP)

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Universidade de Campinas

This research examines the diversity of plant chemicals that deter insect herbivory and how plant chemistry can affect the diversity and productivity of entire forests

Piper hieronymi (Piperaceae). This common pepper plant is host to hundreds of species of arthropods, most of which are undescribed. The defensive chemicals of this and most other pepper plants are completely unstudied. This research will discover and characterize novel toxic compounds from pepper plants across Brazil and Argentina.

CREDIT: LEE DYER, UNIVERSITY OF NEVADA

Update

This year research focused on establishing and integrating novel methods for exploring the diversity of multi-trophic species assemblages associated with *Piper* shrub species in Brazil, Peru, Ecuador, Argentina, and Costa Rica. The team successfully initiated experiments in all countries and hired taxonomists. Teams from all collaborative groups met together in Costa Rica and Brazil to launch projects that will support the overall Dimensions project. They completed metabolomics for species within the major *Radula* clade within *Piper* species and mapped these data onto a new phylogeny for this clade to test specific evolutionary hypotheses. They also created phylogenetic datasets for *Eois*, a hyper-diverse moth genus associated with *Piper*. A Neotropical Lepidoptera course was offered to 25 students in Brazil.

Publications

Dyer, L.A., Forister, M.L. (2015). *The Lives of Lepidopterists.* Springer, New York. In Press.

Forister, M.L., et al. (2015). The global distribution of diet breadth in insect herbivores. *Proc Nat Acad Sci USA* 112: 442-447.

Richards, L.A., et al. (2015). Phytochemical diversity drives plant-insect community diversity. *Proc Nat Acad Sci USA* 112: 10973-10978.

Shimbori, E.M. (2015). A revision of the New World species of the Aleiodes compressor species group (Hymenoptera: Braconidae: Rogadinae). *Can Entomol* 147: 665-673.

Pseudautomeris yourii (Saturniidae) caterpillar parasitized by an unknown wasp (Braconidae: Microgastrinae). This is a generalist caterpillar that feeds on chemically diverse hosts, including plants as different as *Piper* (Piperaceae) and *Chusquea* (Poaceae). The white splotches on the caterpillar are silk cocoons spun by prepupal wasp larvae that have emerged from the caterpillar after consuming internal tissues.

CREDIT: LEE DYER, UNIVERSITY OF NEVADA

Proj. 4 / 12

Taxonomic, genetic and functional biodiversity of above-ground bacterial endophytes in subalpine conifers

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This team seeks to determine the evolutionary and ecological significance of a novel symbiosis between pine trees and the nitrogen-fixing endophytic bacteria living inside their foliage. A deeper understanding of how biodiversity of endophytic bacteria affects the capability of forest conifers to fix nitrogen can solve a long-standing ecological mystery: where does the fixed nitrogen in conifer forests come from?

HTTP://WWW.SCIENCEMAGAZINEDIGITAL.ORG/SCIENCEMAGAZINE/22_MAY_2015?PG=12#PG12

Update

The team developed several new techniques and protocols, contributing to publications. They secured contamination-free 15N labeling and developed new FISH and microscopy protocols to measure endophyte community functions. They optimized bacterial enrichment for single-cell genome sequencing from conifer foliage, and successfully sorted single bacterial cells at the Joint Genome Institute. Bacterial 16S rRNA sequencing data was obtained at UC Merced. Site permits were secured for the sites to be sampled in 2015 and 2016, and undergraduates participated in research with collaborators at Yosemite. Two new graduate students, both from underrepresented minorities, were recruited to the project.

Publications

Moyes, A.B. et al. (2016). Evidence for foliar endophytic nitrogen-fixation in a widely distributed subalpine conifer. *New Phytol* 210: 657-668.

Proj. 5 / 12

The making of biodiversity across the yeast subphylum

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Yeasts of the ancient fungal subphylum Saccharomycotina employ many different resource utilization strategies to allow them to inhabit every continent and every major aquatic and terrestrial habitat. This project seeks to understand the diversification of yeasts by using information written in their genome.

Update

The team has built a database of the 86 published yeast genome sequences from across the subphylum Saccharomycotina and has been adding several new genomes per month. Preliminary analyses of genome content have begun, and a working backbone phylogeny has been produced. Over 300 yeast type strains have been revived and transferred from the United States Department of Agriculture strain collection to the University of Wisconsin-Madison for high-throughput phenotyping and genome sequencing. Several manuscripts have been submitted describing powerful computational and experimental tools for the project, as well as for the broader yeast and genomics communities.

Publications

Alexander, W.G., et al. (2016). Efficient engineering of marker-free synthetic allotetraploids of *Saccharomyces*. *Fungal Genet Biol* 89: 10-17.

Coelho, M.A., et al. (2015). Draft genome sequence of *Sporidiobolus salmonicolor* CBS 6832, a red-pigmented basidiomycetous yeast. *Genome Announc* 3: e00444-15.

Hittinger, C.T., et al. (2015). Genomics and the making of yeast biodiversity. *Curr Opin Genet Dev* 35: 100-9.

CONTINUE >

Wisecaver, J.H., Rokas, A. (2015). Fungal metabolic gene clusters—caravans traveling across genomes and environments. *Front Microbiol* 6: 161.

Zhou, X., et al. (2015). *in silico* Whole Genome Sequencer & Analyzer (iWGS): a computational pipeline to guide the design and analysis of de novo genome sequencing studies. *BioRxiv* doi: http://dx.doi.org/10.1101/028134.

Diverse species of yeasts from the subphylum Saccharomycotina display radically different colony morphologies.

CREDIT: DANA A. OPULENTE AND AMANDA B. HULFACHOR

Proj. 6 / 12

Molecular, ecological and evolutionary dynamics of carbon fixation and diversification in Agavoideae (Asparagaceae) and Oncidiinae (Orchidaceae)

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This project compares the genomic basis of physiological adaptations to water limitation in agaves, yuccas and epiphytic orchids. They identify changes in gene content and function that enabled evolutionary shifts from typical C3/C4 photosynthesis to Crassulacean Acid Metabolism, a rare strategy that makes sugar with less water and less concern about heat stress.

Update

The research team has been involved in characterizing the genomes of several species within the groups of interest, and has evaluated important pathways such as photosynthesis and many developmental processes that have allowed the species to adapt. The team has been heavily involved in synthesizing knowledge of CAM processes across land plants to better understand the diversity of ecophysiological processes enabling epiphytic growth habits, and identifying orthologous CAM genes in multiple species. In addition, physiological, anatomical and transcriptome data have been generated and analyzed for several species in the Agavoideae and Oncidiinae.

Publications

Albert, V.A., Carretero-Paulet, L. (2015). A genome to unveil the mysteries of orchids. *Nat Genet* 47: 3-4.

Heyduk, K., et al. (2016). Gas exchange and leaf anatomy of a C3-CAM hybrid, *Yucca gloriosa* (Asparagaceae). *J Exp Bot* doi: 10.1093/jxb/erv536.

Ming, R., et al. (2015). The pineapple genome and the evolution of CAM photosynthesis. *Nat Genet* 47: 1435-42.

Silvera, K., Lasso, E. (2015) "Ecophysiology... epiphytes." in Goldstein G., Santiago, L.S., eds. *Tropical Tree Physiology*. Springer...

Yang, X., et al. (2015). A roadmap for research on crassulacean acid metabolism (CAM) to enhance sustainable food and bioenergy production in a hotter, drier world. *New Phytol* 207 491-504.

Yang, X., et al. (2016). Plant comparative and functional genomics. *Int J Genomics* doi: 10.1155/2015/924369.

Collaborative Research: Microbial seed banks: processes and patterns of dormancy-driven biodiversity

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When faced with unfavorable conditions, many organisms enter a reversible state of reduced metabolic activity, or dormancy. This project focuses on how dormancy creates 'seed banks', which are important reservoirs of taxonomic, genetic, and functional biodiversity of microbial communities.

Update

The team has been focusing on how and why dormancy varies among microbes as a result of life history trade-offs. Specifically, they are:

1. testing for life history tradeoffs between dormancy and physiological and genomic characteristics by comparing survivorship during prolonged dormancy across a phylogenetically disparate collection of soil bacteria using a traits-based approach,
2. testing predictions regarding the nature of dormancy as a cell-cell communicated response that affects pathogen suppression, plant-soil feedbacks, and ecosystem processes using signaling molecules to directly manipulate microbial seed banks, and
3. developing and testing theoretical predictions regarding the contribution of seed banks to geographic patterns of taxonomic and phylogenetic diversity using communities of soil bacteria from systems with contrasting disturbance histories.

Publications

Aanderud, Z.T., et al. (2015). Resuscitation of the rare biosphere contributes to pulses of ecosystem activity. *Front Microbiol* 6:24.

Bier, R.L., et al. (2015). Linking microbial community structure and microbial processes: an empirical and conceptual overview. *FEMS Microbiol Ecol* 91: doi: 10.1093/femsec/fiv113.

Leff, J.W., et al. (2015). Consistent responses of soil microbial communities to elevated nutrient inputs in grasslands across the globe. *Proc Nat Acad Sci USA* 112: 10967-10972.

Lennon, J.T., Denef, V.J. (2015). "Evolutionary ecology of microorganisms: from the tamed to the wild", in Yates M.V., et al., ed. *Manual of Environmental Microbiology, 4th ed.* ASM Press, Washington, DC.

Lennon, J.T., et al. (2015). Microbial contributions to subterranean methane sinks. *bioRxiv* doi: 10.1101/034801.

Livermore, J.A., Jones, S.E. (2015). Local-global overlap in diversity informs mechanisms of bacterial biogeography. *ISME J* 9: 2413-2422.

Locey, K.J., Lennon, J.T. (2015). Scaling laws predict global microbial diversity. *PeerJ* doi: 10.7287/peerj.preprints.1451v1.

Martiny, J.B.H., et al. (2015). Microbiomes in light of traits: a phylogenetic perspective. *Science* doi: 10.1126/science.aac9323.

Muscarella, M.E., et al. (2015). Species sorting along a subsidy gradient alters community stability. *bioRxiv* doi: 10.1101/031476.

Peralta, A.L., et al. (2015). Crop diversity enhances disease suppressive potential in soils. *bioRxiv* doi: 10.1101/030528.

Rocca, J.D., et al. (2015). Relationships between protein-encoding gene abundance and corresponding process are commonly assumed yet rarely observed. *ISME J* 9:1693-1699.

Shoemaker, W.R., et al. (2015). Do modern theories of biodiversity fail to predict commonness and rarity among microbes? *PeerJ* doi: 10.7287/peerj.preprints.1450v1.

Shoemaker, W.R., et al. (2015). Genome sequence of the soil bacterium *Janthinobacterium sp.* KBS0711. *Genome Announc* 3: e00689-15.

Treseder, K.K., Lennon, J.T. (2015). Fungal traits that drive ecosystem dynamics. *Microbiol Mol Biol Rev* 79: 243-262.

Weitz, J.S., et al. (2015). A multitrophic model to quantify the effects of marine viruses on microbial food webs and ecosystem processes. *ISME J* 9: 1352-1364.

Wiggington, C.H., et al. () Re-examining the relationship between virus and microbial cell abundances in the global oceans. *Nat Microbiol* In press.

Zwart, J.A., et al. (2015). Phytoplankton traits predict ecosystem function in a global set of lakes. *Ecology* 96: 2257-2264.

Proj. 8 / 12

Identifying how the ecological and evolutionary interactions between host and symbiont shape holobiont biodiversity

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This project explores how the diversity and functional integration of social animals and their bacterial gut symbionts are shaped by historical and contemporary environmental interactions. Lessons learned from this unique system will help us to understand the rules governing a ubiquitous but poorly understood partnership—the symbiotic relationship between animals and their gut bacteria.

Update

Having recently started, the team has been planning and training students to explore symbiotic interactions between ants and microbes: The researchers have begun new colony sampling of the host ants across a variety of tropical habitats, and are working toward a complete phylogeny for asking how the ecology and evolution of the ants is connected to the diversity of the microbial symbionts. Such questions include, what are the roles of time, biogeography, and habitat in host diversification, gut community assembly, and co-diversification of the holobiont and host. In addition, progress has been made cultivating representative core symbionts for eventual genomic work. Studies on their in vitro metabolic properties have also been undertaken to lend insight into their functions within the holobiont. The team is also assessing symbiont function through manipulative in vivo experiments and metagenomics, with the long term goal of understanding how symbiont function varies across ecological, geographic, and phylogenetic scales.

Proj. 9 / 12

US-BIOTA-São Paulo: Integrating dimensions of microbial biodiversity across land use change in tropical forests

(CO-FUNDED WITH FAPESP)

US TEAM

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Klaus Rudolf Nusslein
University of Massachusetts Amherst
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Scott Saleska
Joost van Haren
University of Arizona
(1442152)

BRAZIL TEAM

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Dernando Andreote
Plinio Camargo
University of São Paulo

The deforestation of tropical forests for agriculture affects the production and consumption of methane, a potent greenhouse gas. The team seeks to identify the microorganisms involved in methane production and consumption, their physiologies and genetics, and their contribution to the flow of methane from Amazon soils to the atmosphere.

^ Old growth rainforest logs removed from primary Amazon rainforest in Rondonia, Brazil.

CREDIT: KLAUS NÜSSLEIN, UNIVERSITY OF MASSACHUSETTS

CONTINUE >

Update

Several questions are under investigation by the team.

1. Do methanotrophs decrease in diversity across forest to pasture clines, causing pastures to produce more methane?
2. Does the community assembly of the microorganisms determine methane production?
3. Can understanding the biodiversity of microorganisms in an area allow accurate predictions about methane production?

The team conducted novel sampling on a chronosequence of land uses in the Tapajos National Forest within the Amazon. Gas measurements were taken, and total soil DNA was sampled. Soil was physiochemically analyzed. Through the gas measurements, the team demonstrated that methanotroph incidence and diversity is higher in forests compared to pastures, resulting in methane being consumed in forests and methane production in pasture habitats.

Publications

Mueller, R.C., et al. (). Land use change in the Amazon rainforest favors generalist fungi. *Funct Ecol* In Press.

Navarrete, A.A., et al. (2016). Differential response of Acidobacteria subgroups to forest-to-pasture conversion and their biogeographic patterns in the western Brazilian Amazon. *Front Microbiol* 6: 1443.

Ranjan, K., et al. (2015). Forest-to-pasture conversion increases the diversity of the phylum *Verrucomicrobia* in Amazon Rainforest Soils. *Front Microbiol* 6: 779.

Proj. 10 / 12

US-China: How historical constraints, local adaptation, and species interactions shape biodiversity across an ancient floristic disjunction

(CO-FUNDED WITH NSFC)

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In this collaborative project, U.S. and Chinese scientists are conducting analyses of plant and microbial diversity in forests in both the U.S. and China to discover the factors that shape biodiversity through space and time. These forests may be geographically separated, but they share more similarities than many proximate forests.

View of *Magnolia macrophylla* at Talladega National Forest, AL.
CREDIT: PAM SOLTIS, FLORIDA MUSEUM OF NATURAL HISTORY

HTTP://WWW.USA-CHINA-BIODIVERSITY.ORG

Update

During the past year, the team focused on fieldwork, sample acquisition, and developing methods for collecting, analyzing, and managing genetic and ecological data. Working at NEON sites in Florida, Alabama, and Virginia, they sampled genera exhibiting the Eastern Asia – Eastern North America floristic disjunction. Samples for analysis of functional traits, DNA sequences, gene expression, and secondary metabolites of the plants and for microbial analysis of leaves, twigs, and soil from each plant are being processed. They coordinated the sampling plan with colleagues in China and hosted a student from the Chinese team to ensure parallel data collection and sample preparation.

Proj. 11 / 12

Coevolution of scleractinian corals and their associated microorganisms

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The Global Coral Microbiome Project examines the distribution of coral-associated microbes across the phylogenetic, geographic and anatomical diversity of coral reefs. This project investigates whether the composition of coral microbial communities helps to explain the coral vulnerability through studying trans-continental ecosystems, and sampling genome sequences and metabolites of key coral bacteria.

HTTP://OREGONSTATE.EDU/MICROBIOLOGY/VEGATHURBERLAB/SITES/DEFAULT/FILES/MANUAL_PAGES/LEAFLET_SAMPLES_COMBINED.HTML | HTTP://CORALREEFMOVIE.ORG

Update

In the last year and a half the team from Oregon State and Penn State Universities has collected specimens from across the globe that will be sequenced for coral and microbial DNA. Thus far, they have completed expeditions to Saudi Arabia, Colombia, Panama, Réunion, Singapore, Curaçao, and the East and West coasts of Australia. With the assistance from numerous international collaborators, they have compiled thousands of coral microbiome DNA samples and accompanying metadata. Sequencing and open release of this sample set will provide a comprehensive community resource for testing hypotheses of how coral communities have assembled over evolutionary time, and an exemplary platform to investigate how local and global stressors are changing microbial communities on coral reefs.

At each of the sampling localities Vega and colleagues have engaged in outreach activities with local residents and have worked with documentary filmmakers to produce four mini-documentaries about the reefs and cultures visited, emphasizing the perspectives of the scientists and locals that live in each of these areas. These short videos will also build towards a full-length outreach documentary on coral reef documentary.

Proj. 12 / 12

Dimensions: Collaborative Research: Genetic, phylogenetic, and functional microbial diversity in permanently frozen aquatic sediments over geological time

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Karen Lloyd
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This research project addresses the long-pondered question of whether microbes embedded in permafrost are dead (or fossils), representing ancient communities preserved through time, or are living communities that have continued to evolve since becoming buried.

Update

Permafrost of different freezing ages (3 million to 3 thousand years old) are being screened for metabolic activity to determine the archive of time they represent. The team first obtained the late Pleistocene permafrost of both ice complex (Yedoma) and lake-alluvial origin (Siberia) and conducted metagenomic sequencing. Low levels of methane gas, a signal of active metabolic activity, showed the permafrost has living archives, and results suggested that microbial communities in the Yedoma formed under more aerobic conditions than previously thought. Metagenomic sequencing results of similar-age revealed differences in microbial community composition that reflects the conditions under which these deposits were formed. The team had a successful summer field season drilling cores across other sites in Northeastern Siberia.

Publication

Rivkina E., et al. (2016). Metagenome analysis of the late Pleistocene permafrost – additional tools for paleo-reconstructions. *Biogeosciences Discuss* 13:2207-2219.

2014
Image Gallery

Proj. 2/12 — Celebrating a productive summer for REUs at the Dávalos lab working on the Dimensions project. From left: PI Dávalos, Ph.D student Yohe, R.E.U Afzal, PI at PUI Corthals, Ph.D student Mets (back), SUNY STEM Patil (front), REU Bartasunaite, and REU Abubakar.

CREDIT: MARGARITA BARTASUNAITE, JOHN JAY COLLEGE OF CRIMINAL JUSTICE

Proj. 10/12 — University of Florida co-PI Doug Soltis, Senior Research Scientist Mark Whitten, and undergraduate Braden White collect leaf samples and mark trees for future sampling at Talladega National Forest, AL.

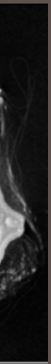
CREDIT: PAM SOLTIS, FLORIDA MUSEUM OF NATURAL HISTORY

Proj. 2/12 — Waterfall and ravine between forests in Peru. Active flight and highly specialized sensory systems enable many noctilionoid bats to travel across gaps and maintain connectivity among plant populations despite natural or anthropogenic barriers.

CREDIT: LAUREL R. YOHE, STONY BROOK UNIVERSITY

Proj. 2/12 — Cross-section micro-CT scans of soft nasal tissues from bat skulls showing sensory epithelia of the olfactory system, as well as papillae of the tongue and portions of the eyes. Artibeus jamaicensis is a primarily frugivorous bat, other species shown visit flowers and consume nectar and, in some cases, pollen.

CREDIT: LAUREL R. YOHE, STONY BROOK UNIVERSITY



Proj. 6/12 — *Erycina pusilla*, a miniature orchid species with fanning leaves growing in a lowland site in Panama. *Erycina pusilla* exhibits Crassulacean Acid Metabolism, a water mode of photosynthesis.

CREDIT: KATIA SILVERA, UC RIVERSIDE AND STRI PANAMA

Proj. 2/12 — Portrait of male *Sturnira*, a primarily frugivorous bat whose epaulettes are sweetly scented and have been described as "inviting a deeper sniff."

CREDIT: LAUREL R. YOHE, STONY BROOK UNIVERSITY

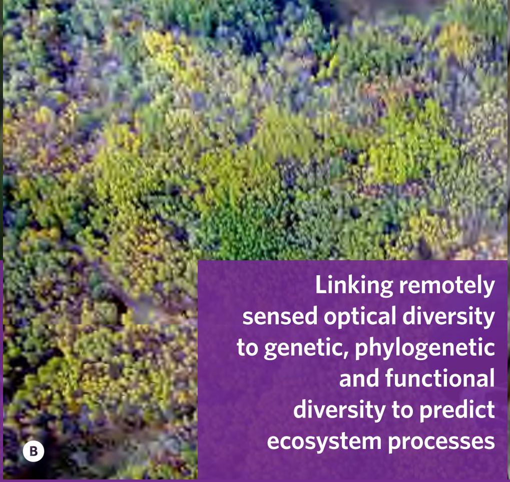
Proj. 10/12 — Temporary microbial lab in the back of a pick-up at Ordway-Swisher Biological Station in northern Florida.

