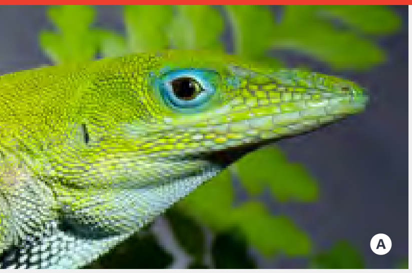
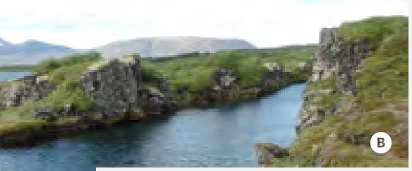
Dimensions of Biodiversity

2010-2016
PROJECTS

NATIONAL SCIENCE FOUNDATION

CO-FUNDED
BY





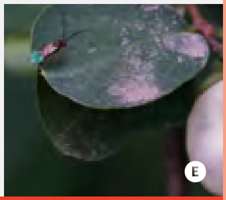


IMAGE CREDIT

THIS PAGE

- A Ian Wang
- B Janette Boughman
- C Theresa Clark & Kirsten Deane-Coe
- D Jack Stanford & Amanda DelVecchia
- E Hannes Schuler

FRONT COVER

- F Hannes Schuler
- G Amanda DelVecchia
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- I Ian Wang
- J Jacques Descloitres
- K Anita Antoninka
- L Christopher Parkinson
- M Priscila Chaverri
- N Deborah Gochfeld
- O Stephanie Anderson
- P Janette Boughman

FIELD SITES

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- Australia
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- Belize
- Bermuda
- Bolivia
- Brazil
- Cayman Islands
- Canada
- China
- Colombia
- Costa Rica
- Curaçao
- Czech Republic
- Dominican Republic
- Ecuador
- Finland
- France
- French Guiana
- French Polynesia
- Germany
- Iceland
- Japan
- Madagascar
- Malaysia
- Mexico
- Norway
- Palau
- Panama
- Peru
- Philippines
- Poland
- Puerto Rico
- Russia
- Saudi Arabia
- Singapore
- South Africa
- Spain
- Suriname
- Sweden
- Switzerland
- Tahiti
- Taiwan
- Thailand
- Trinidad
- United States
- United Kingdom
- Venezuela
- Labrador Sea
- North Atlantic Ocean
- North Pacific Ocean

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- Brazil (FAPESP)

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- Sweden
- United Kingdom

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, Design Specialist, for her important contributions to the abstract booklet. Finally, we are grateful to AAAS Science and Technology Policy Fellows Drs. Sara Chun, Sean M. Watts, Karen Alroy, Rachel S. Meyer, and Catherine L. Malone 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 7th year of research support to characterize the least-well-known aspects of the diversity of life on Earth. The National Science Foundation (NSF) funded 11 new projects in fiscal year 2016 bringing the total number of funded projects to 88.

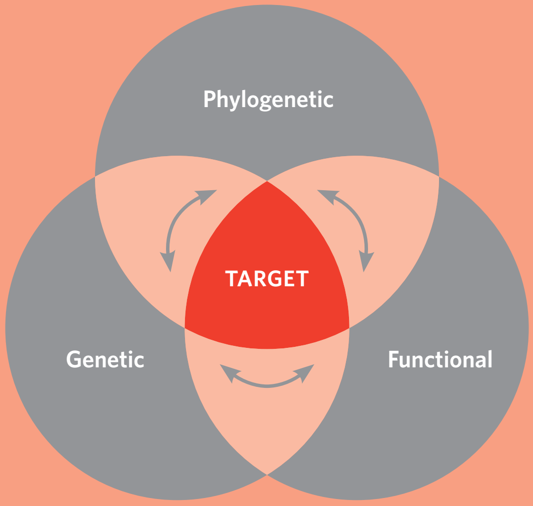
> *These grants will allow us to find new ways of understanding how organisms form, interact, and change through time. This year's Dimensions of Biodiversity awardees will investigate some of the least-known and perplexing 'innovations of nature,' from the ability of plant plankton to metabolize vitamins, to how various types of snake venom developed, to why humidity-loving mosses can tolerate arid conditions.*
>
> **James Olds**
> Assistant Director
> NSF's Biological Sciences Directorate