CREDIT: PAM SOLTIS, FLORIDA MUSEUM OF NATURAL HISTORY

Proj. 2/12 — Developmental series from flower-visiting *Erophylla* bats obtained this year.

CREDIT: KAREN E. SEARS, UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN

US-BIOTA-São Paulo: Improving biodiversity prediction in the Atlantic rainforest



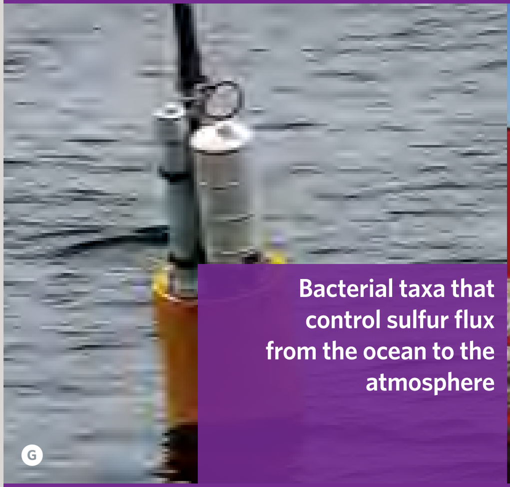
Linking remotely sensed optical diversity to genetic, phylogenetic and functional diversity to predict ecosystem processes

Experimental adaptive radiation — genomics of diversification in bird lice

Biodiversity of the gut microbiome of herbivorous rodents

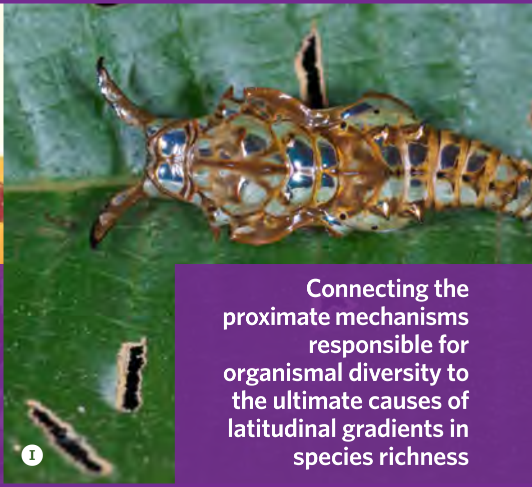
Functional diversity of chemosymbiosis in lucinid bivalves from coastal biomes

US-China: Phylogenetic, functional, and genetic diversity and ecosystem functions in a fragmented landscape



Bacterial taxa that control sulfur flux from the ocean to the atmosphere

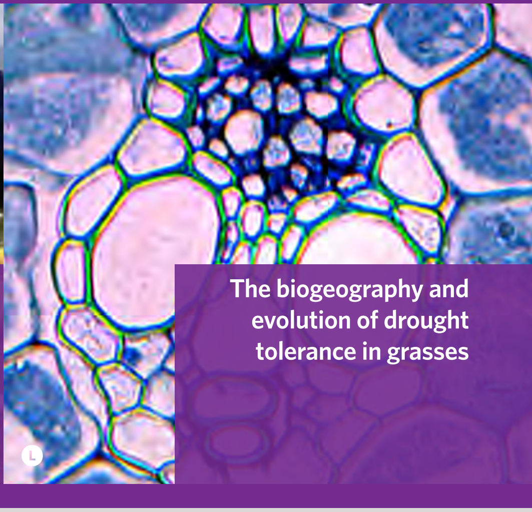
Microbial biodiversity and functionality in deep shale and its interfaces (DSIs)



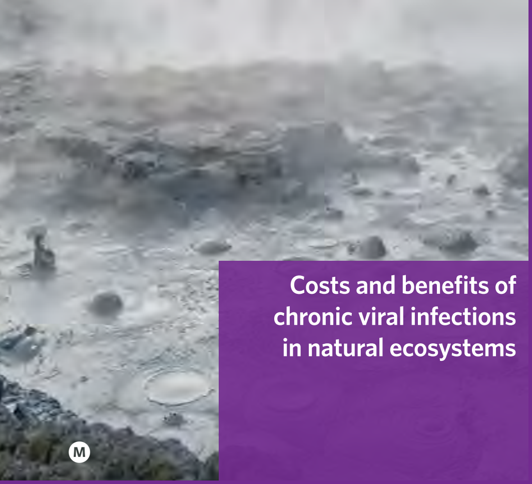
Connecting the proximate mechanisms responsible for organismal diversity to the ultimate causes of latitudinal gradients in species richness

Landscapes of Linalool: scent-mediated diversification of flowers and moths across western North America

Symbiont and transcriptomic niche dimensions of long-term coexistence in *Trifolium* communities



The biogeography and evolution of drought tolerance in grasses



Costs and benefits of chronic viral infections in natural ecosystems

2013 updates

IMAGE CREDIT

Ⓐ Júlia Montesanti
Ⓑ Michael Madritch
Ⓒ S.E. Bush & D.H. Clayton
Ⓓ Kevin Kohl
Ⓔ Audrey T. Paterson
Ⓕ Lin Jiang
Ⓖ M. A. Moran
Ⓗ S. Sharma
Ⓘ Ryan Hill
Ⓙ Rick Overson
Ⓚ Maren Friesen
Ⓛ Joe Craine
Ⓜ Mark Young

US-BIOTA-São Paulo: Improving biodiversity prediction in the Atlantic rainforest

(CO-FUNDED WITH NASA AND FAPESP)

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BRAZIL TEAM

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Ricardo Pinto-da-Rocha
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This project aims to develop a framework for predicting spatial patterns of biodiversity in the highly diverse environment of the Brazilian Atlantic Forest. Models are being constructed by integrating numerous types of data including remote sensing, meteorological, locality, phylogenetic, functional, biotic interaction, and paleoenvironmental data.

Update

The herpetology (Carnaval and Brazilian collaborator M. Rodrigues), ornithology (Miyaki and Brazilian collaborator F. Amaral), invertebrate (Pinto-da-Rocha and Brazilian collaborator A. Freitas), and botany (Michelangeli and Thomas, and Brazilian collaborator L. Lohmann) teams collectively spent four months in the field across seven states of Brazil to sample vertebrates, invertebrates, and plants, being joined by several students. Genetic and sub-genomic data were generated from those collections. Twelve new species and ten taxonomic revisions emerged from those efforts. The Carnaval team also deployed hygrobuttons to measure micro-climatic data from across the forest, which are being compared to estimates of temperature obtained from remote sensing products by the teams of McDonald and Brazilian collaborator T. Silva. The Cruz team, in collaboration with C. Grohman from Universidade de São Paulo, analyzed cave deposit data in Southern Bahia to parameterize paleoreconstruction of climate along the forest. These records were complemented by fossil pollen data collected by French collaborator M. Ledru in southeastern and northeastern Brazil. The Hickerson group developed two novel methods to analyze the sub-genomic data generated by the animal and plant teams, providing new ways to infer community-wide responses to shifts in the biotic or abiotic environment and former range reconstructions.

This team also organized the symposium "The Multiple Dimensions of Biodiversity Science", which took place at the 2015 Meeting of the Society for the Study of Evolution held in Guarujá, Brazil, from 26-30 June 2015.

Tijuca atra; taken at Itamonte, Minas Gerais, Brasil.

CREDIT: JÚLIA MONTESANTI

Publications

Alvarado-Serrano, D.F., Hickerson, M. J. (2015). Spatially explicit summary statistics for historical population genetic inference. *Methods Ecol Evol* doi: 10.1111/2041-210X.12489.

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Poospiza thoracica taken at Cunha, São Paulo, Brasil.

CREDIT: MONTESANTI

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Proj. 2 / 13

Linking remotely sensed optical diversity to genetic, phylogenetic and functional diversity to predict ecosystem processes

(CO-FUNDED WITH NASA)

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Remote sensing methods for monitoring the Earth's biodiversity are being applied to experimental manipulations of plant diversity. This allows scientists to examine the linkages between plant biodiversity, soil microbe diversity, and ecosystem function at multiple scales of spatial resolution.

Aerial photo showing color differentiation of genetically distinct aspen clones. Genotypic differences can be detected via remote sensing techniques.

CREDIT: MICHAEL MADRITCH

Update

Above and belowground dimensions of diversity were studied through their ecosystem components. The team first obtained the aboveground measurements of structural, phenological, biochemical, and physiological plant properties at the scale of individual, haplotype, species, and community. A novel approach using hexacopter data was developed to scan vegetation across prairies, some of which were experimentally manipulated. 35 experimental communities are now being closely monitored using optimized remote sensing and the team is expanding this effort into manipulated forests in Cloquet Minnesota at the IDENT experimental station. One undergraduate joined the team for the summer sponsored by an REU supplement, and measured leaf pigment data from the Cedar Creek reserve that has been sampled the previous year.

Proj. 3 / 13

Experimental adaptive radiation—genomics of diversification in bird lice

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This project will expand the understanding of adaptive radiation using bird-specific ectoparasites as a model system. The researchers are conducting experimental studies that link phylogenetic, genomic, phenotypic, and functional data in order to clarify how micro-and macro-evolutionary processes influence the generation of biodiversity.

Update

A reference genome for the pigeon louse *Columbicola columbae* has been sequenced and assembled and we are now optimizing the assembly. We are also continuing to monitor phenotypic changes in experimental lineages of *C. columbae* that have been evolving on pigeon breeds of different sizes and colors for two years. Lice are measured at six month intervals, and samples of lice are frozen for genomic comparisons to the reference genome. The goal is to document the genomic architecture of phenotypic adaptation to different hosts. The genomes of 64 additional species of *Columbicola* have also been sequenced, and data from 1,107 single copy orthologous genes have been assembled. These genes are being used for a phylogenomic analysis of *Columbicola*. The resulting phylogeny will be compared to a phylogeny constructed for the 64 host species of these lice next year. The team has also focused on outreach, building educational kits that have been distributed locally and internationally.

CONTINUE >

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Proj. 4 / 13

Biodiversity of the gut microbiome of herbivorous rodents

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This project sets out to understand how the evolution and environment of the gut microbiome in herbivorous mammals has helped create a biodiversity hotspot of microbial organisms that in turn may influence the physiology of the host mammal. This work will improve understanding of the metabolism of toxins and diet plasticity in mammals. It has potential applications for improving the health of the human microbiome.

Update

The team has been evaluating the diversity of microbial communities in herbivorous woodrats by collecting woodrats and inventorying regions of the gut through 16S DNA sequencing. Captive woodrats are being functionally analyzed by feeding trials and microbial transplants. Transplants effectively transfer detoxification function from evolutionarily and ecologically experienced animals to naïve species via fecal transplants, measurable by liver gene expression and decreases in toxins such as oxalate. Metagenomic inventories have also been underway to examine microbial community composition across the gut. As outreach, a summer camp was launched for 7th graders to explore gut microbiomes via design of video games.

Publications

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Tannin-degrading microbes isolated from the desert woodrat's gut appear as dark colonies with a ring of white as they clear the tannins added to agar.

CREDIT: KEVIN KOHL, UNIVERSITY OF UTAH

Proj. 5 / 13

Functional diversity of chemosymbiosis in lucinid bivalves from coastal biomes

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Organisms that live within another species (endosymbionts) are common within bivalves, a type of mollusk. These endosymbionts offer chemical nutrients to the host in a relationship called chemosymbiosis. This project explores uncharacterized coastal marine biomes to investigate the phylogenetic, genetic and functional dimensions of biodiversity in modern and ancient lucinid bivalve chemosymbioses.

Update

Multiple habitats were characterized for the presence of lucinids, their ecological conditions, and geochemistry. Fieldwork was expanded to the Bahamas. Community bacterial phylogenetic relationships in porewater exudates and sediment were estimated and compared to lucinid symbiont communities. Symbionts were rarely encountered in the habitat. Metabolically relevant genes were mined using targeted pyrosequencing. Whole genome and metagenome sequencing were completed for several species, which reveals surprising symbiont diversity. Morphometrics methods revealed that internal shell features can significantly vary between stable seagrass and sand. These results reveal the potential use of intraspecific morphologic variations to reconstruct habitat changes in the fossil record.

Publications

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Proj. 6 / 13

US-China: Phylogenetic, functional, and genetic diversity and ecosystem functions in a fragmented landscape

(CO-FUNDED WITH NSFC)

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CHINA TEAM

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The major goal of this project is to use the Thousand Island Lake (TIL) region of Southern China as an idealized model of habitat fragmentation to study the ecological determinants of multiple dimensions of biodiversity of woody plant and arthropod assemblages, and their linkage to ecosystem functions.

CONTINUE >

Update

The team held several meetings and pursued ambitious data collection objectives. 75 plots were established on 29 islands. Litterbags were placed on nearly 1000 individuals of common woody plant species and measured semi-annually. In-depth habitat diversity measurements including soil microbial community analyses and arthropod surveys have been completed. Genetic stratification from fragmentation of common plant species was characterized in the common pine. Acorn weevil infestation studies established a model system for future work. Land use over the TIL was recorded using Landsat remote sensing imagery. Species disturbance and island effects were quantified. Observations were combined with laboratory experiments to test Darwin's naturalization hypothesis.

Publications

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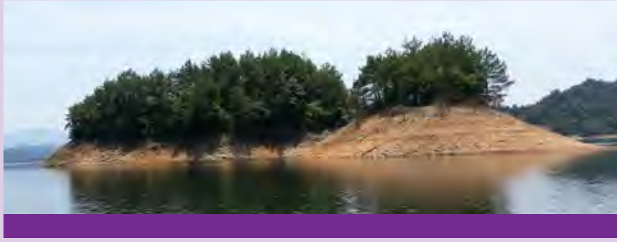

A small island that supports tree growth.
CREDIT: LIN JIANG

Proj. 7 / 13

Bacterial taxa that control sulfur flux from the ocean to the atmosphere

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This project seeks to understand how the regulation of dimethylsulfoniopropionate (DMSP) metabolism in marine bacteria affects the climate-relevant sulfur cycle between the ocean and the atmosphere. The goal is to understand how the diversity and community structure of microbial life impacts the fate of oceanic and atmospheric chemicals.

Update

The ecology and physiology of DMSP-degradating marine bacteria was studied at different levels of biological complexity: (1) pure culture studies of a model marine bacterium, *Ruegeria pomeroyi*, (2) model systems consisting of three co-cultured microbes (one bacterium and two phytoplankton representing a high and low DMSP producer), (3) time series sampling in coastal California waters using an autonomous sampling device, the Environmental Sample Processor, during a month-long study that spanned a natural phytoplankton bloom, and (4) natural marine bacterial populations in the Gulf of Mexico. Correlating gene expression with DMSP concentrations, uptake, and gaseous end products allowed for elucidation of the dominant pathways of bacterial degradation in these systems, and investigation into the biological and physical factors at play. The studies suggest that the availability of osmolytes (of which DMSP is one), the need to manage bacterial oxidative stress, and the presence of alternate organic sulfur sources correlated with DMSP fate. Ongoing studies are focusing of the mechanisms by which each affects bacterial DMSP degradation strategies.

Proj. 8 / 13

Microbial biodiversity and functionality in deep shale and its interfaces (DSIs)

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This project will characterize the diversity of microbes living at deep shale interfaces, identify the origin of these microbes within geologic time, and assess how this community is adapting to changing environments. With increased hydraulic fracturing, these deep shale environments may be particularly at risk for biodiversity change.

Update

To identify the geological and paleoenvironmental factors contributing to microbial diversity, the team explored three Marcellus shale well cores from regions with different maturity within the Appalachian Basin. Geochemistry, including trace element and lipid abundance, was analyzed. They integrated geochemical (major and trace elements), isotopic, and biomarker signatures from shale core samples to elucidate environmental conditions of deposition, source and provenance of detritus, thermal maturity, and the paleo redox environment. The team also developed a protocol for lab culturing microbes that require high pressure and temperature. Results at this stage have traced the paleoenvironmental shifts that predict the total organic carbon abundance via mitigation of microbial diversity.

Publications

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Proj. 9 / 13

Connecting the proximate mechanisms responsible for organismal diversity to the ultimate causes of latitudinal gradients in species richness

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This project connects genetic, molecular, and cellular mechanisms underlying adaptive variation within species to the ultimate causes of higher-order species diversity. Using the radiation of neotropical Adelpha butterflies, this team integrates phylogenetic and genomic insights about the evolution of adaptive traits with data from the ecology and natural history of the butterflies.

CONTINUE >

Update

Proposing a hypothesis that latitudinal gradients in species richness arise from increased diversification rates resulting from more intense biotic interactions in tropical than temperate communities, Mullen and colleagues completed a RAD phylogeny for the genus Adelpha and improved the Limenitis genome assembly by adding PacBio reads, creating frameworks that helped reveal patterns of mimicry and host plant-driven diversification, and platforms for testing their hypothesis. The team showed that while predation studies confirmed more intense predation in tropical environments, diversification in adaptive traits such as pigment visualization opsins evolve to have optimized thermostability along environmental clines. Solving this puzzle of adaptation drivers is being aided by tests of evolution rates of trait-related genes.

Publication

Ebel, E.R., et al. (2015). Rapid diversification associated with ecological specialization in Neotropical *Adelpha* butterflies. *Molec Ecol* 24: 2392-2405.

Francesca, D., et al. (2014). Opsin clines in butterflies suggest novel roles for insect photopigments. *Mol Biol Evol* 32: 368-379.

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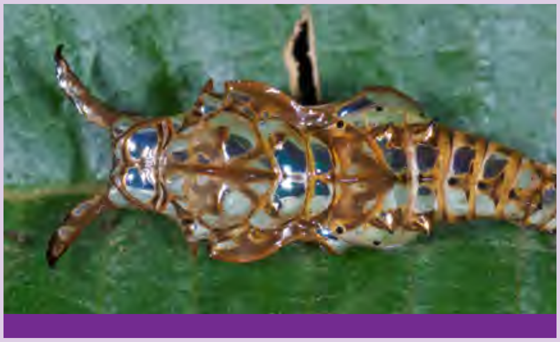
^ A male *Adelpha capucinus* dries its wings after emerging from its pupa at the Napo Wildlife Center in the east Ecuadorian Amazon.

CREDIT: KEITH WILLMOTT, UNIVERSITY OF FLORIDA



^ Larvae of a species in the "*Adelpha serpa* group" photographed in Honduras. The larvae was found feeding on a plant in the family Melastomataceae.

CREDIT: RYAN HILL, UNIVERSITY OF THE PACIFIC

Proj. 10 / 13

Scent-mediated diversification of flowers and moths across western North America

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We commonly think of floral scent for its role in attracting pollinators, but it can also be a cue for floral and seed predators. This project integrates chemical ecology and comparative genomics to explore the impact of past selective pressures on current patterns of diversity in non-model organisms: evening primroses, hawkmoths, bees and micromoths.

HTTP://ONAGMOTH.ORG

Update

During the past year the team collected extensive ecological data on 43 populations of 15 focal taxa and started population genetic and phylogenetic work of the plants and herbivores using genotyping-by-sequencing and MYbaits 300-gene sequence capture methods. Hundreds more species were vouchered and distributed to numerous herbaria. Draft genomes of three focal plants are also near completion. Larvae were collected and reared, and common garden pilot experiments to complement the fieldwork were initiated at Northern Arizona University. All scent and floral morphology data have been analyzed, producing exciting results linking pollination syndromes and functional specialization.

Publication

Rhodes, M., et al. (2014). Local topography shapes fine-scale spatial genetic structure in the Arkansas Valley evening primrose, *Oenothera harringtonii* (Onagraceae). *J Hered* 105: 806-815.

Proj. 11 / 13

Symbiont and transcriptomic niche dimensions of long-term coexistence in *Trifolium* communities

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This project expands on a long-term record of clover (*Trifolium*) species distributions to examine the role of genetic variation in rhizobial root symbionts in biological nitrogen fixation and clover coexistence.

Update

The team has been heavily involved in data collection and some analysis. Greenhouse experiments growing *Trifolium* species in different combinations tested different soil origins and rhizobium treatments. Experiments looking at the effects of the previous biotic environment's effect on the next generation of plant growth were also conducted using various permutations to evaluate the affects of competition and mutualism. Results advance competition theory, suggesting plants benefit from mutualists, and soil microbes also mediate the relative strength of intraspecific and interspecific plant interactions. All these effects varied among species, and are now being investigated at the molecular level.

Publication

Jones, E.I., et al. (2015). Cheaters must prosper: reconciling theoretical and empirical perspectives on cheating in mutualism. *Ecolog Lett* 18:1270-1284.

Proj. 12 / 13

The biogeography and evolution of drought tolerance in grasses

(CO-FUNDED WITH NASA)

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Christopher J Still
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The goal is to understand the dimensions of biodiversity of drought tolerance in grasses. This project examines interspecific variation in drought tolerance among related species, intraspecific variation in drought tolerance of geographically widespread species, and physiological and genomic aspects of the evolutionary transition from C3 to C4 photosynthesis.

Update

The team focused on 250 grasses and 30 non-grass outgroups, analyzing plastomes, 3D leaf anatomy, root anatomy, and drought tolerance phenotypes. Congeneric susceptible and tolerant species pairs were identified and analyses of gene expression changes during drying conditions (dry-down) are underway. Students have been involved in morphological modeling, leaf clearing, and vouchering, and have found adaptation to open fields from dense forest habitat played a major role in the evolution of leaf traits. The team has also revised placement of the economically-important Panicoideae clade in the grass phylogeny, and revealed numerous intermediates between C3 and C4 photosynthesis strategies. Surprisingly, C4 and CAM grasses appear more functionally constrained; plasticity of some cell shapes in those grasses influences drought tolerance.