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 selection pressures. The Dimensions of Biodiversity program is a platform for exploration of species and population-level diversity, recognizing that genetic diversity is best understood in a **phylogenetic** context to reveal how biodiversity is shaped over time. For instance, researchers using a 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

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, decision makers and the public
APPROACH	Planning & partnering → Baselining & synchronizing → Assessing progress → Aligning investments with emerging priorities



> *This research will help us understand, for example, the incredible diversity of marine life and how it functions. In a time of changing seas, that knowledge is of great importance in comprehending, and conserving, the species in Earth's vast oceans.*
>
> **Roger Wakimoto**
> Assistant Director
> NSF's Geosciences Directorate

the expression of traits to their effects on our environment. Researchers are pioneering investigations on what impact the feedback from those environmental functions have on species and communities, while others are assessing the impacts of diversity on ecosystems over time. 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 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)
2010		16		$2.9M	$9.3M	$18.9M		$31.1M	¥750k	
2011		12	$6.5M	$1.5M	$2.5M	$17.5M		$28.0M	¥610k	
2012	C, B, N	14	$3.2M	$168K	$2M	$22.8M	$720k	$29M	¥6M	R$2.8M
2013	C, B, N	13			$1M	$21.7M	$2.5M	$25.2M	¥3M	R$2.7M
2014	C, B	12			$1M	$22.5M		$23.5M	¥3M	R$3.1M
2015	C, B	10		$3.6M	$2.5M	$17.7M		$23.8M	¥3M	
2016	C, B	11				$20.3M		$20.3M		R$7.2M

Broader Impacts

Dimensions of Biodiversity Projects have innovative outreach activities. Some examples and concepts connected to these activities are given here in the broad categories of citizen science, databases and cyberinfrastructure, undergraduate and graduate education, and K-12 education.

CITIZEN SCIENCE

Dimensions projects connect the public with...

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

DATABASE & CYBERINFRASTRUCTURE

Through Dimensions, projects are connected with...

- Extreme Weather Events
- Parasitoid Wasps
- Extinction Risk
- Phylogenetic Frameworks
- Plant Traits
- Parallel Sequencing
- Predictive Ecology
- Satellite Imagery
- Soil Organic Matter
- Worm Biology
- Protein Fingerprints
- Oxygen Minimum Zone
- Paleobiology
- Single Cell Genomics
- Coral Reefs
- Oceanography
- Arthropod Diversity
- Flowering Plants
- Museums
- Deep Subsurface

UNDERGRADUATE & GRADUATE EDUCATION

Through Dimensions, students are connected with projects on...

- Herbaria
- Copepods
- Microbiomes
- Symbioses
- Fungi
- Genomics
- Isotope Ratios
- Sensory System Evolution
- Gene Expression
- Phytoplankton
- Adaptive Radiation
- Extinction Risk
- Science Festivals
- Oxygen Minimum Zone
- Nutrient Cycling
- Plant Pathogens
- Deep Shale
- Nutrient Ratios
- Dry Valleys

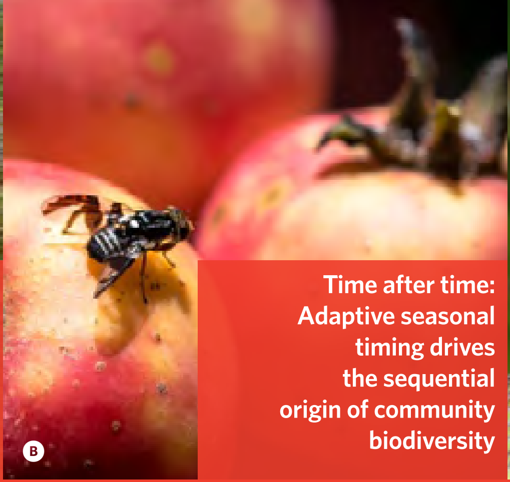
K-12 EDUCATION

Through Dimensions, educators and students are connected with...