Publications

Cotton, J. L., et al. (2015). Resolving deep relationships of PACMAD grasses; a phylogenomic approach. *BMC Plant Biol* 15: 178.

Costs and benefits of chronic viral infections in natural ecosystems

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Georgia Institute of Technology
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Rachel Whitaker
University of Illinois Urbana-Champaign
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Hot springs in Yellowstone National Park are prone to chronic viral infections, and this project investigates the genetic and functional basis of them. The study of this tractable hot spring model system can broaden our understanding of biodiversity and clarify the ways in which viruses influence the composition of microbial communities over time.

Update

The team continued collection and analysis of Yellowstone hot spring environmental samples for host and viral community structure and dynamics. Over 20,000 single cells were isolated and hundreds of genomes were partially sequenced, as were over 100 virus strains. A new anti-viral microbial host defense system was discovered in hot springs—and analyzed in the lab—where induced dormancy blocks viral entry. Viral FISH assays are being developed to link metagenomic sequences of viruses directly to their hosts in natural environments. An initial high-resolution temporal dataset of host and virus fluctuations and a model of contact-mediate dormancy are advancing understanding of this system.

A boiling Yellowstone mud hot spring sampled for this project.
CREDIT: MARK YOUNG, MONTANTA STATE UNIVERSITY

Publications

Bolduc, B., et al. (2014). Viral community composition in Yellowstone acidic hot springs assessed by network analysis. *ISME J* 9: 2162-2177.

Bautista, M., et al. (2015). Virus-induced dormancy in the Archaeon *Sulfolobus islandicus*. *mBIO* 6: e02565-14.

Childs, L.M., et al., (2014). CRISPR-Induced distributed immunity in microbial populations. *PLoS One* 9: e101710.

Dellas,N. et al. (2014). Archaeal viruses: diversity, replication, and structure. *Ann Rev Virol* 1: 399-426.

Gulbudak, H., Weitz, J.S. (2015). A touch of sleep: biophysical model of contact-mediated dormancy of Archaea by viruses. *Proc R Soc B. In review.*

Hochstein, R., et al. (2015). Large tailed spindle viruses of Archaea: A new way of doing viral business. *J Virol* doi: 10.1128/JVI.00612-15.

Snyder, J., et al. (2015). 40 years of archaeal virology: expanding viral diversity. *Virology* 479: 369-378.

Munson-McGee, J., et al. (2015). Nanoarchaeota, its Sulfolobales host, and Nanoarchaeota virus distribution across Yellowstone National Park Hot Springs. *Appl Environ Microbiol* 81: 7860-7868.

Typical high temperature Yellowstone hot spring.
CREDIT: MARK YOUNG, MONTANTA STATE UNIVERSITY

2013 Image Gallery

^ **Proj. 1/13** — Rupornis magnirostris picture, taken at Cambará do Sul, Rio Grande do Sul, Brasil.

CREDIT: JÚLIA MONTESANTI

^ **Proj. 7/13** — REU student Diano Cordero prepares to filter water samples during experiments to test for sulfur gas production from the DMSP analogs, dimethylsulfonioacetate and S- methylmethionine.

CREDIT: RONALD KIENE

^ **Proj. 10/13** — Hyles lineata drinks nectar from an *Oenothera californica* subsp. *avita* flower at the Mojave National Preserve, CA.

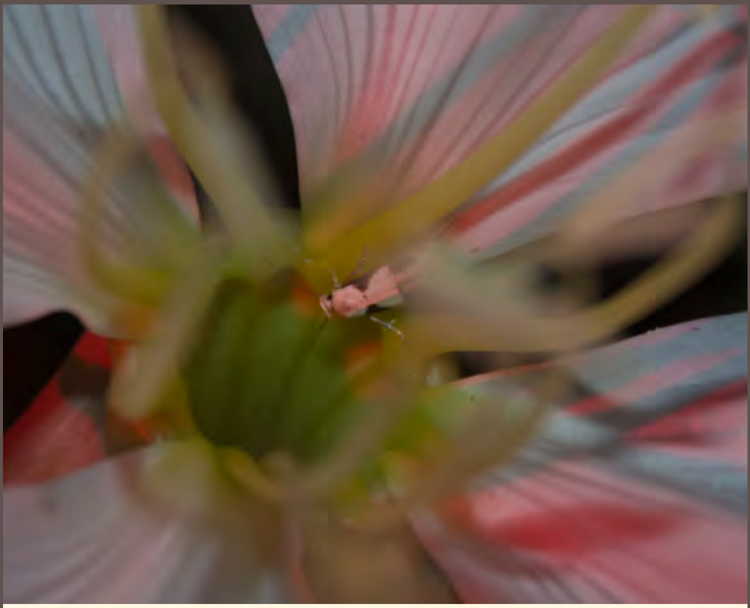
CREDIT: KRISSA SKOGEN, CHICAGO BOTANIC GARDEN

^ **Proj. 10/13** — A *Lasioglossum* bee visits a flower of *Oenothera gayleana* in NM.

CREDIT: RICK OVERSON, CHICAGO BOTANIC GARDEN

Proj. 7/13 — Advanced Placement biology students from Cedar Shoals High School, Athens, GA traveled to the University of Georgia Marine Institute in April 2015 to isolate marine bacteria and learn about coastal ecosystems.

CREDIT: MARY ANN MORAN



Proj. 10/13 — An adult Mompha moth visits *Oenothera cespitosa* subsp. *marginata* in Utah.

CREDIT: RICK OVERSON, CHICAGO BOTANIC GARDEN

Proj. 10/13 — *Oenothera xylocarpa*, Bakeoven Meadow, CA.

CREDIT: LAURA STEGER, CHICAGO BOTANIC GARDEN

Proj. 1/13 — Amazilia versicolor taken at Itatiaia, Rio de Janeiro, Brasil.

CREDIT: JÚLIA MONTESANTI

Proj. 10/13 — *Hyles lineata*, the white -lined sphinx moth, use many members of the Onagraceae as larval host plants. Here, a larva eats the flower bud of *Oenothera lavandulifolia*.

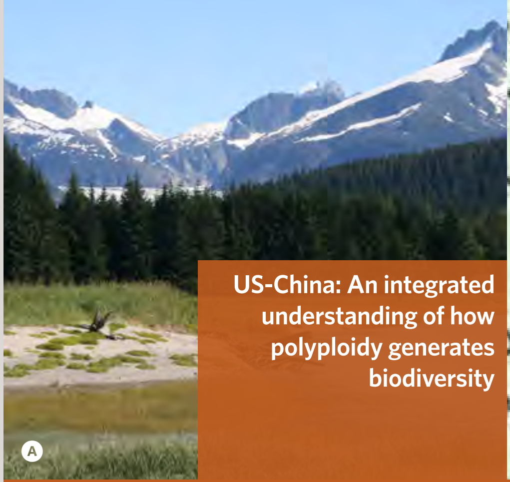
CREDIT: RICK OVERSON, CHICAGO BOTANIC GARDEN

Proj. 10/13 — Lighttrapping for moths.

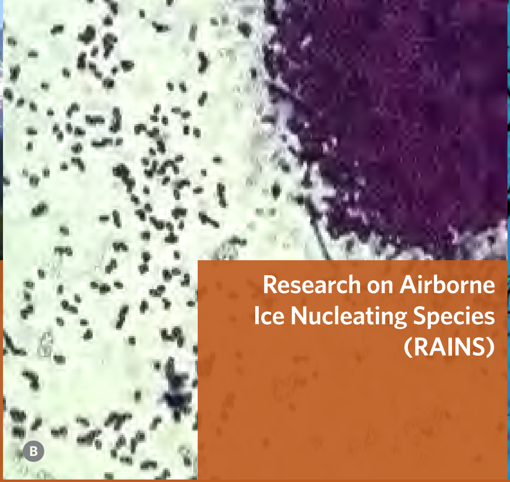
CREDIT: RICK OVERSON, CHICAGO BOTANIC GARDEN

Proj. 10/13 — *Oenothera neomexicana* field site in the Pinaleno Mountains, AZ.

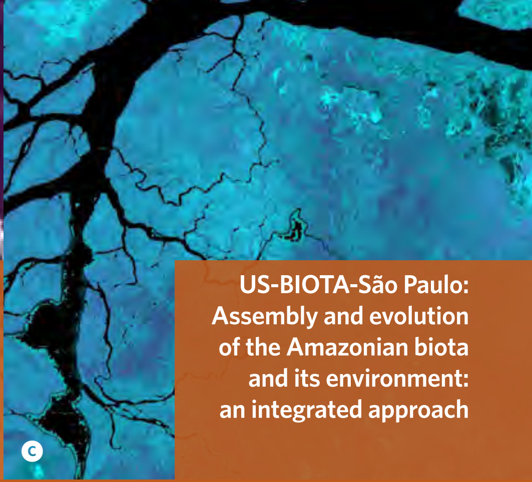
CREDIT: RICK OVERSON, CHICAGO BOTANIC GARDEN



US-China: An integrated understanding of how polyploidy generates biodiversity

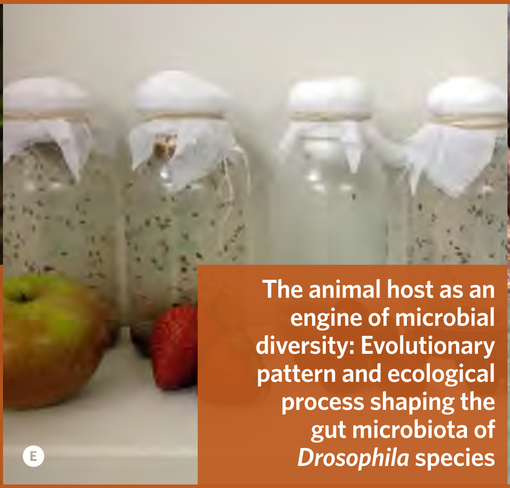


Research on Airborne Ice Nucleating Species (RAINS)



US-BIOTA-São Paulo: Assembly and evolution of the Amazonian biota and its environment: an integrated approach

Do parallel patterns arise from parallel processes?



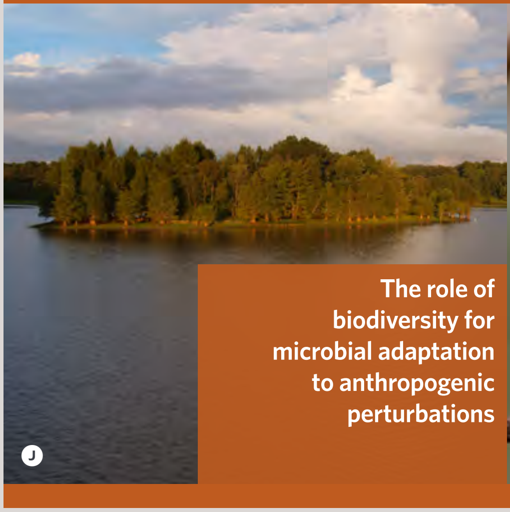
The animal host as an engine of microbial diversity: Evolutionary pattern and ecological process shaping the gut microbiota of *Drosophila* species

Community assembly and decomposer function of aquatic fungi along a salinity gradient

A community level approach to understanding speciation in Hawaiian lineages

The taxonomic, genomic, and functional diversity of soil carbon dynamics

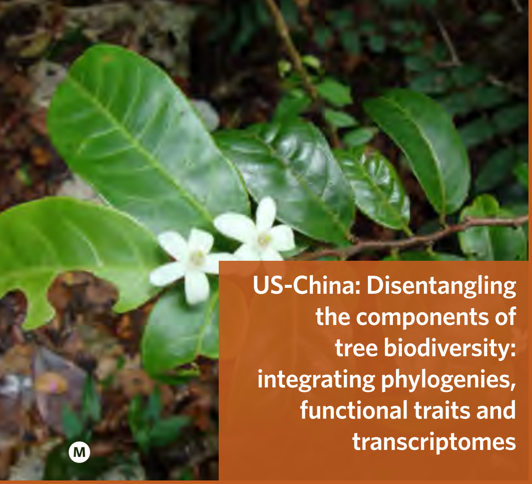
The role of taxonomic, functional, genetic, and landscape diversity in food web responses to a changing environment



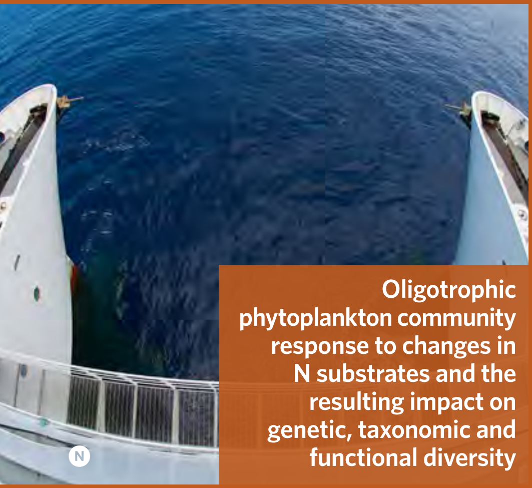
The role of biodiversity for microbial adaptation to anthropogenic perturbations

Historical and contemporary influences on elevational distributions and biodiversity tested in tropical Asia

US-China: Anthropogenic nutrient input drives genetic, functional and taxonomic biodiversity in hypereutrophic Lake Taihu, China



US-China: Disentangling the components of tree biodiversity: integrating phylogenies, functional traits and transcriptomes



Oligotrophic phytoplankton community response to changes in N substrates and the resulting impact on genetic, taxonomic and functional diversity

2012 updates

IMAGE CREDIT

Ⓐ Arlo Midgett
Ⓑ Brent Christner
Ⓒ Joel Cracraft
Ⓓ Michael N. Dawson
Ⓔ Alyssa Bost & Angela E Douglas
Ⓕ A. Ferrer
Ⓖ Karl Magnacca
Ⓗ Paul Dijkstra
Ⓘ Anthony R. Ives
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Ⓚ T. E. Martin
Ⓛ Hans Paerl
Ⓜ Nathan Swenson
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US-China: An integrated understanding of how polyploidy generates biodiversity

(CO-FUNDED WITH NSFC)

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CHINA MEMBERS	**Ming Dong** **Jiliang Pang** Hangzhou Normal University	**Jumin Li** **Shisheng Ke** Taizhou University	**Minghua Song** Chinese Academy of Sciences

Polyploid species have undergone recent whole genome duplications. This project examines the role that polyploidy has played in the evolution of strawberry species, using species in US and in China. The strawberry genus, with generally small genomes and cytogenetic compatability, is ideal for exploring patterns of genetic diversity arising from polyploidization.

HTTP://WILDSTRAWBERRY.ORG

Update

Taking on the challenge of studying polyploids, the team released several community resources in the past year, including a script to perform phylogenetics of linkage-map-anchored polyploidy subgenomes. All the collection (2013 + 2014) and haplotype data of 18 *Fragaria* species have been put online. The team published their findings on genetic processes involved in high order polyploidization—the events that create an octoploid strawberry—and found that placement of octoploids in phylogenetic analyses suggests potential breakage in linkage disequilibrium of cytoplasmic genomes during allopolyploidization. Exploring mitochondrial patterns, they also detected intracellular gene transfer events that might function in reducing nuclear-mitochondrial incompatibilities.

Fragaria collecting in Sichuan, China. Jing-Song Chen, Yao-Bin Song, and Tia-Lynn Ashman.

CREDIT: AARON LISTON, OREGON STATE UNIVERSITY

Publication

Ashman, T.L., et al. (2013). Revisiting the dioecy-polyploidy association: alternate pathways and research opportunities. *Cytogenet Genome Res* 140: 241-255.

Gonda, R., et al. (2015). "The Strawberry Caper": Using scenario-based problem solving to integrate middle school science topics. *Am Biol Teacher* 77: 50-54.

Govindarajulu R., et al. (2015). Comparison of nuclear, plastid, and mitochondrial phylogenies and the origin of wild octoploid strawberry species. *Am J Bot* doi: 10.3732/ajb.1500026.

Johnson, A.L., et al. (2014). Bioclimatic evaluation of range in *Fragaria* (Rosaceae): consequences of variation in mating system, ploidy and species age. *Bot J Linnean Soc* 176: 99-114.

Liston, A., et al. (2014). *Fragaria*: A genus with deep historical roots and ripe for evolutionary and ecological insights. *Am J Bot* 101: 1686-1699.

Tennessen, J.A., et al. (2014). Evolutionary origins and dynamics of octoploid strawberry subgenomes revealed by dense targeted capture linkage maps. *Genome Biol Evol* 6: 3295-3313.

Fragaria collecting in Sichuan, China. Junmin Li, Yao-Bin Song, and Ming Dong.

CREDIT: TIA-LYNN ASHMAN, UNIVERSITY OF PITTSBURGH

Research on Airborne Ice Nucleating Species (RAINS)

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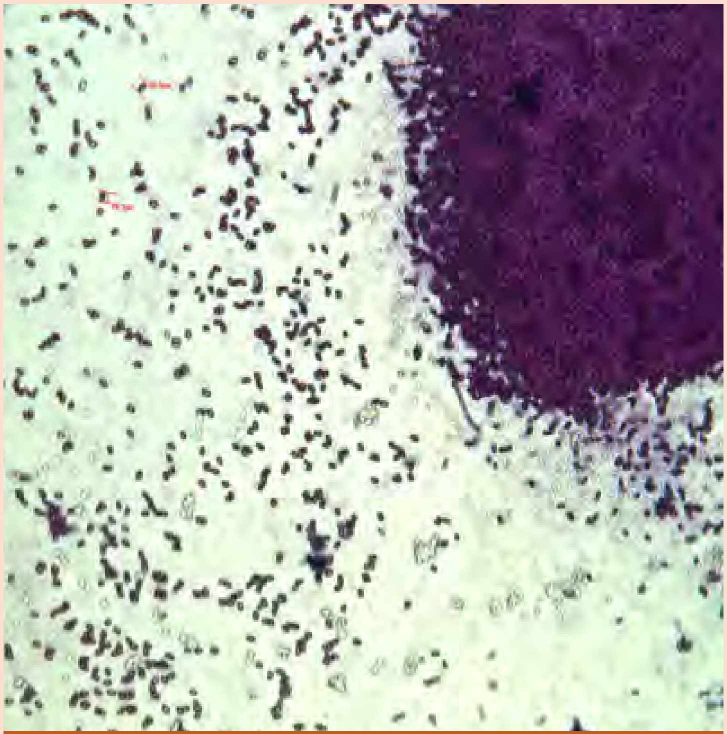
This project examines the diversity and activity of airborne microbes that catalyze the formation of ice crystals in the atmosphere. RAINS seeks to understand the role of microbial ice nucleation in atmospheric microbial dispersal, and ultimately, precipitation generation.

HTTPS://SCHOLAR.GOOGLE.COM/CITATIONS?USER=H7YZSPYAAAAJ&HL=EN
HTTPS://BIOICE.WORDPRESS.COM

Update

The RAINS team completed collection of aerosols and precipitation in Louisiana, Virginia, and Idaho, to characterize the seasonal diversity of microbial assemblages available before, during, and after precipitation events. Thick in analysis, the group is pursuing an interesting gene family called ina that conveys the ice nucleation phenotype. At the end of October 2015, the RAINS team assembled in Baton Rouge, LA for a week long sampling campaign intended to take advantage of the collaborative, interdisciplinary aspect of the project. During this time, they collected and analyzed samples from the remnants of Hurricane Patricia, which produced ~10 inches of rain in the region over two days.



^ Balloons floating into the stratosphere collect microorganisms that are brought back to the lab and studied. Some of them travel hundreds of kilometers through the air.

CREDIT: BRENT CHRISTNER, UNIVERSITY OF FLORIDA

Publication

Bryan, N.C., et al. (2014). A method for sampling microbial aerosols using high altitude balloons. *J Microbiol Methods* 107: 161-168.

Cameron, K.A., et al. (2015). Diversity and potential sources of microbiota associated with snow on western portions of the Greenland Ice Sheet. *Environ Microbiol* 17: 594-609.

Weber, C.F. (2014). Hormones and antibiotics in nature: a laboratory module designed to broaden undergraduate perspectives on typically human centered topics. *J Microbiol Biol Educ* 15: 277-286.

Weber, C.F, Werth, J.T. (2015). Is the lower atmosphere a vast, readily accessible reservoir of culturable antimicrobial compound-producing Actinomycetales? *Front Microbiol* 6: 802.

Weber, C.F. (2016). *Polytrichum commune* spores nucleate ice and associated microorganisms increase the temperature of ice nucleation activity onset. *Aerobiologia* 2: 353-361.

Weber, C.F., Werth, J.T. (2015). Culturing life from air: using a surface air system to introduce discovery-based research in aerobiology into the undergraduate biology curriculum. *J Microbiol Biol Educ* doi: 10.1128/jmbe.v16i1.813.

US-BIOTA-São Paulo: Assembly and evolution of the Amazonian biota and its environment: an integrated approach

(CO-FUNDED WITH NASA AND FAPESP)

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Jose Diniz Filho
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This project seeks to understand the evolutionary and ecological history of Amazonia, the most diverse ecosystem on Earth. A goal is to build a comprehensive database of plants, birds and primates, which, together with phylogenetic, population genetic, remote sensing, geology, and Earth-systems modeling, will illuminate the historical development of Amazonian biota.

Update

Members of the team organized a November 2015 symposium at the Geological Society of America in Baltimore integrating Amazonian biotic and geological data. This was followed by a successful PI meeting and symposium in São Paulo. The AMNH, FMNH and Brazilian colleagues continued large-scale sampling of multiple bird species complexes and primates to reveal fine-grain endemism and phylogeographic patterns with next-gen sequencing. Databasing of geo-referenced specimens of Amazonian birds, primates, and several plant families continued. The botany group obtained whole chloroplast genomes for 14 species representing major Lecythidaceae lineages that will be used for phylogenetic studies.

Publications

Brower, A.V.Z. (2015). What is a cladogram and what is not? *Cladistics* doi: 10.1111/cla.12144.

Cracraft, J. (2014). “Avian higher-level relationships and classification: Passeriformes” in Dickinson, E.C., Christidis, L., eds. *The Howard & Moore complete checklist of the birds of the world Fourth edition*. Aves Press. Northhampton, UK.

Cracraft, J., et al. (2015). Response to comment on “Whole-genome analyses resolve early branches in the tree of life of modern birds”. *Science* 349: 1460.

Claramunt, S., Cracraft, J. (2015). A new time tree reveals Earth history’s imprint on the evolution of modern birds. *Science Advances* 1: e1501005

Garzón-Orduña, I.J., et al. 2015. An alternative, plant-based time-tree implies conflicting dates for the diversification of ithomiine butterflies (Lepidoptera: Nymphalidae: Danainae). *Syst Biol* 64: 752-767.

Garzón-Orduña, I.J., et al. (2015). Competing paradigms of Amazonian diversification and the Pleistocene refugium hypothesis. *J Biogeography* 42: 1357-1360.

Gubili, C., et al. (2015). Isolation and characterization of polymorphic microsatellite DNA markers from an Amazonian white-sand vegetation specialist bird, *Xenopipo atronitens* (Aves: Pipridae). *J Field Ornithol* Submitted.

Huang, Y-Y, et al. (2015). Toward a phylogenetic-based Generic Classification of Neotropical Lecythidaceae–I. Status of *Bertholletia, Corythophora, Eschweilera* and *Lecythis*. *Phytotaxa*. 203: 85-121.

Mori, S.A., et al. (2015). The utility of placentation in the circumscription of genera of new world Lecythidaceae (Brazil nut family). *Phytoneuron* 13: 1–46.

Mori, S.A., et al. (2015). Toward a phylogenetic-based generic Classification of Neotropical Lecythidaceae–II. Status of *Allantoma, Cariniana, Couratari, Couroupita, Grias and Gustavia. Phytotaxa.* 203: 122-137.

Patitucci, K.F., et al. (2015). *Mosesia ovalis n. sp.* (Digenea: Phaneropsolidae) from the green manakin *Xenopipo holochlora* from Peruvian Amazon with notes on morphology of *Mosesia mosesi* Travassos, 1921. *Comparative Parasitol* 83: 49-53.

Savit. A., Bates, J. (2015). Right around the Amazon: The origin of the circum-Amazonian distribution in *Tangara cayana* (with A. V. Savit). *Folia Zoologica* 64: 273.

Do parallel patterns arise from parallel processes?

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Julian P. Sachs
University of Washington
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This project is to survey the dimensions of diversity of the organisms found in marine lakes, and investigate the processes that cause gains and losses in this biodiversity. Marine lakes formed as melting ice sheets raised sea level after the last glacial maximum and flooded hundreds of inland valleys around the world.

MARINE LAKES: EXPERIMENTS IN ECOLOGY AND EVOLUTION | HTTP://MARINELAKES.UCMERCED.EDU

PAPAPRO COLLABORATIVE RESEARCH ENVIRONMENT | HTTP://PAPAPRO.PBWORKS.COM/W/PAGE/77654363/PAPAPRO%20HOME

PAPAPRO : DO PARALLEL PATTERNS ARISE FROM PARALLEL PROCESSES? | HTTP://WWW.BCO-DMO.ORG/PROJECT/2238

BCO-DMO PROJECT WEBSITE AND DATA REPOSITORY | HTTP://WWW.BCO-DMO.ORG/DATASET/54118

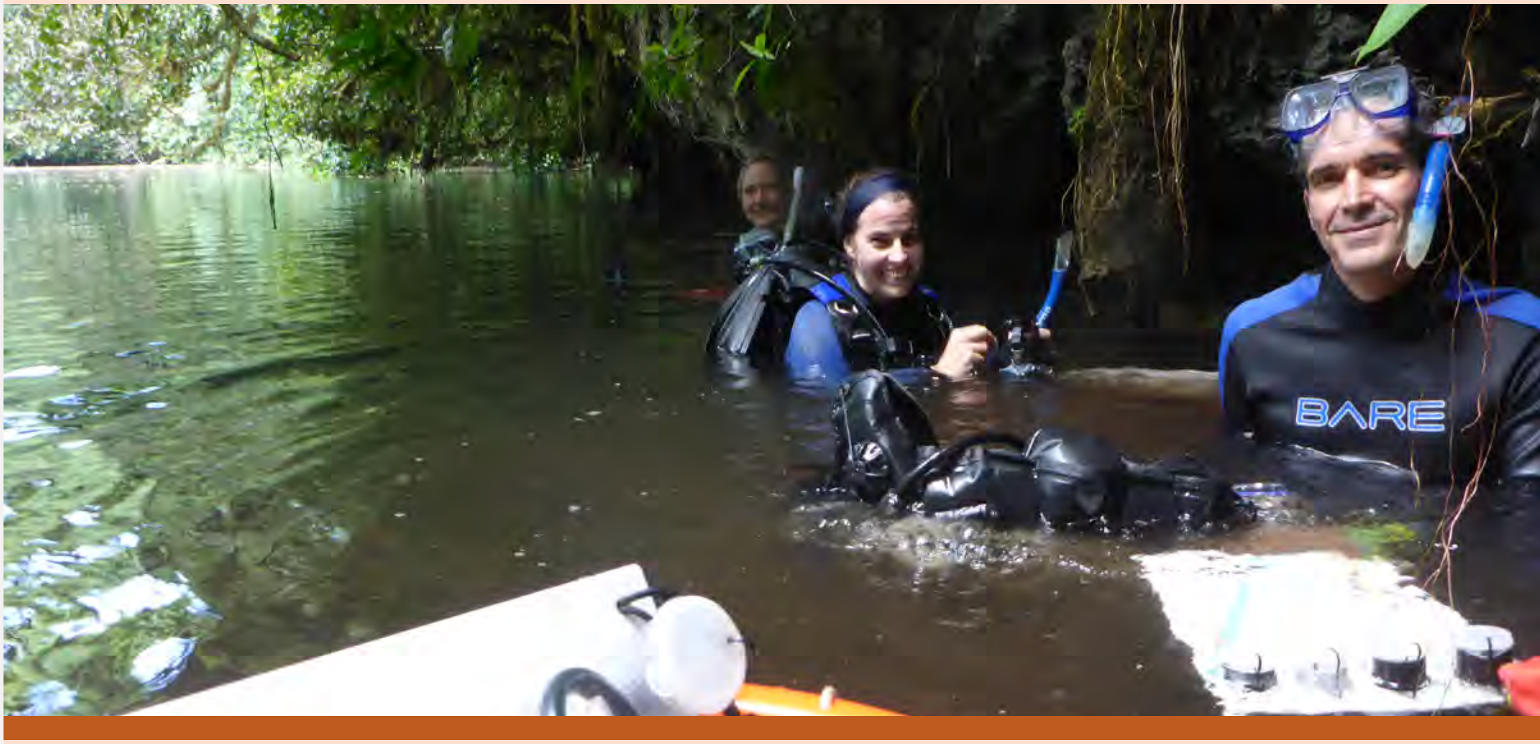
Update

Since 2013, the team has spent 7 months conducting fieldwork in Palau. These field trips involved survey and collection of modern marine microbe, invertebrate, fish, and algae communities and recovery of sediment cores up to 11 m deep and 10,000 years old. Over 15 lakes have been surveyed for species diversity—with a total of 14,726 geolocated datapoints describing invertebrate and algae species distributions—and 21 species of macrobiota sampled in detail for genetic information. Experiments with microbial communities are exploring how functional diversity is shaped by, and shapes, environmental variation, with potential knock-on effects for macrobiota. These datasets are now being integrated to find out how communities have changed through time, leading to today's distributions of functions, genes and species.

Publications

Dawson, M.N. (2015). Islands and island-like marine environments. *Global Ecol Biogeograph* doi: 10.1111/geb.12314.

Ladd, S.N., Sachs, J.P. (2015). Influence of salinity on hydrogen isotope fractionation in Rhizophora mangroves from Micronesia. *Geochimica et Cosmochimica Acta* 168: 206-221.



^ Having snorkeled and dived to photograph and collect samples, the team of scientific divers transfers each sample into an uniquely labeled tube of preservative for shipping back to the lab for genetic analyses and long-term storage.

CREDIT: LAUREN SCHIEBELHUT

Proj. 5 / 14

The animal host as an engine of microbial diversity: Evolutionary pattern and ecological process shaping the gut microbiota of *Drosophila* species

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Gregory Loeb
Cornell University
(1241099)

John Jaenike
University of Rochester
(1241099)

This project investigates the significance of mutually-beneficial interactions in promoting the diversity of bacterial communities and their animal hosts in fruit flies and their relatives.

Update

In this project, Douglas and colleagues have applied metagenomic and transcriptomic tools to demonstrate that *Drosophila* is a key driver of the microbial communities in the immediate environment by altering microbial community composition and promoting microbial diversity. The bacteria have substantial effects on animal fitness, including development rates, starvation tolerance and behavior, all with profound ecological consequences. Through their transcriptome work, they have also successfully distinguished the key effects of diet (fruit and fungi) and gut microbiota composition on the molecular function of the *Drosophila* gut.

Publications

Douglas, A.E. (2013). Microbial brokers of insect-plant interactions revisited. *J Chem Ecol* 39: 952-961.

Douglas, A.E. (2014). Symbiosis as a general principle in eukaryotic evolution. *CSH Perspect Biol* 6: a016113.

Douglas, A.E. (2014). The molecular basis of bacterial–insect symbiosis. *J Molec Biol* 23: 3830-3837.

Wong, A, et al. (2015). The host as driver of the microbiota in the gut and external environment of *Drosophila melanogaster*. *Appl Environ Microbiol* 81: 6232-6240.

Proj. 6 / 14

Community assembly and decomposer function of aquatic fungi along a salinity gradient

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James Dalling
Katy Heath
University of Illinois
Urbana-Champaign
(1241212)

Diverse groups of freshwater and marine fungi remain to be described from tropical waters. This project examines the roles of aquatic fungi in the decomposition of wood along salinity gradients in Panamanian coastal rivers, asking how gene expression patterns among diverse fungi influence the rate and trajectory of wood decay in water.

HTTP://PUBLISH.ILLINOIS.EDU/AQUATICFUNGI

Update

A total of 600 morphospecies have been described using traditional methods that allow fungal identification based on isolation from fruiting bodies. Spore-derived cultures provided internal transcribed spacer (ITS) barcode sequences for ~70% of the 600. DNA was also obtained from completed decomposition field experiments. Fluidigm/HiSeq sequencing applications were employed to capture fungi, bacteria, and archaea, producing a snapshot of the decomposition community. Fungal diversity assays were completed along the entire salinity gradient and throughout the decomposition series. Dozens of primer sets, that amplify genes encoding lignocellulolytic enzymes from 380 fungi, will be used in combination with the ITS phylogeny to investigate evolution of the gene family. Transriptome profiling of four fungal cultures is also underway.

Proj. 7 / 14

A community level approach to understanding speciation in Hawaiian lineages

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Daniel Gruner
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(1240774)

Kerry Shaw
Cornell University
(1241060)

Donald Price
University of Hawaii
Hilo
(1241228)

The arthropod communities on Hawaiian islands that differ in age have different natural histories and may express different patterns and rates of evolution. This research will transform our thinking of how biodiversity is impacted by the dynamic community.

Update

The large team has just completed intensive field studies, which involved setting up plots, collecting soil and litter, then Malaise, pitfall, power aspirator and beating sampling to collect arthropods. Vegetation sampling was conducted in parallel. Specimen sampling has been a rigorous multi-institutional effort. ddRAD sequencing protocols were applied to target mitochondrial DNA sets. Exon capture was used for population genomics of 4 *Drosophila* species on three islands. The macroecological data analysis has contributed to theoretical development, showing that the Maximum Entropy Theory of Ecology is compatible with most metrics but fails for systems undergoing rapid change such as this island chronosequence.

Publications

Brewer, M.S., Carter, R., Croucher, P.J.P, Gillespie, R.G. (2015). Shifting habitats, morphology and selective pressures: developmental polyphenism in an adaptive radiation of Hawaiian spiders. *Evolution* 69: 162-178.

Brewer, M.S., Cotoras, D.D., Croucher, P.J.P, Gillespie, R.G. (2014). New sequencing technologies, the development of genomics tools, and their applications in evolutionary arachnology. *J Arachnol* 42: 1-15.

Gillespie, R.G. (2014). "Island Biogeography". *International Encyclopedia of Geography* Douglas Richardson. Wiley-Blackwell and the Association of American Geographers: Hoboken, New Jersey.

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Warren, B.H., et al. (2015). Islands as model systems in ecology and evolution: prospects fifty years after MacArthur-Wilson. *Ecol Lett* 18: 200.

Yim, K., et al. (2014). Comparative transcriptomics of maturity-associated color change in Hawaiian spiders. *J Hered* 105: 771-781.

A Hawaiian carnivorous caterpillar, *Eupithecia palikea*.

CREDIT: KARL MAGNACCA

The taxonomic, genomic, and functional diversity of soil carbon dynamics

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This project examines the roles that taxonomic and genetic diversity of microbes play in the processing of new and old carbon in soils. Of particular interest is the concept of 'priming': a pulse increase of carbon causes an acceleration in soil organic matter degradation.

Update

In the midst of microbiome analysis, the team has been publishing their ecological results linking soil bacterial biodiversity to soil carbon stability. They first developed and published a new microbial ecology method for stable isotope probing. Then, they used isotope probes to study fast- and slow-growing bacterial groups. 16S rRNA genes were sequenced from a ponderosa pine ecosystem with plots pulsed with single or repeated carbon treatments. Both bacterial groups, with extra carbon, became less dominated by a single microbial genus and increased diversity. The team is preparing pipelines for massive bacterial community characterization; these will become publically available web-based bioinformatics.

Publications

Hungate B.A., et al. (2015). Quantitative microbial ecology through stable isotope probing. *Appl Environ Microbiol* 81: 7570-7581.

Mau, R.L., et al. (2015). Linking soil bacterial biodiversity and soil carbon stability. *ISME J* 9: 1477-1480.

Collecting soil for microbial diversity analysis.

CREDIT: PAUL DIJKSTRA, NORTHERN ARIZONA UNIVERSITY

The role of taxonomic, functional, genetic, and landscape diversity in food web responses to a changing environment

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State University
Fargo
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Ives and colleagues are examining how genetic, taxonomic, ecological, and landscape diversity influence the control of agricultural pests by their natural enemies. They have accrued an array of remote-sensing ecological and molecular tools to examine this system, using aphids and pea family plants as the central interaction of interest.

Update

Focusing on aphids as the pests, and then expanding to the entire community of organisms in a field, the team completed experiments looking at temperature fluctuations on aphid population and predation. They performed a temporal survey of aphid dynamics and evolution. Broad-scale spatial surveys of bacterial endosymbionts of aphids from different locations were initiated. Then, choosing a single alfalfa field, the team screened bacteria associated with all common herbivorous insects and their natural enemies. The team has brought these natural systems into the lab, completing experiments on the aphid-microbe-parasitic wasp relationships that confer resistance and susceptibility, and manipulating environmental conditions to understand their effects on communities.

Publication

Barton, B.T. (2014). Reduced wind strengthens top-down control of an insect herbivore. *Ecology* 95: 2375-2381.

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Oliver, K.M., Martinez, A.J. (2014). How resident microbes modulate ecologically-important traits of insects. *Curr Opin Insect Sci* 4: 1-7.

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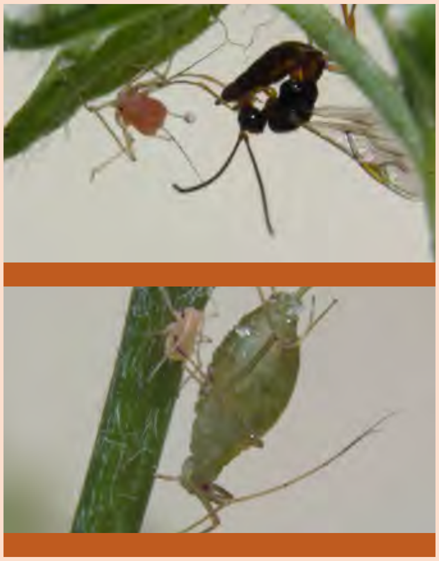
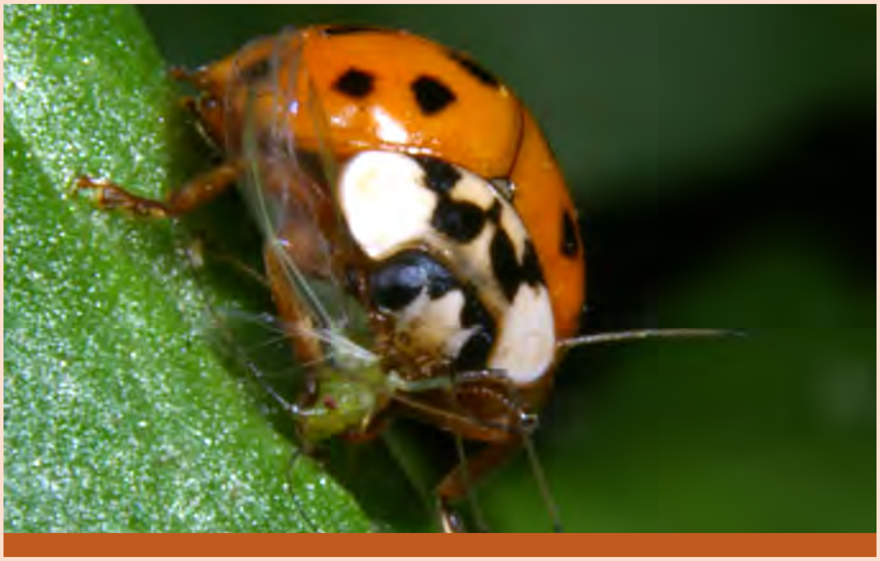


Top: The parasitoid *Aphidius ervi* attacking a pea aphid.
Bottom: The pea aphid, *Acyrthosiphon pisum*.
CREDIT: ANTHONY R. IVES, UW-MADISON



The multicolored Asian ladybeetle, *Harmonia axyridis*.
CREDIT: ANTHONY R. IVES, UW-MADISON

The role of biodiversity for microbial adaptation to anthropogenic perturbations

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This project examines how low-abundance (rare) members of microbial communities enable community adaptation and resilience to disturbances and to the presence of new organic compounds such as petroleum hydrocarbons, pesticides, and antibiotics.

Update

To quantify the importance of the rare biosphere and its function for microbial community adaptation to environmental perturbations, the team set up lab mesocosms of natural plankton from Lake Lanier (GA) and perturbed them with manmade organic compounds that the community had rarely seen previously. Time-series metagenomic analysis of the plankton revealed that rare species were commonly responsible for the degradation of important organic pollutants, and identified new biodegradation genes and transmissible plasmids. Further, these data revealed that horizontal gene transfer of genes under selection was rampant during the enrichment period and caused a reduction in intra-specific diversity in the natural populations. Experimental patterns from the laboratory mesocosms are being cross-examined in the Lake Lanier, in-situ, with dynamic models built for the entire lake community of >18,000 bacterial species.

Publication

Caro-Quintero, A., Konstantinidis, K.T. (2015). Inter-phylum HGT has shaped the metabolism of many mesophilic and anaerobic bacteria. *ISME J* 9: 958-967.

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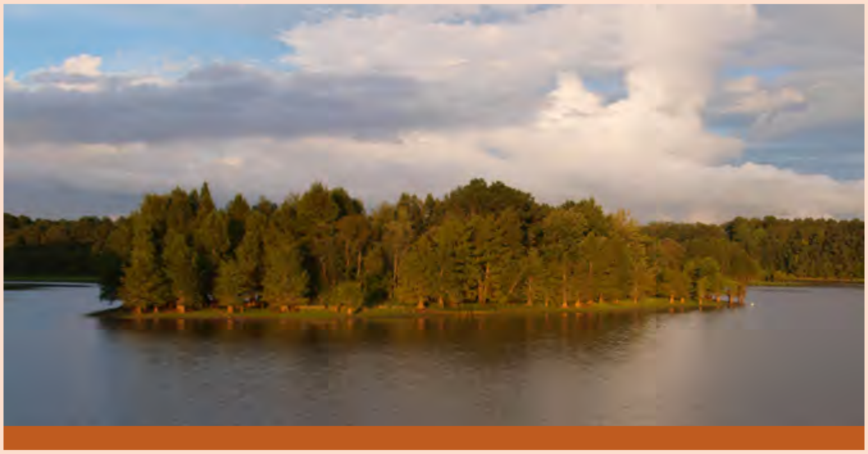

< Photo of Lake Eufaula, Alabama.