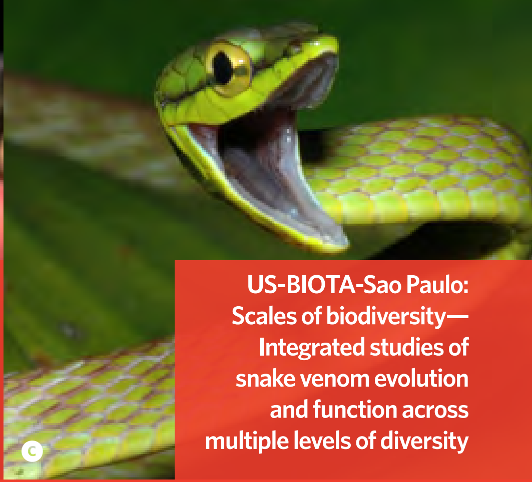
- The Pacific Northwest
- Color Pattern Divergence
- Avian Malaria
- Drought Tolerance
- Elevation Ranges
- Coastal Ecosystems
- Microbial Sciences
- Trophic Interactions
- Wild Nightshades
- Adaptive Radiation
- Video Game Design
- Plant Mating Systems
- Soil Organic Matter
- Mathematical Modeling
- Weather Station Data
- Genetic Architecture
- Nitrogen Cycling


A

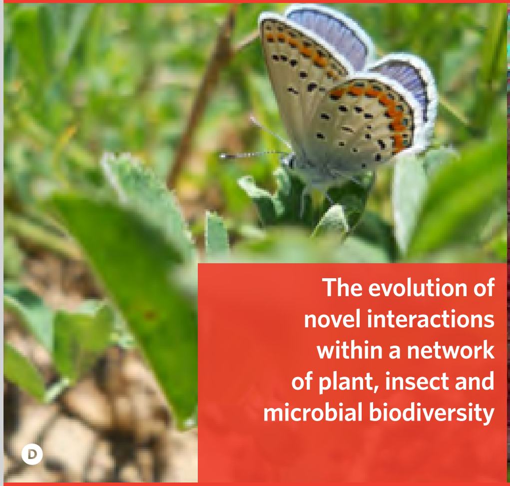
Diversification of sensory systems in novel habitat: Enhanced vision or compensation in other modalities?


B

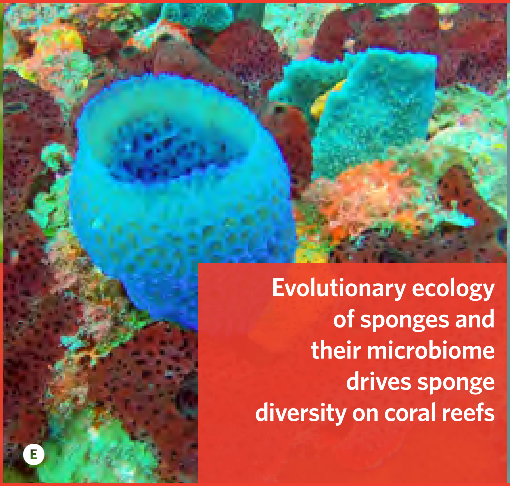
Time after time: Adaptive seasonal timing drives the sequential origin of community biodiversity


C

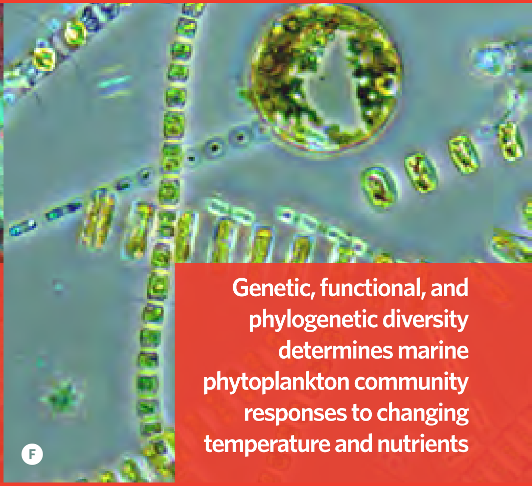
US-BIOTA-Sao Paulo: Scales of biodiversity—Integrated studies of snake venom evolution and function across multiple levels of diversity


D

The evolution of novel interactions within a network of plant, insect and microbial biodiversity