CREDIT: K. KONSTANTINIDIS AND D. TSEMENTZI, GEORGIA TECH

Historical and contemporary influences on elevational distributions and biodiversity tested in tropical Asia

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This project examines multiple factors that may contribute to the maintenance of elevational gradients in biodiversity, using diverse tropical bird fauna in Borneo as a model system. Bird blood parasites, nesting behavior, and other life history variables will be examined with genetic and environmental differentiation.

Update

The team has monitored 718 nests of 45 species across the elevational gradient, assessing risk, behavior, and development. Sensitivity of adult metabolism to temperature was measured on 99 individuals of 20 species. Nearly 1000 birds were banded to further estimate adult mortality and dispersal. Nest manipulations allowed a student to test the effect of harsh weather on the birds. Hundreds of DNA and RNA samples are being analyzed. There are now 4000 blood samples available for DNA analysis of 76 species. Microsatellite and other markers were developed, and a microarray platform of adaptive SNP variation is being run. Fitness consequences related to ecological and evolutionary theories have been published, supporting novel and conventional allometric, growth rate, and life history hypotheses.

Publications

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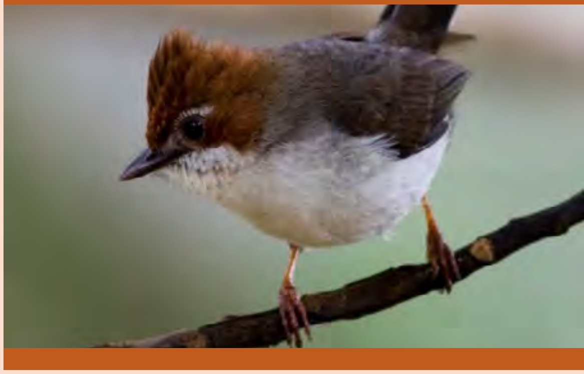

Top: *Pellorneum*, an endemic species in Borneo, standing at its nest entrance, has a narrow elevational distribution, potentially associated with the greater sensitivity to temperature of its embryos.

Bottom: *Yuhina*, an endemic species in Borneo, has a wide elevational distribution, potentially associated with the lower sensitivity to temperature of its embryos.

CREDIT: T. E. MARTIN

Anthropogenic nutrient input drives genetic, functional and taxonomic biodiversity in hypereutrophic Lake Taihu, China

(CO-FUNDED WITH THE CHINESE MINISTRY OF SCIENCE AND TECHNOLOGY)

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Paerl and colleagues are examining the genetic diversity of microbial involved in production and nutrient cycling dynamics in a lake that experiences massive blooms of toxic cyanobacteria. They are linking diversity to the inputs and processing of nitrogen that is the cause of the toxic blooms.

Update

Increased nitrogen (N) input into many rivers and lakes is a key factor promoting harmful algal (dominated by cyanobacteria) blooms; this project confronts needed environmental management with an ecosystem scale systems biology approach. Research trips to Lake Taihu, China where N input, biogeochemical cycling, biodiversity measurements, experimental mesocosm nutrient manipulations and modeling efforts were completed, has led to publications used to develop nutrient reduction strategies aimed at controlling blooms. In situ mesocosm experiments examined nitrogen fixation potential, hypothesized to be positively selected for when nitrogen availability controls bloom development. This hypothesis was rejected, indicating that external N inputs play a critical role in bloom dynamics. Observations are integrated into a mechanistic model of cyanobacteria – N interaction that spans the molecular and ecosystem scales. Results from this study are being used as a "looking glass" for other lakes and estuaries worldwide threatened with bloom development and expansion.

Publications

Deng, J., et al. (2014). Earlier and warmer springs increase cyanobacterial (*Microcystis* spp.) blooms in subtropical Lake Taihu, China. *Freshwater Biol* 59: 1076-1085.

Deng, J., et al. (2014). Effects of nutrients, temperature and their interactions on spring phytoplankton community succession in Lake Taihu, China. *PLOS ONE* 9: e113960.

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Havens, K.E., Paerl, H.W. (2015). Climate change at a crossroad for control of harmful algal blooms. *Environmental Science & Technology* 49: 12605-12606.

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Otten, T.G., Paerl, H.W. (2015). Health Effects of Toxic cyanobacteria in U.S. Drinking and Recreational Waters: Our Current Understanding and Proposed Direction. *Curr Envir Health Rpt* 2: 75-84.

Paerl, H.W. (2013). "Combating the global proliferation of harmful cyanobacterial blooms by integrating conceptual and technological advances in an accessible water management toolbox" in Crystal ball – 2013. *Environ Microbiol Rep* 5: 12-14.

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Steffen, M.M., et al. (2014). Nutrients drive transcriptional changes that maintain metabolic homeostasis but alter genome architecture in *Microcystis. ISME J* 8: 2080-2092.

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Watson, S.B., et al. (2015). "Harmful algal blooms." in Wehr, J.D., et al., eds. *Freshwater Algae of North America*. Academic Press, San Diego, CA. pp. 873-920.

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Proj. 13 / 14

US-China: Disentangling the components of tree biodiversity: integrating phylogenies, functional traits and transcriptomes

(CO-FUNDED WITH NSFC)

US MEMBERS

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Michigan State University
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CHINA MEMBERS

Keping Ma
Zhanging Hao
Lixin Zhang
Lanzhu Ji
Chinese Academy of Sciences

A pioneer of the emergent community functional phylogenomics field, this study of tree biodiversity is developing a predictive framework that can address classic questions about the functional similarity of species, the dynamic functional responses of species to environmental stimuli and help us understand processes that generate and maintain forest diversity.

Update

The project has produced the first inventories of transcriptomes for tree communities in Wisconsin and subtropical China (> 125 non-model species) and it has quantified community-wide gene expression response to drought for tree species in the Wisconsin forest. The data are being used in functional phylogenomic analyses of community dynamics, to relate plant resistance transcripts to seedling mortality rates, to explore tree species co-occurrence and their soil fungal assemblage, to quantify the phylogenetic signal in gene expression in response to drought and explore whether co-expression promotes co-occurrence. Additionally, species in the genera *Acer* and *Prunus* were subjected to phylogenetically structured competition experiments and evaluated for gene expression response.

Proj. 14 / 14

Oligotrophic phytoplankton community response to changes in N substrates and the resulting impact on genetic, taxonomic and functional diversity

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Matthew Church
University of Hawaii
(1241263)

Kevin Arrigo
Stanford University
(1241093)

Genomics, molecular biology, and stable isotope tracers become tools to investigate how changes in the form and availability of nitrogen affect the dimensions of biodiversity in marine phytoplankton. Focusing on the North Pacific Subtropical Gyre, they use innovative nanomethodologies for characterizing seawater and a number of state-of-the-art methods for comprehensive community evaluation.

Update

The team conducted the Nutrient Effects on Marine microOrganisms (NEMO) cruise in 2014, collecting complex comprehensive datasets about water, element availability, phytoplankton ecotypes and communities, excitation, light, and nitrogen fixation capacity. They have been analyzing the data since, leading to numerous publications showing patterns drawn from understanding the basic properties of the gyre blooms. Idealized one-dimensional modeling studies show how internal waves can modify biogeochemical dynamics in oligotrophic conditions. And two-dimensional modeling studies reveal more complex physical/biogeochemical interactions. Novel microarray-based gene-centric approaches for analysis of metatranscriptomic data have been developed (called MAGC bioinformatics), revealing the transcriptional patters underlying the whole microbial community response.

Publications

Bench, S.R., et al. (2013). Whole genome comparison of six Crocosphaera watsonii strains with differing phenotypes. *J Phycol* 49: 786-801.

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Shilova, I.N., et al. (2014). A microarray for assessing transcription from pelagic marine microbial taxa. *ISME J* 8: 1476-1491.

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2012
Image Gallery

Proj. 5/14 — Fungi isolated from field-collected *Drosophila melanogaster* include *Penicillium* species and unidentified yeasts.

CREDIT: JOHN MCMULLEN AND ANGELA E DOUGLAS, CORNELL UNIVERSITY

Proj. 12/14 — A top down view of an in situ mesocosm experiment on a *Microcystis* cyanobacterial bloom in Lake Taihu, China.

CREDIT: HANS PAERL, UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL

Proj. 12/14 — Alex Hounshell (left), a PhD graduate student at the University of North Carolina at Chapel Hill Institute of Marine Sciences, conducts mesocosm experiments with colleagues from the Nanjing Institute of Geography and Limnology and Taihu Laboratory for Lake Ecosystem Research in Wuxi, China.

CREDIT: HANS PAERL, UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL

Proj. 5/14 — Drosophila fruit diets: *Drosophila* fruit flies are cultured on fruit-supplemented diets to investigate how the gut microbiota influences fitness on different food substrates, a first measure of microbiota effects on the ecological amplitude of the fruit fly host.

CREDIT: ALYSSA BOST AND ANGELA E DOUGLAS, CORNELL UNIVERSITY

Proj. 4/14 — Having hiked to the lake, a member of the team snorkels to collect specimens from a randomized series of points in the lake.

CREDIT: MICHAEL N. DAWSON

Proj. 12/14 — Dr. Hans Paerl collects samples of *Microcystis* from water taken from Lake Taihu, China.

CREDIT: HANS PAERL, UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL

Proj. 2/14 — RAINS PIs Carolyn Weber (left) and Boris Vinatzer harvest Louisiana rain collected during a sampling campaign in late October 2015.

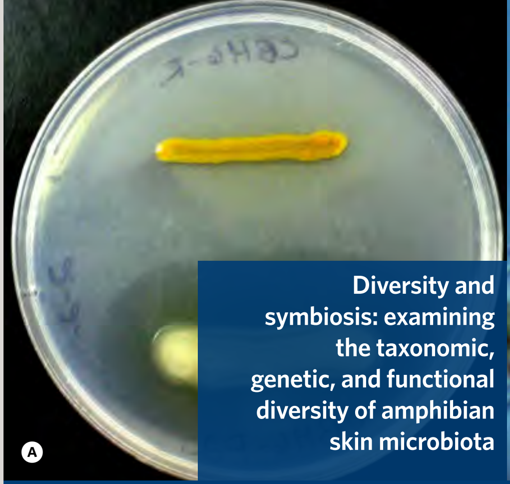
CREDIT: BRENT CHRISTNER, UNIVERSITY OF FLORIDA

Proj. 12/14 — A Microcystis cyanobacterial bloom in Lake Taihu, China (June, 2015).

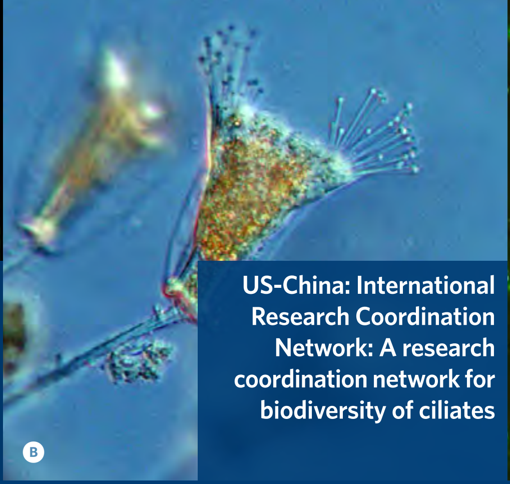
CREDIT: HANS PAERL, UNIVERSITY OF NORTH CAROLINA AT CHAPEL HILL

Proj. 4/14 — A selection of the sponges that occur on fallen trees in the shallowest waters of 'Big Crocodile Lake,' Mecherchar, Palau.

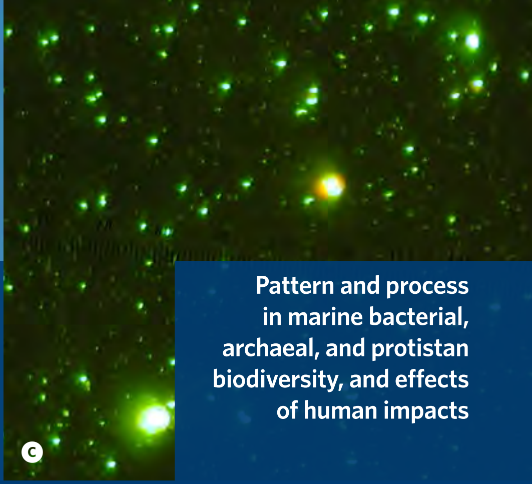
CREDIT: MICHAEL N. DAWSON



Diversity and symbiosis: examining the taxonomic, genetic, and functional diversity of amphibian skin microbiota

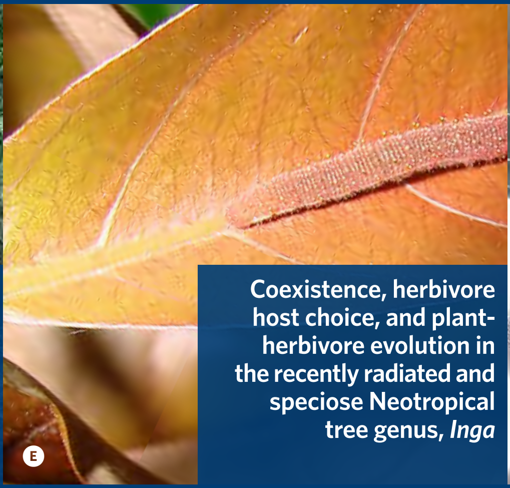


US-China: International Research Coordination Network: A research coordination network for biodiversity of ciliates



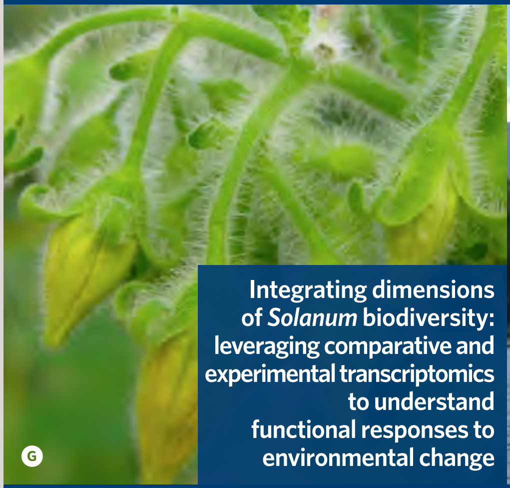
Pattern and process in marine bacterial, archaeal, and protistan biodiversity, and effects of human impacts

Testing the potential of pathogenic fungi to control the diversity, distribution, and abundance of tree species in a Neotropical forest community

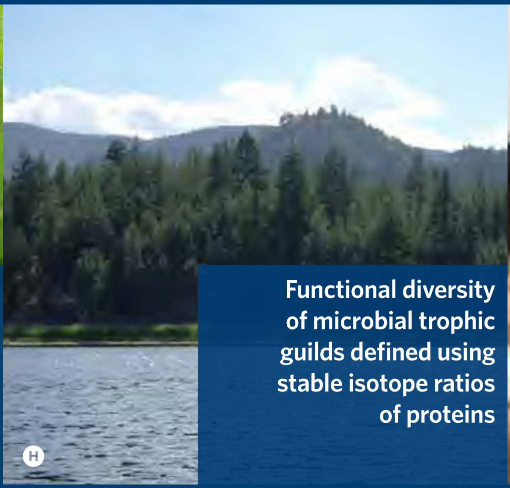


Coexistence, herbivore host choice, and plant-herbivore evolution in the recently radiated and speciose Neotropical tree genus, *Inga*

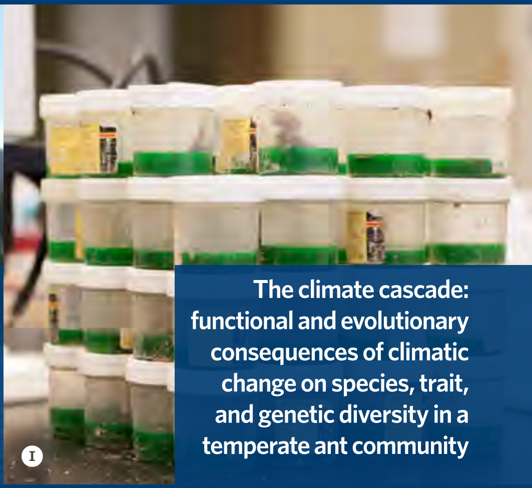
Lake Baikal responses to global change: The role of genetic, functional and taxonomic diversity in the plankton



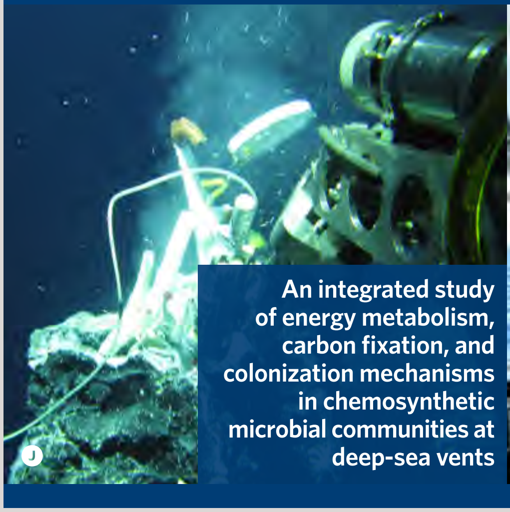
Integrating dimensions of *Solanum* biodiversity: leveraging comparative and experimental transcriptomics to understand functional responses to environmental change



Functional diversity of microbial trophic guilds defined using stable isotope ratios of proteins



The climate cascade: functional and evolutionary consequences of climatic change on species, trait, and genetic diversity in a temperate ant community



An integrated study of energy metabolism, carbon fixation, and colonization mechanisms in chemosynthetic microbial communities at deep-sea vents

Functional diversity of marine eukaryotic phytoplankton and their contributions to the C and N cycling

Integrating genetic, taxonomic, and functional diversity of tetrapods across the Americas and through extinction risk

2011
updates

IMAGE CREDIT

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Diversity and symbiosis: examining the taxonomic, genetic, and functional diversity of amphibian skin microbiota

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This project investigates the diverse microbial communities on the skin of amphibian species and their role in controlling a critical disease that threatens amphibian biodiversity in the Neotropics. They use a Kolmogorov-Smirnov Measure to determine the key species that drives community differences.

Update

A total of 138 samples of three amphibian species were collected in Panama in 2012. From these, the bacterial community was analyzed, as were the fungi and metabolites, and results were published. A new statistical tool called KS measure was also published. Environment-microbiome studies using these data are in press. Laboratory experiments in Panama were also completed, where fungus exposure was manipulated and skin microbiomes were analyzed. Collaborations were made and comparative immunogenetics studies were completed and published from these experimental frogs. Numerous multi-state student projects on various species of frog have been completed and presented, focusing on under-represented groups.

Publication

Becker, M.H., et al. (2015). Composition of symbiotic bacteria as a predictor of survival in Panamanian golden frogs infected with *Batrachochytrium dendrobatidis*. *Proc Biol Soc* 282: doi: 10.1098/rspb.2014.2881.

Becker, M.H., et al. (2015). Phylogenetic distribution of symbiotic bacteria from Panamanian amphibians that inhibit growth of the lethal fungal pathogen *Batrachochytrium dendrobatidis*. *Mol Ecol* 24: 1628-1641.

Belden, L.K., et al. (2015). Panamanian frog species host unique skin bacterial communities. *Front Microbiol* 6:1161.

Ellison, A.R., et al. (2015). More than skin deep: functional genomic basis for resistance to amphibian chytridiomycosis. *Genome Biol Evol* 7: 286-298.

Hughey, M.C., et al. (2014). *Batrachochytrium dendrobatidis* in Virginia amphibians: within and among site variation in infection. *Herpetol Rev* 45: 428-438.

Loftus, S.C., et al. (). Dimension reduction for multinomial models via a Kolmogorov-Smirnov Measure (KSM). *Ecol Lett* Submitted.

Rebollar, E.A., et al. (2016). Skin bacterial diversity of Panamanian frogs is associated with host susceptibility and presence of *Batrachochytrium dendrobatidis* *ISME J* 10: 1682-1695.

Walke, J.B., et al. (2015). Most of the dominant members of amphibian skin bacterial communities can be readily cultured. *Appl Environ Microbiol* 81: 6589-6600.

Walke, J.B., et al. (2015). Community structure and function of amphibian skin microbes: an experiment with bullfrogs exposed to a chytrid fungus. *PLoS One* 10: e0139848

Woodhams D.C., et al. (2015). Antifungal isolates database to centralize data on amphibian skin-associated bacteria and their function against emerging fungal pathogens including *Batrachochytrium dendrobatidis. Ecology* 96: 595.

US-China: International Research Coordination Network: A research coordination network for biodiversity of ciliates

(CO-FUNDED WITH NSFC)

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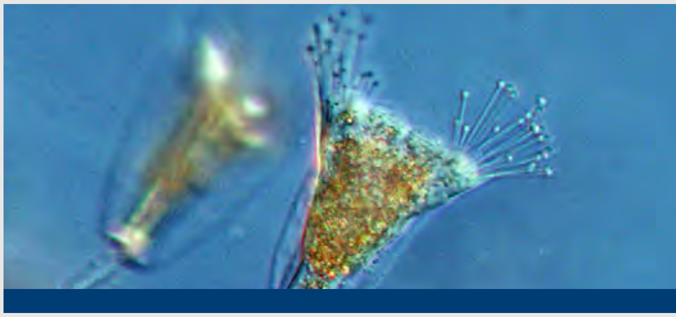
This project establishes an international research coordination network (IRCN) for the biodiversity of ciliates, including researchers from the US, China, the United Kingdom, and Brazil. This IRCN is an 'engine' for generating new ideas, projects, and procedures for archiving complex data needed to facilitate exploration of these important protists.