E

Evolutionary ecology of sponges and their microbiome drives sponge diversity on coral reefs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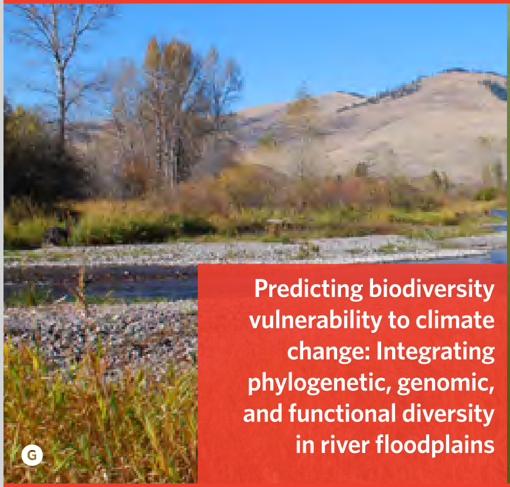
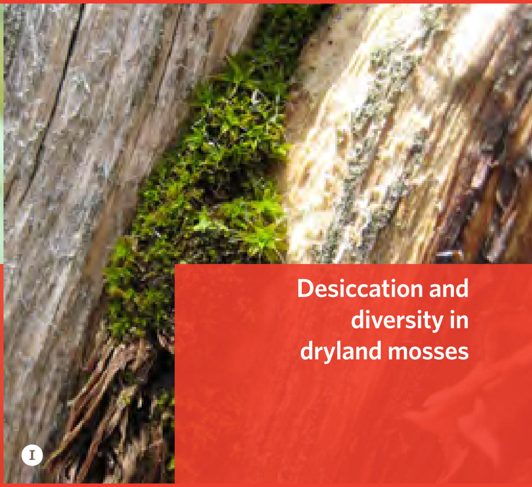
Genetic, functional, and phylogenetic diversity determines marine phytoplankton community responses to changing temperature and nutrients


G

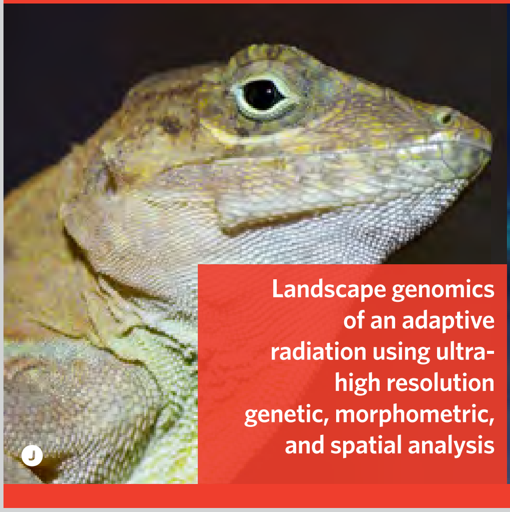
Predicting biodiversity vulnerability to climate change: Integrating phylogenetic, genomic, and functional diversity in river floodplains


H

Secondary metabolites as drivers of fungal endophyte community diversity


I

Desiccation and diversity in dryland mosses


J

Landscape genomics of an adaptive radiation using ultra-high resolution genetic, morphometric, and spatial analysis


K

Functional and genomic diversity in vitamin B_1 metabolism and impacts on plankton networks and productivity

2016 abstracts

IMAGE CREDIT

Ⓐ Janette W. Boughman
Ⓑ Hannes Schuler
Ⓒ Christopher L. Parkinson
Ⓓ Lauren Lucas
Ⓔ Deborah J. Gochfeld
Ⓕ Stephanie Anderson
Ⓖ Amanda DelVecchia
Ⓗ Priscila Chaverri
Ⓘ Theresa Clark
Ⓙ Ian J. Wang
Ⓚ Jacques Descloitres

Proj. 1 / 11

Diversification of sensory systems in novel habitat: Enhanced vision or compensation in other modalities?

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Icelandic stickleback fishes provide a compelling testing ground and lots of statistical power to investigate how evolutionary change in sensory systems facilitates survival and persistence of species in rapidly changing environments.

Iceland's dynamic landscape is shaped by volcanoes, glaciers, and severe storms. Like much of the Arctic it is also experiencing unprecedented environmental change. Against this backdrop only a few species adapt quickly enough to persist. One, the threespine stickleback fish, is found in the ocean surrounding Iceland, and in many of the islands' lakes and rivers. Adaptation to the freshwater environments has occurred in the brief time since colonization. In Iceland, one can reconstruct evolutionary time by using extant marine sticklebacks (ancestral to all freshwater populations), young freshwater populations (100s of years old from lakes newly formed near the ocean), and older freshwater populations (15,000 years old from highland lakes formed just after the glaciers retreated).