Acineta tuberosa.

CREDIT: JOHN C. CLAMP, DEPARTMENT OF BIOLOGY, NORTH CAROLINA CENTRAL UNIVERSITY

HTTP://IRCN-BC.ORG

Update

With the goal of advancing the rate at which knowledge is gained about taxonomy, phylogeny, geographical distribution, ecology, and genomics of core groups of ciliated protists, groups of specialists continued integrated investigations on ciliate biodiversity. The IRCN sponsored an annual workshop in Qingdao, China, during October 2015, led to improved archiving strategies for the community resource "Ciliate Guide". This led to a publication on recommended minimal requirements for the description of biodiversity of ciliated protists. The IRCN also compiled a database of science programs at minority serving institutions to broaden participation. Travel funds were provided for young researchers to present at international conferences and to attend trainings.

Publication

Dunthorn M., et al. (2015). Ciliates—Protists with complex morphologies and ambiguous early fossil record. *Marine Micropaleontol* 119: 1-6.

Dunthorn M., et al. (2015). Report of the 2014 joint workshop of the International Research Coordination Network for Biodiversity of Ciliates and the British Society for Protist Biology. European Journal of Protistology. *Eur J Protistol* 51: 118-119.

Liu W., et al. (2015). Two new genera of planktonic ciliates and insights into the evolution of the family Strombidiidae (Protista, Ciliophora, Oligotrichia). *PLoS ONE* 10: e0131726.

Pattern and process in marine bacterial, archaeal, and protistan biodiversity, and effects of human impacts

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Fuhrman and colleagues compare heavily disturbed harbor regions and relatively pristine ocean habitat in the Los Angeles basin to better understand links between marine microbial diversity and ecosystem function. The team uses time series approaches in three coastal locations to evaluate relationships among microorganisms of different complex natural communities.

HTTP://BITBUCKET.ORG/CHARADE/ELSA
HTTP://WWW-RCF.USC.EDU/~FSUN/PROGRAMS/NGS-MC/NGS-MC.HTML

Update

This project had numerous accomplishments. Computational advances included speedy software allowing association network analysis with massive datasets. rRNA:rDNA ratios in protists and bacteria proved valuable to examine the active microbes and their distribution patterns at our 3 sites. Analytical biases of popular 16S rRNA sequencing protocols were shown via mock communities, and we reported an alternative protocol that yielded high fidelity. Analysis of 16S rRNA (prokaryotes and chloroplasts) from a daily-resolved spring bloom showed 10 different dominant phytoplankton over 18 days, and an unexpected Euryarchaeal bloom. Highly resolved sequences showed single base differences (out of 400bp) could show taxa with remarkably different seasonal patterns.

Publications

Bialonski, S., et al. (2015). Time-series dataset of phytoplankton indicates a complex mixture of transport and ecology in a coastal ecosystem. *J Phytoplankton Res* In press.

Cram, J.A., et al. (2015). Cross-depth analysis marine bacterial networks suggests downward propagation of temporal changes. *ISME J* 9: 2573-2586.

Cram, J., et al. (2016). Dilution reveals how viral lysis and grazing shape microbial communities. *Limnol Oceanogr* doi: 10.1002/lno.10259.

Das, J., et al. (2015). Data-driven robotic sampling for marine ecosystem monitoring. *Int J Robot Res* 34: 1435-1452.

Needham, D., Fuhrman, J. (2016). Pronounced daily succession of phytoplankton, archaea and bacteria following a spring bloom. *Nature Microbiol* 1: 16005.

Fuhrman, J.A, et al. (2015). Marine microbial dynamics and their ecological interpretation. *Nat Rev Microbiol* 13: 133-146.

Hu, S., et al. (2015). Marine microbial eukaryote diversity and biogeography inferred from three different approaches for processing DNA information. *J Euk Microbiol* 62: 688-693.

Lie, A.A.Y., et al. (2014). Investigating microbial eukaryote diversity: Insights from a comparison of pyrotag and full-length sequences of 18S rDNA from a global survey. *Appl Environ Microbiol* 80: 4363-4373.

Martiny, A.C., et al. (2015). Biogeochemical interactions control a temporal succession in the elemental composition of marine communities. *Limnol Oceanogr* doi: 10.1002/lno.10233.

Parada, A., et al. (2015). Every base matters: assessing small subunit rRNA primers for marine microbiomes with mock communities, time-series and global field samples. *Envir Microbiol* doi: 10.1111/1462-2920.1302.

Ren J., et al. (2015). Inference of Markovian properties of molecular sequences from NGS data and applications to comparative genomics. *Bioinformatics* doi: 10.1093/bioinformatics/btv395.

Xia, L.C., et al. (2015). Statistical significance approximation in local trend analysis of high-throughput time-series data using the theory of Markov chains. *BMC Bioinformatics* 6: 301.

Testing the potential of pathogenic fungi to control the diversity, distribution, and abundance of tree species in a Neotropical forest community

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The abundance and diversity of tropical trees and fungal pathogens of trees are functionally interconnected with forest dynamics. This project is testing a mechanistic hypothesis for why so many tropical tree species are rare (occur at low population density) in a well-studied tropical forest on Barro Colorado Island (BCI), Panama.

Update

During the past year, the team established a mycological collection of pathogenic heart-rot fungi. They collected and analyzed wood-core samples from trees having infected heartwood that were identified during earlier tomographic scans. They collected and characterized leaves infected by fungi, and improved the ITS amplification system used for pathogen identification, employing a novel fusion-style next generation method. A new approach was taken to infer phylogenies across Basidiomycete and Ascomycete fungi. The team also expanded their work in new directions: they successfully established a collaboration with the City of Panama and the Municipal Parks system to apply tree decay diagnostics knowledge and techniques to help evaluate decay status of city trees.

Publications

Faircloth, B.C., Glenn, T.C (2012). Not all sequence tags are created equal: designing and validating sequence identification tags robust to indels. *PLoS ONE* 7: e42543.

Gilbert, G.S., et al. (2015). The impact of plant enemies shows a phylogenetic signal. *PLoS ONE* 10: e0123758.

Hubbell, S.P. (2013). Tropical Rainforest conservation and the twin challenges of diversity and rarity. *Ecol Evol* 3: 3263-3274.

Parker, I.M., et al. (2015). Phylogenetic structure and host abundance drive disease pressure in communities. *Nature* 520: 542-544.

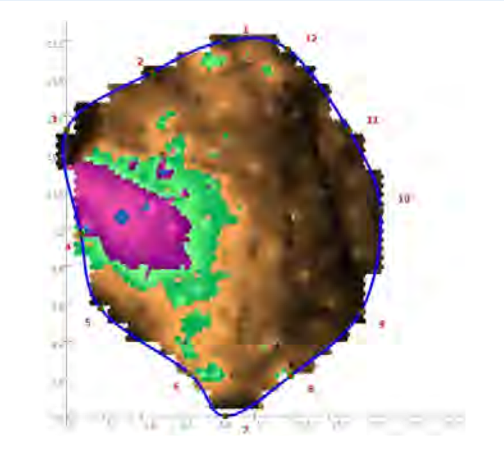
Shaw, T.I., et al. (2013). STRAW: species TRee analysis web server. *Nucleic Acids Res* 41: W238-W241.

Untergasser, A., et al. (2012). Primer3—new capabilities and interfaces. *Nucleic Acids Res* 40: e115.

Zhu, Y., et al. (2015). Conspecific and phylogenetic density-dependent survival differs across life stages in a tropical forest. *J Ecol* 103: 957-966.

^ A crew of project interns collecting data on internal decay of mature living trees.

CREDIT: GREGORY S. GILBERT, UC SANTA CRUZ



^ A tomographic image showing internal decay in the trunk of a living rainforest tree.

CREDIT: GREGORY S. GILBERT, UC SANTA CRUZ

Coexistence, herbivore host choice, and plant-herbivore evolution in the recently radiated and speciose Neotropical tree genus, *Inga*

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This project studies interactions between members of the tree genus *Inga* (>300 species) and their insect herbivores at five sites in Central and South America. This work is shedding light on the coevolution of plants and herbivores and its influence on the ecology of the most diverse forest communities on Earth.

HTTP://STORIES.RBGE.ORG.UK/ARCHIVES/16411

Update

The team continued the metabolomic analyses of Inga, discovering cryptic species along the way. Complementary work to understand the phytochemical changes in *Inga* due to abiotic variables such as light was completed, and transcriptomics work added *Inga* leaf developmental information and estimates of metabolic gene divergence among species. The team barcoded thousands of herbivores from five countries. Sanger sequencing was used for Lepidoptera phylogenetics and sequence capture of >1400 loci is being used for *Inga* phylogenetics to resolve *Inga* population history. Emerging publications include one on Peru, supporting that herbivore pressure plays a key role in species divergence, and another examining host choice in phylogenetic and orthogonal anti-herbivore trait contexts.

Publications

Endara, M.J., et al. (2015). Divergent evolution in antiherbivore defences within species complexes at a single Amazonian site. *J Ecol* 103: 1107-1118.

Nicholls, J.A., et al. (2015). Using targeted enrichment of nuclear genes to increase phylogenetic resolution in the neotropical rain forest genus *Inga* (Leguminosae: Mimosoideae). *Front Plant Sci* doi: 10.3389/fpls.2015.00710.

Wiggins, N.L., et al. (2016). Quantitative and qualitative shifts in defensive metabolites define chemical defense investment during leaf development in *Inga*, a genus of tropical trees. *Ecol Evol* 6: 478-492.

^ An unidentified caterpillar consuming *Inga marginata* (Nouragues, French Guiana).

CREDIT: TOM KURSAR, UNIVERSITY OF UTAH

Lake Baikal responses to global change: The role of genetic, functional and taxonomic diversity in the plankton

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This project studies the planktonic food web of the world's largest, oldest, and most biologically diverse lake—Lake Baikal in Siberia—to predict how native vs. non-native plankton will respond to accelerating environmental change in this system.

HTTP://WWW.WELLESLEY.EDU/NEWS/2015/AUGUST/NODE/69576

Update

Temporal and spatial community structure was assessed across all three basins of the lake spanning 69 sampling stations; this included phylogenomics study on Lake Baikal's unique planktonic amphipod. Metagenomics and functional diversity/redundancy characterization using RNA abundance was completed on bacteria and microeukaryotic plankton to examine the spatial and temporal factors explaining population structure. Correlations were made with gene abundance, environmental traits, and microeukaryotic community composition. They used seal teeth to measure decades of metal contamination, enriching environmental datasets. A variety of experiments were completed to understand and model the roles of nutrients and grazing on the food web dynamics, and to obtain physiological trait data. The team also published an analysis of climate and meteorological effects on the endemic algae.

Publications

Bowman, Jr., L.L., et al. (). RNA:DNA ratios suggest capital breeding strategy in Lake Baikal endemic *Epischura baikalensis* (Copepoda: Calanoida). *Oecologia.* Submitted.

Hampton, S.E., et al. (2015). Heating up a cold subject: prospects for under-ice plankton research in lakes. *J Plankton Res* doi: 10.1093/plankt/fbv002.

Izmest'eva, L.R., et al. (2016). Lake-wide physical and biological trends associated with warming in Lake Baikal. *J Great Lakes Res* 42: 6-17.

Katz, S.L., et al. (2015). The "Melosira years" of Lake Baikal: winter environmental conditions at ice onset predict under-ice algal blooms in spring. *Limnol Oceanogr* doi: 10.1002/lno.10143.

Litchman E., et al. (2015). Microbial resource utilization traits and trade-offs: implications for community structure, functioning and biogeochemical impacts at present and in the future. *Front Microbiol* 6: doi: 10.3389/fmicb.2015.00254

Nakov, T., et al. (2015). Molecular phylogeny of the *Cymbellales* (Bacillariophyceae, Heterokontophyta) with a comparison of models for accommodating rate variation across sites. *Phycologica* 53: 359.

Nakov, T., et al. (2015). Towards a phylogenetic classification of species belonging to the diatom genus *Cyclotella* (Bacillariophyceae): Transfer of species formerly placed in *Puncticulata*, *Handmannia*, *Pliocaenicus* and *Cyclotella* to the genus *Lindavia*. *Phylotaxa* 217: 249.

Theriot, E.C., et al. (). Evidence for a recent origin of the modern *Stephanodiscus* Ehrenb. (Bacillariophyta: Thalassiosirales) flora through multiple rapid divergences: An example of morphological evolution greatly outpacing molecular evolution in diatoms. *Protist* Submitted.

Processing samples from a bag experiment conducted in Baikal to determine what the dominant pelagic grazer (a copepod, *Epischura baikalensis*) eats.

CREDIT: BART DE STASIO, JR., BIOLOGY DEPARTMENT, LAWRENCE UNIVERSITY

Proj. 7 / 12

Integrating dimensions of *Solanum* biodiversity: leveraging comparative and experimental transcriptomics to understand functional responses to environmental change

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The research aims to generate an integrated understanding of natural adaptive trait variation in response to abiotic and biotic environmental variation in the wild tomato plant group *Solanum* sect. *Lycopersicon*. It highlights the role of drought and herbivore defense in driving remarkable diversity.

Update

Comparative evolutionary transcriptomics studies were completed with 29 genotypes, representing 13 species from the wild tomato group, and an additional 10 species within the closely related, ecologically diverse sister groups to *Solanum*. They have shown that constitutive and induced defense phenotypes are highly variable between species, and respond rapidly to local ecological conditions. They have confirmed that different *Solanum* show different patterns of individual response to jasmonic acid induction, drought stress, and their combination, at the phenotypic level. The team generated two recombinant F2 populations showing variation for drought and defense response and are analyzing co-segregation of traits and genotypes. They are sharing these resources and results with public bioinformatics tools and platforms.

Publications

Haak, D.C., et al. (2014). No evidence for phylogenetic constraint on natural defense evolution among wild tomatoes. *Ecology* 95: 1633-1641.

Haak, D.C., et al. (2014). Merging ecology and genomics to dissect diversity in wild tomatoes and their relatives. *Adv Exp Med Biol* 781: 273-298.

Muir, C.D., et al. (2014). Quantitative genetic analysis indicates selection on leaf phenotypes across wild tomato species (*Solanum* sect. *Lycopersicon*). *Genetics* 198: 1629-1643.

Muir, C.D., et al. (2014). Morphological and microanatomical determinants of mesophyll conductance in wild relatives of tomato (*Solanum* section. *Lycopersicon*, sect. *Lycopersicoides*; Solanaceae). *Plant Cell Environ* 37: 1415-1426.

Proj. 8 / 12

Functional diversity of microbial trophic guilds defined using stable isotope ratios of proteins

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This project uses isotopic ratios of carbon, nitrogen, and sulfur from microbial metabolism to link guilds of microbes to their roles in biogeochemical processes. This novel approach is improving our understanding of the role of microbes in ecosystems.

Update

The team pioneered the use of natural carbon isotope (13C) measurements of individual biomolecules to understand the biogeochemical processes mediated by uncultured communities of prokaryotes. Their results have also opened opportunities to interpret the fundamental differences in the molecular isotopic signatures of prokaryotes and eukaryotes. They also spearheaded lipidomics research for geochemistry, intersecting metagenomics, microbial genetics, and environmental lipid profiling. They developed protein stable isotope fingerprinting (P-SIF), a multidimensional protein chromatography coupled to stable isotope-ratio mass spectrometry, and applied this technology to *microbial mat* systems, *environments,* and *host-symbiont relationships.*

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Publications

Bovee R.J., Pearson, A. (2014). Strong influence of the littoral zone on sedimentary lipid biomarkers in a meromictic lake. *Geobiology* 12: 529-541.

Hamilton, T.L., et al. (2014). Coupled reductive and oxidative sulfur cycling in the phototrophic plate of a meromictic lake. *Geobiology* 12: 451-468.

Hamilton, T.L., et al. (2016). Carbon and sulfurcycling below the chemocline in a meromictic lake and the identification of a novel taxonomic lineage inthe FCB superphylum, *Candidatus aegiribacteria*. *Front Microbiol* 7: 598.

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Newman, D.K., et al. (2015). Cellular and molecular biological approaches to interpreting ancient biomarkers. *Annu Rev Earth Planet Sci* 44: 493-522.

Pearson, A. (2013). "Lipidomics for geochemistry." In Falkowski, P.G., Freeman, K.H., eds. *Treatise on Geochemistry (2nd Edition)* 12, Elsevier London., pp. 291-336.

Proj. 9 / 12

The climate cascade: functional and evolutionary consequences of climatic change on species, trait, and genetic diversity in a temperate ant community

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Sanders and colleagues study adaptations to climate change in a common foraging ant in eastern US forests to understand the mechanisms that allow some species to adapt to shifts in climate rather than migrating or going extinct.

Clint Penick, a postdoctoral researcher at NC State University, samples leaf litter inside one of the Warming Chambers.

CREDIT: LAUREN NICHOLS, NC STATE UNIVERSITY

Update

They continued to maintaining experimental warming plots and working with collaborators at Vermont and Harvard Forest to examine gene and protein expression. Former students, who are now postdocs, have broadened the project to include herbivores, plants, fungi, bacteria, and archaea. The team is finishing a meta-analysis to elucidate the relative responses of 31 distinct response variables, including 11 taxonomic groups and 10 ecosystem functions, to the treatments at both sites. Results are suggesting strong evidence of local adaptation to thermal environments, producing a blueprint of the thermal reactionome. Above ground community responses were strong, but underground responses were stable.

Publications

Bewick, B., et al. (2014). Predicting future coexistence in a North American ant community. *Ecol Evol* 4: 1804-1819.

Burt, M.A., et al. (2014). Interactions in a warmer world: The relative effects of experimental warming, intraspecific density, and insect herbivory on seedling dynamics. *Ecosphere* 5: 1-12.

Cregger, M.A., et al. (2014). Microbial communities respond to experimental warming, but site matters. *Peer J* 2: e358.

Del Toro, I., et al. (2015). Ant-mediated ecosystem functions on a warmer planet: effects on soil movement, decomposition and nutrient cycling. *J Animal Ecol* 85: 1233-1241.

Del Toro, I., et al. (2015). Predicted impacts of climatic change on ant functional diversity and distributions in eastern North American forests. *Divers Distrib* 21: 781-791.

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Fowler, D., et al. (2014). Niche filtering rather than partitioning shapes the structure of forest ant communities. *J Anim Ecol* 83: 943-952.

Gibb, H., et al. (2015). Climate mediates the effects of disturbance on ant assemblage structure. *Proc R Soc B* 282: doi: 10.1098/rspb.2015.0418.

Gotelli, N.J. and J. Stanton-Geddes (2015). Climate change, genetic markers and species distribution modeling. *J Biogeograph* 42: 1577-1585.

Graham, C.H., et al. (2014). The origin and maintenance of montane biodiversity: integrating evolutionary and ecological processes. *Ecography* 37: 711-719.

Jing, X. et al. (2015). The links between ecosystem multifunctionality and above- and belowground biodiversity are mediated by climate. *Nat Commun* 6: 8159.

Marchin, R. M., et al. (2015). Temperature alone does not explain phenological variation of diverse temperate plants under experimental warming. *Global Change Biol* 21: 3138-3151.

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Pelini, S.L., et al. (2014). Geographic differences in effects of experimental warming on ant species diversity and community composition. *Ecosphere* 5: 125.

Pelini S.L., et al. (2015). Higher trophic levels overwhelm climate change impacts on terrestrial ecosystem functioning. *Plos One*: 10: e0136344.

Peters, M.K., et al. (2014). Variation in nutrient use by ant assemblages along an extensive environmental gradient on Mt Kilimanjaro. *J Biogeograph* 41: 2245-2255.

Read Q.D., et al. (2014). Convergent effects of elevation on functional leaf traits within and among species. *Funct Ecol* 28: 37-45.

Resasco, J., et al. (2014). Testing sodium limitation of fire ants in the field and laboratory. *Ecol Entomol* 39: 267-271.

Resasco, J., et al. (2014). Using historical and experimental data to reveal warming effects on ant assemblages. *PLoS One* 9: e88029.

Stanton-Geddes, J. et al. (2014). In Defense of P-values: comment on the statistical methods actually used by ecologists. *Ecology* 95: 637-642.

Stuble, K.L., et al. (2014). Ant-mediated seed dispersal in a warmed world. *Peer J* 2: e286.

^ Open-top chambers at the Duke Forest site in North Carolina. Built in 2009 at sites in both North Carolina and Massachusetts, the warming chambers consist of 12 open-top warming chambers, nine of which are pumped with warm air to simulate predicted global warming.

CREDIT: LAUREN NICHOLS, NC STATE UNIVERSITY

An integrated study of energy metabolism, carbon fixation, and colonization mechanisms in chemosynthetic microbial communities at deep-sea vents

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Deep-sea hydrothermal vents,first discovered in 1977, are 'poster child' ecosystems where microbial chemosynthesis rather than photosynthesis is the primary source of organic carbon. This project establishes an interdisciplinary international research program to better understand the underlying microbiology and biogeochemistry in these poorly-understood deep-sea hydrothermal vent ecosystems.

Update

The major activities of the last year were related to analyzing the samples obtained during a research expedition to the deep-sea vents in 2014. During the expeditions, novel experiments incubating microbes under high pressure successfully determined the inorganic carbon fixation rates by the cells in different environments. Single cell genomes from these experiments were also analyzed. Biomass was collected from the vents and metagenomic analyses are near completion. This work showed oxygen and nitrate respiration support primary production in the subseafloor biosphere that is coupled to the oxidation of both sulfide and hydrogen. Suites of microbes were identified that were able to grow under a range of different oxygen levels.

Publications

Bertrand, E.M., et al. (2013). Identity and mechanisms of alkane-oxidizing metalloenzymes from deep-sea hydrothermal vents. *Front Microbiol* 4: 109.

Foustoukos, D.I., Pérez-Rodríguez I. (2015). A continuous culture system for assessing microbial activities in the piezosphere. *Appl Environ Microbiol* 81: 6850-6856.

Houghton, J.L., et al. (2016). Thiosulfate oxidation by *Thiomicrospira thermophila*: metabolic flexibility in response to ambient geochemistry. *Environ Microbiol* doi: 10.1111/1462-2920.13232.

Kminek, G., et al. (2014). Report of the workshop for life detection in samples from Mars. *Life Sci Space Res* 2: 1-5.

Labonté, J.M., et al. (2015). Single cell genomics-based analysis of virus-host interactions in marine surface bacterioplankton. *ISME J* 9:2386-2399.

Labonte, J.M., et al. (2015). Single cell genomics indicates horizontal gene transfer and viral infections in a deep subsurface Firmicutes population. *Front Microbiol* 6: 649.

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Pérez-Rodríguez, I., et al. (2015). From deep-sea volcanoes to human pathogens: A conserved quorum sensing signal in Epsilonproteobacteria. *ISME J* 9: 1222-1234.

Pérez-Rodríguez, I., et al. (). Rate-yield trade-offs and nitrogen isotope fractionation during dissimilatory nitrate reduction are conserved among chemolithoautotrophic deep-sea vent e-Proteobacteria and Aquificae. *Environ Microbiol* Submitted.

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Functional diversity of marine eukaryotic phytoplankton and their contributions to the C and N cycling

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This project uses two North Atlantic sites in two seasons to link genetic diversity and species composition of phytoplankton communities to the biogeochemistry of the surface ocean, tracking the complex changes occurring during late summer blooms of algae.

Update

The second Subarctic North Atlantic cruise, involving both sample collection and incubation experiments, was accomplished. Transects show a clear ecological, nutrient, and primary production gradient from the warm low nutrient waters to the cooler nutrient richer waters, contributing to identification of exciting new nitrate cycling patterns. Metagenomic analyses of thousands of samples revealed major picoeukaryotic groups dominating different seasons and ocean layers. The group generated a custom database, PhyloDB, comprising tens of millions of peptides, and developed new methods for taxonomic binning. They are currently analyzing samples collected on the completed four cruises, especially the flow cytometric sorting of incubation samples and subsequent isotope analysis, and publishing results.

Publications

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Integrating genetic, taxonomic, and functional diversity of tetrapods across the Americas and through extinction risk

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Volker Radeloff
University of Wisconsin Madison
(1136592)

Catherine Graham
State University of New York Stony Brook
(1136705)

Blair Hedges
Temple University
(1455761)

Young and colleagues have assembled a database of 13,000 land vertebrates of the Americas to investigate how changes in one dimension of biodiversity influences changes in others. Understanding how species composition influences the vibrant diversity of animal functional traits will improve understanding of how different communities are assembled and change over time.

Update

After expanding their tetrapod database to include thorough information on reptiles and amphibians, including traits, ranges, and extinction risk assessment, Young and colleagues have successfully imputed missing natural history trait data across the Americas. They have finished developing predictive models of global mammalian extinction and are working on predictive geospatial analysis of the other tetrapod groups. Sharing these macroecological data among universities and NGOs, collaborative publications have addressed the identification of key biodiversity areas, re-examined theories of evolution and extinction, and developed methods needed to improve global sustainability efforts.

Publication

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2011 Image Gallery

^ **Proj. 9/12** — Julia Stevens, postdoctoral researcher at NC State University and the NC Museum of Natural Sciences, extracts soil cores inside one of the warming chambers in Duke Forest in NC.

CREDIT: LAUREN NICHOLS, NC STATE UNIVERSITY

^ **Proj. 6/12** — Wellesley College students and Dr. Marianne Moore process samples from a copepod grazing experiment conducted in L. Baikal, Siberia with Dr. Bart De Stasio, Jr. of Lawrence University. This information will be used to parameterize an eco-evolutionary model that will predict how climate warming will affect the abundance of endemic and cosmopolitan plankton species in the lake.

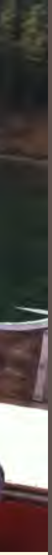
CREDIT: BART DE STASIO, JR., BIOLOGY DEPARTMENT, LAWRENCE UNIVERSITY

^ **Proj. 6/12** — The team is trying to determine if the cold-loving endemic species in Lake Baikal will be replaced by warm-loving cosmopolitan species found in lakes throughout the world.

CREDIT: BART DE STASIO, JR., BIOLOGY DEPARTMENT, LAWRENCE UNIVERSITY

^ **Proj. 9/12** — Undergraduates sift leaf litter to collect arthropods inside one of the heated warming chambers.

CREDIT: LAUREN NICHOLS, NC STATE UNIVERSITY



Proj. 9/12 — Researchers sort through ant colonies collected earlier that day from within the warming chambers.

CREDIT: LAUREN NICHOLS, NC STATE UNIVERSITY

Proj. 6/12 — Vasya is a Russian undergraduate student at Irkutsk State University in Russia.

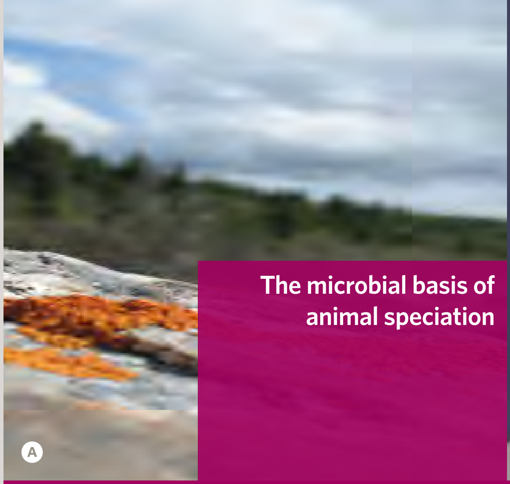
CREDIT: BART DE STASIO, JR., BIOLOGY DEPARTMENT, LAWRENCE UNIVERSITY

Proj. 9/12 — Pitfall traps collected each month from within the warming chambers allow researchers to track changes in ground foraging arthropod communities.

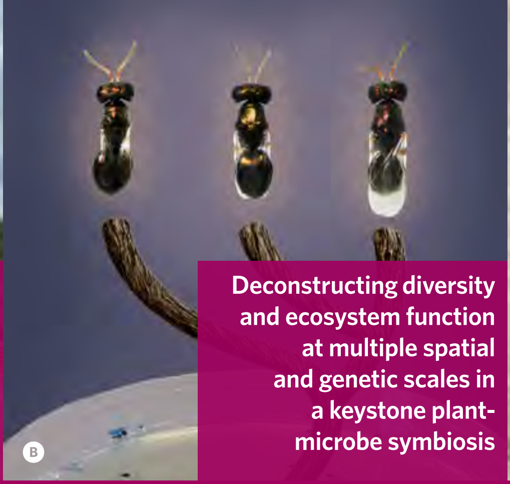
CREDIT: LAUREN NICHOLS, NC STATE UNIVERSITY

Proj. 9/12 — *Aphanogaster rudis* (Winnow Ant) carries its brood. *A. rudis* is one of the most common ants in forests of North Carolina. Researchers are studying how gene expression and protein levels of *A. rudis* change in response to different temperature treatments and are investigating how these responses have evolved.

CREDIT: LAUREN NICHOLS, NC STATE UNIVERSITY

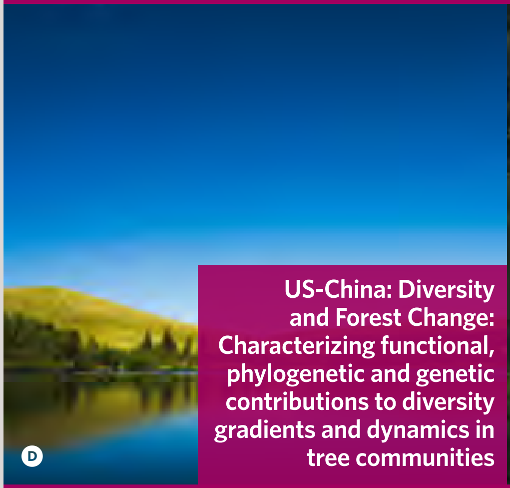


The microbial basis of animal speciation

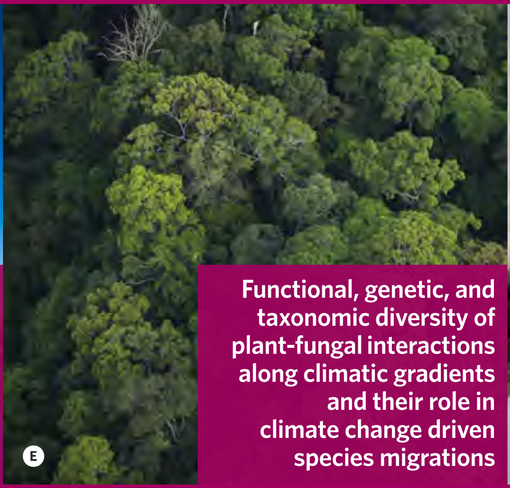


Deconstructing diversity and ecosystem function at multiple spatial and genetic scales in a keystone plant-microbe symbiosis

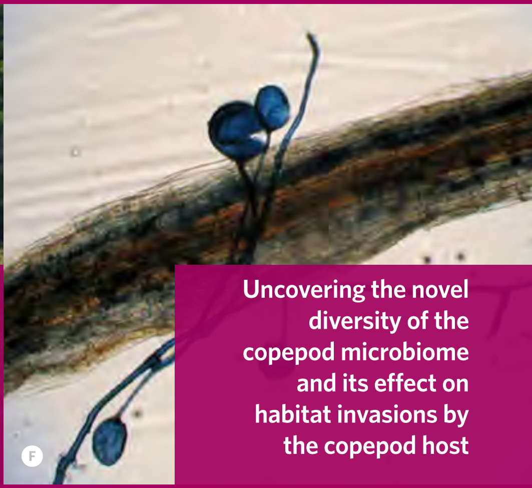
Can evolutionary history predict how changes in biodiversity impact the productivity of ecosystems?



US-China: Diversity and Forest Change: Characterizing functional, phylogenetic and genetic contributions to diversity gradients and dynamics in tree communities



Functional, genetic, and taxonomic diversity of plant-fungal interactions along climatic gradients and their role in climate change driven species migrations

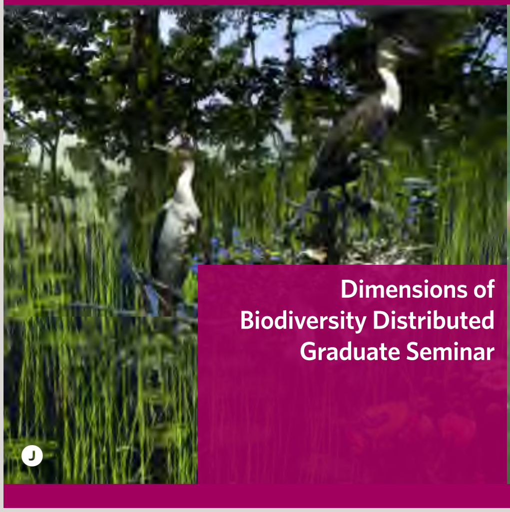


Uncovering the novel diversity of the copepod microbiome and its effect on habitat invasions by the copepod host

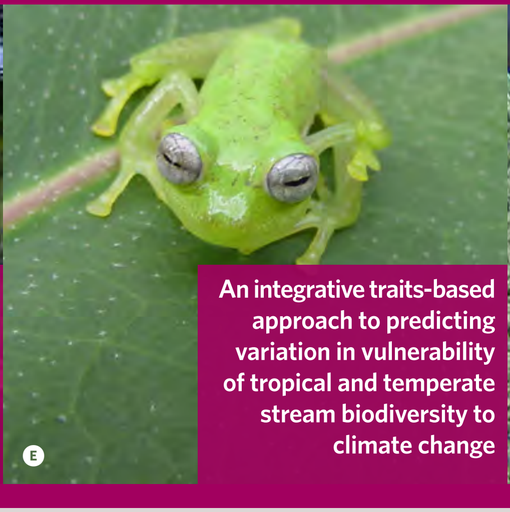
An interdisciplinary study of hyperdiverse endophytic fungi and their function in boreal forests

Biological Controls on the Ocean C:N:P ratios

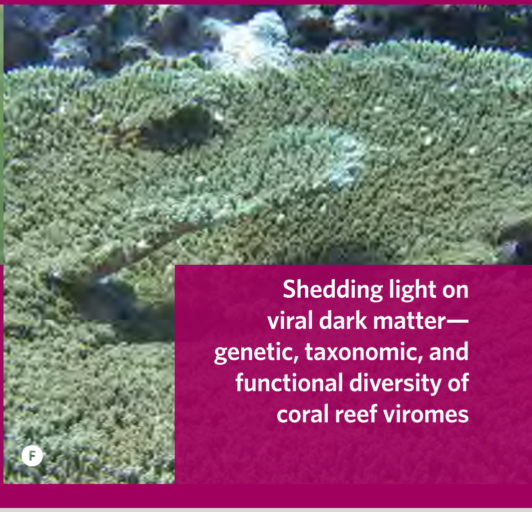
Genomics, functional roles, and diversity of the symbiotic gut microbiotae of honey bees and bumble bees



Dimensions of Biodiversity Distributed Graduate Seminar



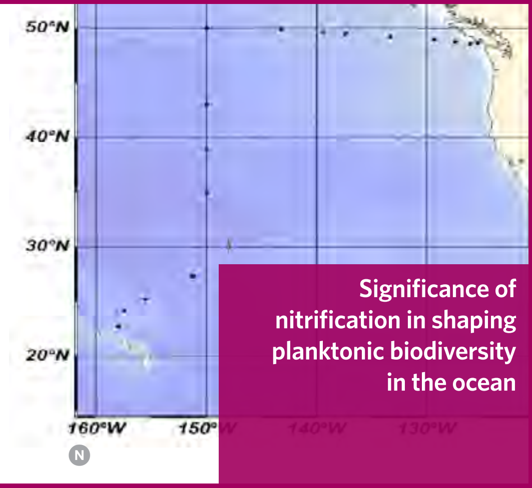
An integrative traits-based approach to predicting variation in vulnerability of tropical and temperate stream biodiversity to climate change



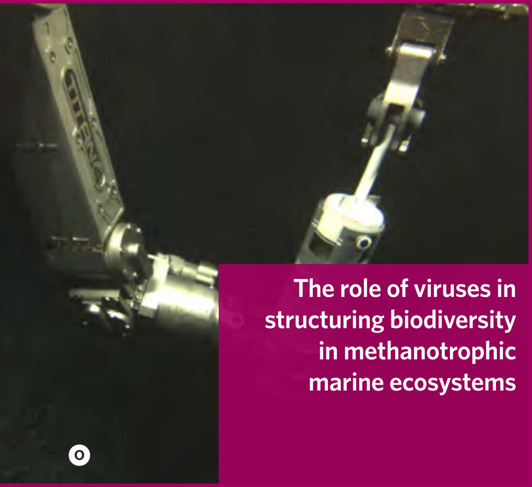
Shedding light on viral dark matter—genetic, taxonomic, and functional diversity of coral reef viromes

2010 updates

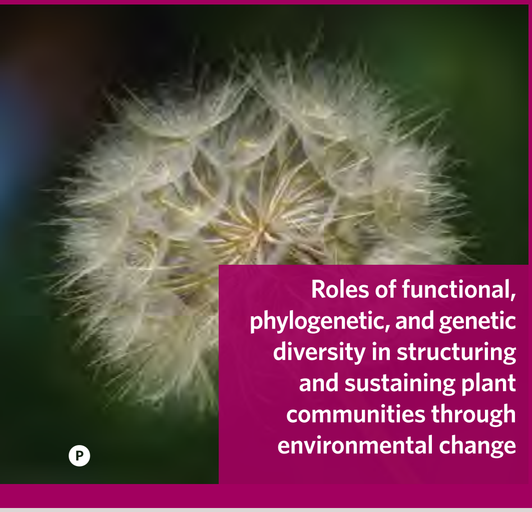
Parallel evolutionary radiations in *Protea* and *Pelargonium* in the Greater Cape Floristic Region



Significance of nitrification in shaping planktonic biodiversity in the ocean



The role of viruses in structuring biodiversity in methanotrophic marine ecosystems



Roles of functional, phylogenetic, and genetic diversity in structuring and sustaining plant communities through environmental change

IMAGE CREDIT

Ⓐ A. Elizabeth Arnold
Ⓑ Robert Brucker & Seth Bordenstein
Ⓒ Kabir G. Peay
Ⓓ Bradley Cardinale
Ⓔ Christian Ziegler
Ⓕ Richard Lankau
Ⓖ iStock
Ⓗ Adam Martiny
Ⓘ Jay Evans
Ⓙ Jes Coyle, David Gonthier, Jonathan Moore & the Brookhaven National Lab
Ⓚ W. Chris Funk
Ⓛ Forest Rohwer
Ⓜ C.D. Schlichting
Ⓝ Anitra Ingalls & David Stahl
Ⓞ David Valentine
Ⓟ Gregory Sonnier

The microbial basis of animal speciation

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This project studies the role that host-associated microbial communities play in structuring species complexes and diversification in a genus of parasitoid wasps.

Publications

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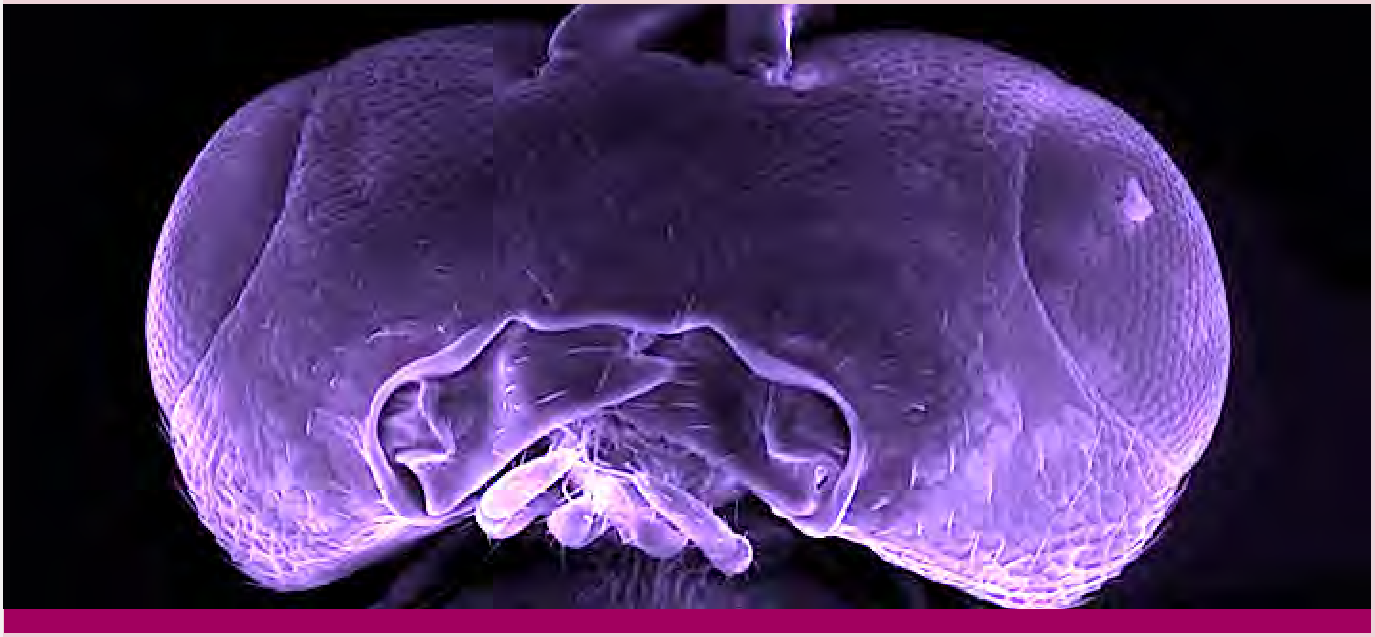

^ The head of *Nasonia* wasp that was captured in detail by a scanning electron microscope. The image is false colored purple.

CREDIT: ROBERT BRUCKER AND SETH BORDENSTEIN, VANDERBILT UNIVERSITY

Deconstructing diversity and ecosystem function at multiple spatial and genetic scales in a keystone plant-microbe symbiosis

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This project is investigating soil fungal communities associated with pine-dominated forests in North America, which are poorly known and may serve as a model system for understanding microbial community dynamics.

HTTP://WEB.STANFORD.EDU/~KPEAY/DOB_HOME.HTML

Publications

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^ *Top:* Plant and fungal tissue intermingle in roots to form a new absorptive organ—the mycorrhiza. In ectomycorrhizas, fungal tissue encases the plant roots and nutrients are absorbed by hyphal filaments that forage the soil.

Bottom: Many of the fungi involved in ectomycorrhizal symbiosis produce conspicuous fruiting bodies, commonly known as mushrooms.

CREDIT: KABIR G. PEAY

Can evolutionary history predict how changes in biodiversity impact the productivity of ecosystems?