A conspicuous ecological feature is that some Iceland lakes are spring fed and clear, whereas others are glacially fed and turbid — akin to looking through dense fog. Sensory systems are key for survival and reproduction because animals gather information on the external environment using sight, smell, taste, sound, and touch to find prey, avoid predators, and mediate social interactions. Have these fish evolved better vision in glacial lakes where visual information is obscured? Or instead, have they shown evolutionary tradeoffs in sensory systems, reducing vision and compensating by increased reliance on the mechanosensory lateral lines or olfaction?

This project studies the integrated evolution of visual, olfactory, and mechanosensory systems in the novel sensory environment of glacial lakes. It assesses how differences in sensory systems affect predator detection in clear versus turbid waters. Gene expression data will be used to help identify novel candidate genes for sensory adaptation. A key strength of the study is to marshall novel methods to determine colonization history, placing adaptive evolution within an explicitly phylogeographic context, thereby revealing the rate of adaptation and extent of parallel evolution. And lastly, the project explores the role of plasticity in initial colonization and subsequent evolution. The project combines the phenotypic, functional, and genetic dimensions, all within a historical context to help understand what has facilitated rapid adaptation to novel environments; crucial information in an era of global change.

Undergraduates, laboratory technicians, graduate students, post doctoral researchers, and early career faculty will be trained in a variety of cutting-edge approaches that can be used in a diversity of science careers. Key findings from this research will be disseminated broadly in schools and museums to create a more scientifically literate American public.

PI Boughman used a field spectrometer to record the spectral quality of light in Þristikla, a glacial lake in the northern highlands.

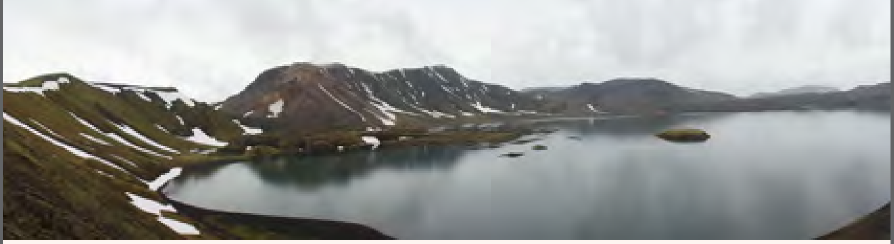
CREDIT: JANETTE W. BOUGHMAN

PI Boughman setting a trap from the shore into Frostastaðavatn, a spring fed lake in the southern highlands of Iceland.

CREDIT: JANETTE W. BOUGHMAN

Lagarfljót is a very turbid glacial lake in eastern Iceland fed by meltwater from Iceland´s largest glacier, Vatnajökull. Visibility in this lake is restricted to just a few centimeters.

CREDIT: JANETTE W. BOUGHMAN

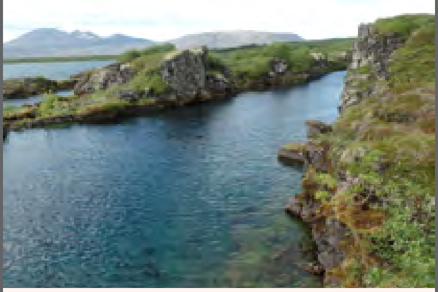


Frostastaðavatn is a clear spring fed lake in the southern highlands near Landmannalaugar, Iceland. It has abundant stickleback as well as arctic charr. Charr are the primary predators of stickleback. The project tests the ability of stickleback from glacial and spring fed lakes to avoid predatory attacks in both turbid and clear water conditions.

CREDIT: JANETTE W. BOUGHMAN

Data on the sensory environment are collected and traps for stickleback fish are set from small boats. Few lakes are on roads and none have launch sites, so access can be challenging.

CREDIT: JANETTE W. BOUGHMAN



Spring fed and situated in a rift valley, Þingvallavatn is a mid-elevation lake with clear visibility to 70+ meters. It has two morphs of stickleback and four morphs of arctic charr.

CREDIT: JANETTE W. BOUGHMAN

Some lakes have other fish species that prey upon stickleback. Research technician Jared Thompson caught many arctic charr in this spring fed highland lake.