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(1046307)

This project asks how the evolution of genetic differences among species of freshwater algae influences species coexistence and primary production in freshwater.

Publications

Alexandrou, M.A., et al. (2014). Genome duplication and multiple evolutionary origins of complex migratory behavior in Salmonidae. *Molec Phylog Evol* 69: 514-523.

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US-China: Diversity and Forest Change: Characterizing functional, phylogenetic & genetic contributions to diversity gradients & dynamics in tree communities

(CO-FUNDED WITH NSFC)

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Institute of Botany, CAS

Wanhui Ye
South China Botanical Garden, CAS

Min Cao
Jie Li
Xishuangbanna Tropical Botanical Garden, CAS

Xiangcheng Mi
Institute of Botany, CAS

Xugao Wang
Institute of Applied Ecology, CAS

This Dimensions project was the first to be funded by the partnership between NSF and the National Natural Science Foundation of China (NSFC). A group of forest scientists from the US, China, and other parts of Asia have created an international research coordination network (IRCN) to explore the resilience of forests to global change.

^ Research plot at Yasuni, Ecuador.

CREDIT: STUART DAVIES

HTTP://CTFSNEWS.BLOGSPOT.COM/2014/09/2014-CTFS-FORESTGEO-WORKSHOP.HTML

Publications

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^ Research plot at Changbaishan, China.

CREDIT: STUART DAVIES

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Canopy of the plot at Lambir, Malaysia.

CREDIT: CHRISTIAN ZIEGLER

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Functional, genetic, and taxonomic diversity of plant-fungal interactions along climatic gradients and their role in climate change driven species migrations

Richard Lankau
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(1552412)

The largely unseen world of soil fungi is intimately linked to plant communities. This award supports research to understand how the taxonomic diversity of soil fungi interacts with the genetic diversity of two tree species.

Publications

Lankau, R.A. Keymer, D.P. (). Disassociation of tripartite plant-soil-microbial relationships may inhibit gene flow and range expansion within and beyond tree species ranges. *New Phytol* Submitted.

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^ External hyphae of arbuscular mycorrhizal fungi with spores growing around sycamore (*Platanus occidentalis*) roots.

CREDIT: RICHARD LANKAU

Proj. 6 / 16

Uncovering the novel diversity of the copepod microbiome and its effect on habitat invasions by the copepod host

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This project characterizes diversity and metabolic functions of the microbiome of a copepod, and is testing how diversity and functions (metabolic and ecological) change when the saline copepod invades a novel habitat: freshwater.

Publications

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Proj. 7 / 16

An interdisciplinary study of hyperdiverse endophytic fungi and their function in boreal forests

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The EnDoBiodiversity project aims to understand the diversity of endophytic fungal symbionts of plants and lichens in threatened boreal systems, and to identify the fundamental processes that generate and maintain that diversity.

HTTP://WWW.ENDOBIODIVERSITY.ORG
HTTP://SNAP.HPC.NCSU.EDU

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Boreal lichens harbor a diverse array of secondary fungi (Endolichenic fungi).

CREDIT: A. ELIZABETH ARNOLD, UNIVERSITY OF ARIZONA

Biological Controls on the Ocean C:N:P ratios

Adam Martiny
Steven Allison
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Michael Lomas
Bigelow Laboratory for Ocean Sciences
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Benjamin Van Mooy
Woods Hole Oceanographic Institution
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The Redfield ratio is the ratio of nitrogen to phosphorus in seawater. Understanding how biodiversity regulates the Redfield ratio will provide important insights for understanding the role of biodiversity in regulating global nutrient cycles.

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A sampling rosette from R/V Atlantic Explorer Dimensions of Biodiversity project.

CREDIT: ADAM MARTINY, UNIVERSITY OF CALIFORNIA, IRVINE

Genomics, functional roles, and diversity of the symbiotic gut microbiotae of honey bees and bumble bees

Nancy Moran
University of Texas
Austin
(1415604)

Jay Evans
U.S. Department of Agriculture
Research Service Beltsville Area
(1046153)

Most of the Earth's biodiversity is microbial. This project examines the microbiota in the guts of bees from two genera — *Apis* (honey bees) and *Bombus* (bumble bees). The research offers important insights into the ecological resilience of organisms that provide economic, ecological and agricultural value through their pollination services.

HTTP://WEB.BIOSCI.UTEXAS.EDU/MORAN/RESEARCH_DIMENSIONS.HTML

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^ Honey bee queen being tended by her workers on the comb.

CREDIT: WALDAN KWONG, YALE UNIVERSITY

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^ Honeybee workers and queen on the hive (*Apis mellifera*).

CREDIT: JAY EVANS, USDA

Dimensions of Biodiversity Distributed Graduate Seminar

Julia Parrish
University of Washington
(1050680)

A distributed graduate seminar served as a baseline for the planned 10-year Dimensions of Biodiversity program, building databases and blogs that describe the state of biodiversity science.
The seminar unites >100 students from dozens of universities to build the next generation of biodiversity scientists through inquiry-based peer-led learning.

HTTP://WWW.BIODIVERSEPERSPECTIVES.COM

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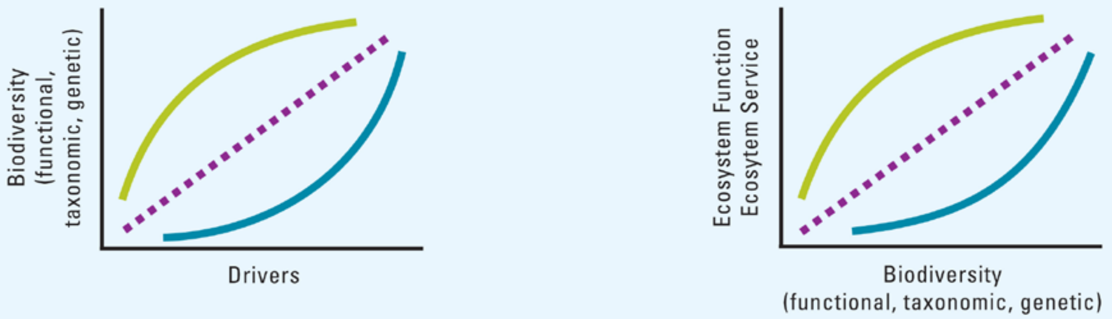

^ DBDGS teams addressed one of two broad framing questions: 1) What forces create/maintain biodiversity pattern, and 2) What patterns of system function, service, or even associated human well-being does biodiversity drive?

CREDIT: CATHY SCHWARTZ

An integrative traits-based approach to predicting variation in vulnerability of tropical and temperate stream biodiversity to climate change

LeRoy N. Poff
William C. Funk
Cameron Ghalambor
Boris Kondratieff
Colorado State University
(1046408)

Steven Thomas
University of Nebraska Lincoln
(1045991)

Alexander Flecker
Joseph Bernardo
Kelly Zamudio
Cornell University
(1045960)

Predicting the effects of rapid climate change on biodiversity is an important and urgent scientific challenge. This project examines the influence of climate change on stream biodiversity in small streams spanning an elevation gradient of 2000+ meters in the tropical Andes of Ecuador and in the Colorado Rockies.

HTTP://WWW.EEB.CORNELL.EDU/EVOTRAC/WELCOME.HTML

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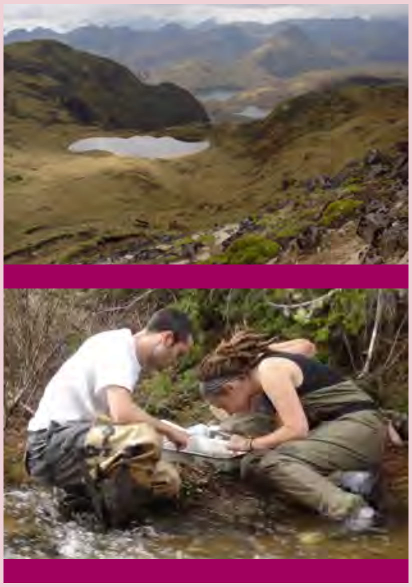

Top: The Papallacta drainage on the eastern flank of the Ecuadorian Andes.

Bottom: Two students sample aquatic insects in a Colorado stream.

CREDIT: KELLY ZAMUDIO, CORNELL UNIVERSITY

Rio Santa Maria, in the Oyacachi Basin, Ecuador, is one of the streams sampled by EVOTRAC.

CREDIT: KELLY ZAMUDIO, CORNELL UNIVERSITY

Students on their way to sample aquatic insects in streams in the Colorado Front Range for the ECOTRAC project.

CREDIT: KELLY ZAMUDIO, CORNELL UNIVERSITY

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Proj. 12 / 16

Shedding light on viral dark matter—genetic, taxonomic, and functional diversity of coral reef viromes

Forest Rohwer
Anca Segall
Robert A. Edwards
San Diego State University
(1046413)

This project examines virus diversity on coral reefs along a human impacts gradient at both regional and global scales.

HTTPS://VDM.SDSU.EDU
HTTPS://VDM.SDSU.EDU/IVIREONS

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^ *Acropora* corals.

CREDIT: FOREST ROHWER, SAN DIEGO STATE UNIVERSITY

Parallel evolutionary radiations in *Protea* and *Pelargonium* in the Greater Cape Floristic Region

Carl Schlichting
Kent Holsinger
Cynthia Jones
John Silander
University of Connecticut
(1046328)

Andrew Latimer
University of California Davis
(1045985)

Justin Borevitz
University of Chicago
(1046251)

The Fynbos and Succulent Karoo biomes in South Africa's Greater Cape Floristic Region are two of the world's plant biodiversity hotspots. Using two plant genera as model systems, this project looks at the ways in which functional diversity of traits evolves and influences community dynamics.

HTTPS://FIGSHARE.COM/ARTICLES/DIMENSIONS_OF_BIODIVERSITY%3A_PARALLEL_EVOLUTIONARY_RADIATIONS_IN_PROTEA_AND_PELARGONIUM_IN_THE_GREATER_CAPE_FLORISTIC_REGION/94286

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^ *Pelargonium peltatum.*

CREDIT: CARL D. SCHLICHTING, ECOLOGY AND EVOLUTIONARY BIOLOGY, UNIVERSITY OF CONNECTICUT

^ *Pelargonium sericifolium.*

CREDIT: CARL D. SCHLICHTING, ECOLOGY AND EVOLUTIONARY BIOLOGY, UNIVERSITY OF CONNECTICUT

Significance of nitrification in shaping planktonic biodiversity in the ocean

David Stahl
Virginia E. Armbrust
Allan Devol
Anitra Ingalls
University of Washington
(1046017)

James Moffett
University of Southern California
(1046098)

The Stahl research team examines the diversity and function of ammonia oxidizing Archaea (AOA) in the ocean and they are determining the role of these newly discovered organisms in structuring the diversity of phytoplankton.

Publications

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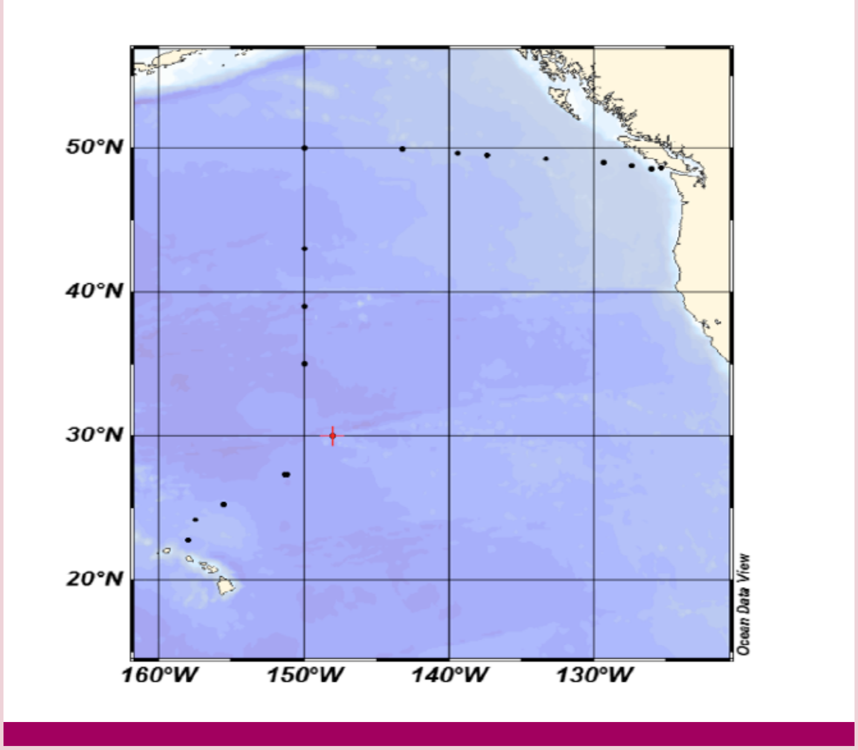

^ Research stations sampled for analyses of biological and chemical controls of nitrogen form and availability. Research conducted in August 2013 on the Kilo Moana.

CREDIT: ANITRA INGALLS AND DAVID STAHL

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Proj. 15 / 16

The role of viruses in structuring biodiversity in methanotrophic marine ecosystems

David Valentine
University of California
Santa Barbara
(1046144)

Microbes in ocean sediments form a unique ecosystem. There, methane is consumed, preventing large amounts of this potent greenhouse gas from entering the atmosphere. This research is shedding light on a dark corner of the biosphere, and could identify new and novel genes that support life in these environments.

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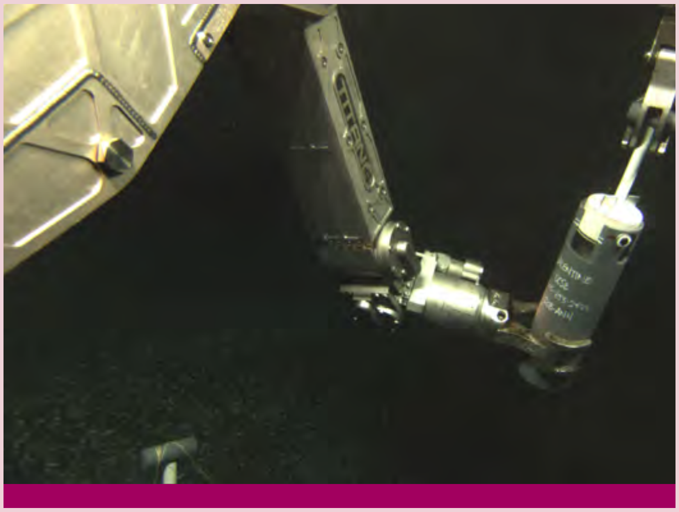

Deployment of an incubator at one study site in 2011, open to the environment and ready to be colonized by local microbial communities. Here, the manipulator arms of ROV Jason are seen locking the top of the incubator into the open position.

CREDIT: DAVID VALENTINE, UCSB

Preparing to inject tracer into a sealed incubator after the two-year colonization period.

CREDIT: DAVID VALENTINE, UCSB

Roles of functional, phylogenetic, and genetic diversity in structuring and sustaining plant communities through environmental change

Donald Waller
Kenneth Cameron
Thomas Givnish
Kenneth Sytsma
University of Wisconsin
Madison
(1046355)

Waller and colleagues are examining the functional traits, phylogenetic relationships, geographic distributions, and patterns of genetic variation in native and introduced plants in Wisconsin forests and grasslands. Their goal is to identify how climate change, habitat fragmentation, invasive species, and overabundant deer are acting to drive ecological change.

< *Tragopogon sp*, a typical example of a wind-dispersed species.

CREDIT: GREGORY SONNIER, BOTANY DEPARTMENT, UNIVERSITY OF WISCONSIN-MADISON

HTTP://BOTANY.WISC.EDU/DOB

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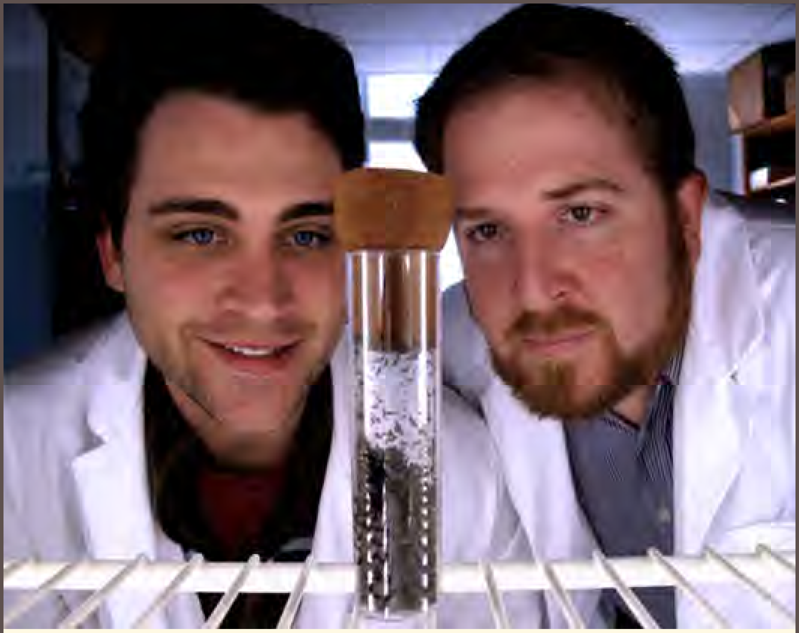
2010
Image Gallery

Proj. 6/16 — Copepods are a major food source for some of the world's most important fisheries, such as herring, anchovy, salmon and flounder.

CREDIT: ISTOCK



Proj. 1/16 — Seth Bordenstein (right) and Robert Brucker, examining a bottle filled with *Nasonia* wasps.

CREDIT: ROBERT BRUCKER AND SETH BORDENSTEIN, VANDERBILT UNIVERSITY

Proj. 4/16 — Seeds from the plot at Huai Kha Khaeng, Thailand.

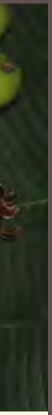
CREDIT: STUART DAVIES

Proj. 3/16 — Undergraduate research assistant samples algae from lab experiment and maintains chemostats.

CREDIT: BRADLEY CARDINALE

Proj. 4/16 — Understory in the plot at Wabikon Lake Forest, USA.

CREDIT: STUART DAVIES

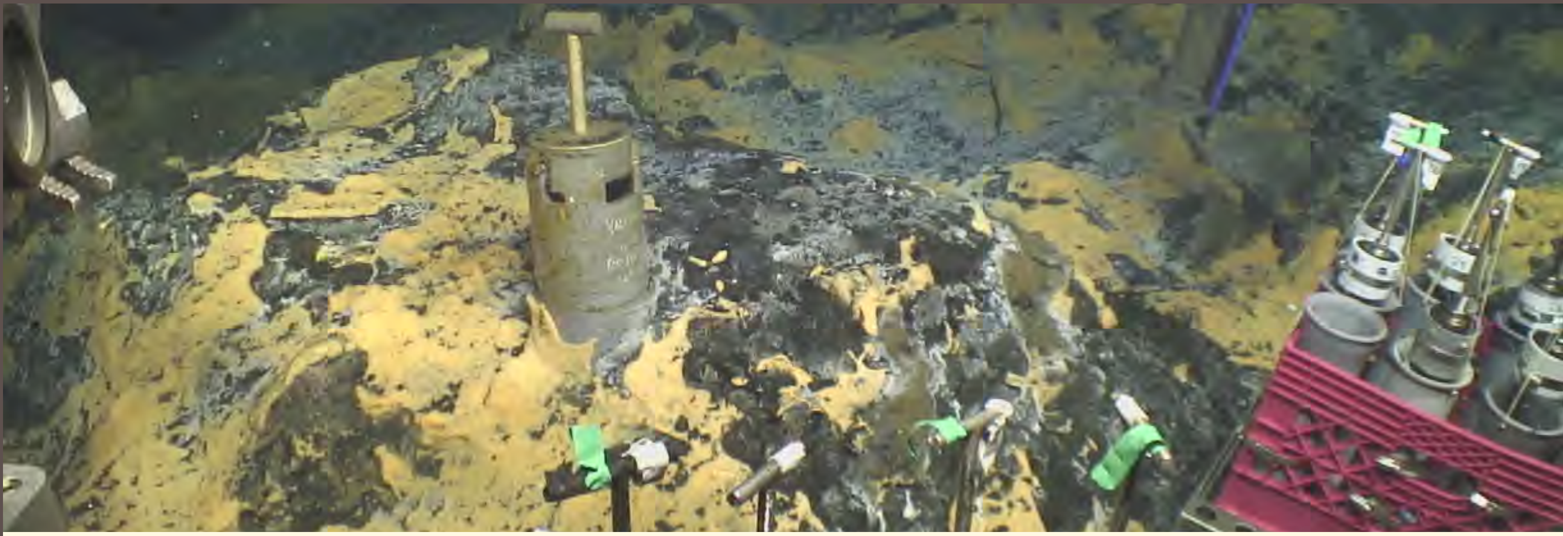


Proj. 13/16 — *Pelargonium crithmifolium.*

CREDIT: CARL D. SCHLICHTING, ECOLOGY AND EVOLUTIONARY BIOLOGY, UNIVERSITY OF CONNECTICUT

Proj. 9/16 — *Bombus impatiens* individual foraging on flowers.

CREDIT: NANCY MORAN, UNIVERSITY OF TEXAS, AUSTIN



Proj. 15/16 — An incubator as first seen on the return to a second study site in 2013, showing substantial growth of microbial mats on the outer surfaces.

CREDIT: DAVID VALENTINE, UCSB

Dimensions of Biodiversity

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