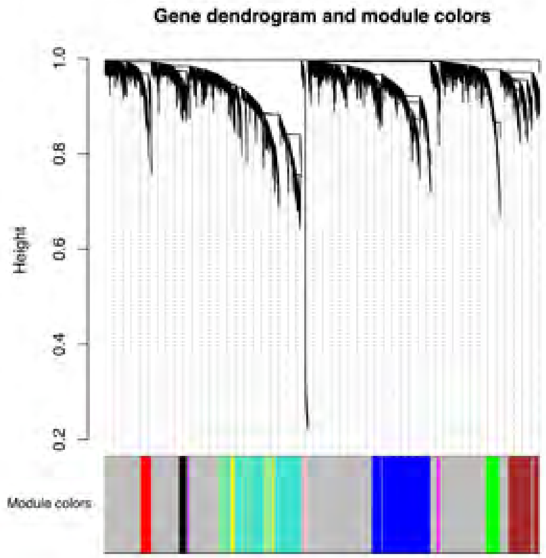
CREDIT: JANETTE W. BOUGHMAN

These threespine stickleback were captured in a spring fed lake. Males are colorful during the breeding season.

CREDIT: JANETTE W. BOUGHMAN

Blautaver is a glacial highland lake connected to the Tungnaá River in Iceland. Note the spectral shift of the water, which is both turquoise and turbid.

CREDIT: JANETTE W. BOUGHMAN



Thousands of genes can be expressed simultaneously in a tissue, making analyses difficult. Here, whole-brain gene expression in a female stickleback fish is analyzed after grouping genes with similar expression patterns into modules.

CREDIT: JASON KEAGY, MICHIGAN STATE UNIVERSITY

Proj. 2 / 11

Time after time: Adaptive seasonal timing drives the sequential origin of community biodiversity

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Daniel Hahn
University of Florida
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This research project will study rapid evolution of a new agricultural pest, the apple maggot fly, and a community of coevolving parasitoid wasps to understand how diversification in one lineage can help generate greater diversity across trophic levels.

In seasonal environments, organisms must cope with unfavorable periods (e.g., winter). Seasonal coping strategies are familiar: trees drop leaves, birds migrate, and bears hibernate. Animals and plants must synchronize their life cycles to seasonal conditions like temperature or moisture, and also synchronize their periods of activity with other organisms, including prey, competitors, predators, etc. This seasonal response and synchronization is a critical organizing aspect of many different ecological communities.

Seasonal adaptation can help create and maintain biodiversity. Speciation, the generator of biodiversity, occurs when populations become reproductively isolated, and reproduction is often seasonal. Therefore, shifts in seasonal timing can disrupt reproductive timing among populations, catalyzing speciation. Moreover, speciation does not occur in isolation. Formation of new taxa creates opportunities for other, interacting organisms to also diversify. Shifts in seasonal timing can have reverberating effects generating new biodiversity "sequentially" through ecosystems. Contemporary environmental change is driving changes in seasonality. The capacity of ecological communities to evolve in concert with changing conditions will impact whether interactions among community members will be maintained or disrupted under new environmental conditions.

This project will investigate the role of seasonal adaptation in the origin and maintenance of insect biodiversity. *Rhagoletis pomonella,* the apple maggot fly, evolved a fruit-feeding habit in the mid 1880's to feed on earlier ripening apple fruits and is now a major agricultural pest. Superimposed on seasonal partitioning of plant-feeding flies are additional "sequential" radiations involving parasitic wasps. Three wasps have similarly diverged in life cycle timing to match the seasonal shift of their *R. pomonella* hosts to earlier fruiting apples. This project will test whether the same physiological, molecular, and genomic mechanisms underlying the shift in life history timing allowing *Rhagoletis* to consume apples are also involved in sequential shifts and seasonal adaptation of the wasps that parasitize apple flies. Environmental conditions will be manipulated to assess the potential for environmental change to disrupt the fly and wasp communities, or if sufficient genetic diversity exists within these insect populations for them to rapidly respond and co-evolve.

Impacts of this research range from novel findings on adaptation and response to environmental change to educational and societal benefits. These researchers have strong commitments to fostering participation of underrepresented groups in science through mentoring and outreach. The scientists will partner with high school teachers to use this story of ecological divergence and co-speciation in their own backyards to develop and disseminate a curriculum unit on evolution as an important on-going process in nature. *Rhagoletis* flies are also important agricultural pests. This work on life history timing of flies and their parasites will contribute to both better management practices and understanding of how new crop pests emerge.

A parasitoid wasp searching for snowberry fly larvae to parasitize.

CREDIT: HANNES SCHULER, UNIVERSITY OF NATURAL RESOURCES AND LIFE SCIENCES VIENNA (FORMER POST DOC AT NOTRE DAME)

PI Jeff Feder and graduate student Glen Hood.

CREDIT: HANNES SCHULER, UNIVERSITY OF NATURAL RESOURCES AND LIFE SCIENCES VIENNA

PhD student Qinwen Xia working at a microscope attached to a microinjector needle rig used to treat diapausing flies and wasps with the developmental hormone ecdysone.

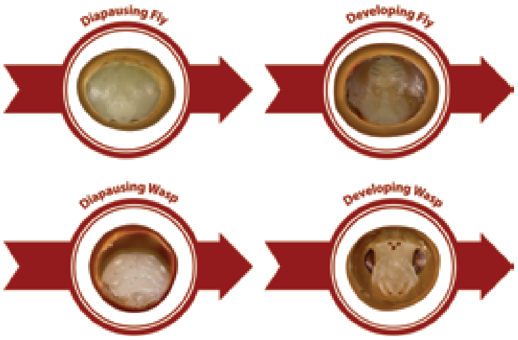
CREDIT: ALEX CATALANO, UNIVERSITY OF FLORIDA

Edgewater High School students use curriculum developed through the project.

CREDIT: MARGARITA HERNANDEZ, CENTER FOR PRE-COLLEGIATE EDUCATION AND TRAINING, UNIVERSITY OF FLORIDA

A hawthorn fly preparing to lay eggs within a hawthorn fruit where the larvae will feed, grow, and sometimes be parasitized by hawthorn wasps.

CREDIT: HANNES SCHULER, UNIVERSITY OF NATURAL RESOURCES AND LIFE SCIENCES VIENNA



A conceptual diagram showing diapausing flies and diapasuing wasps on the left, and developing flies and wasps on the right. The timing of diapasue versus development regulates diversification and seasonal timing in this community of interacting organisms.

CREDIT: QINWEN XIA, UNIVERSITY OF FLORIDA

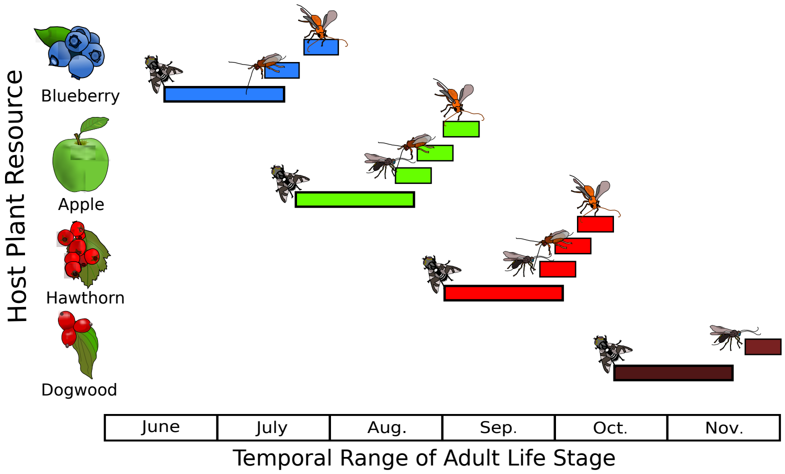


Diagram showing how *Rhagoletis* flies and their parasitoid wasps are adapted to different seasonal resources.

CREDIT: THOMAS POWELL, BINGHAMTON UNIVERSITY

Proj. 3 / 11

US-BIOTA-Sao Paulo: Scales of biodiversity— Integrated studies of snake venom evolution and function across multiple levels of diversity

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Understanding how groups of organisms have become exceptionally species-rich requires identifying the features and mechanisms that promote diversification. This research assesses the role that venom diversity, from the genetic to the functional level, has played in the diversification in front and rear-fanged venomous snakes from North, Central and, South America.

A major challenge in evolutionary biology is identifying the traits that promote diversification in species-rich groups of organisms. The derived snakes (superfamily Colubroidea) are one such diverse group of vertebrates; comprised of more than 2,500 species including front- and rear-fanged venomous species. Venom diversity, both genetic and functional, is hypothesized to have been the key feature initiating and maintaining this radiation by expanding feeding opportunities. This project will assess whether changes in the venom system have contributed to diversification patterns within Colubroidea snakes and whether venom has evolved in a repeatable or predictable way in different species.

In the first part of the study, researchers will test for relationships between venom function and diversification rates by collecting venomous snakes from areas of exceptionally high species diversity in the United States, Central America, and Brazil through field expeditions. Venom variation will then be assessed at the molecular level in the laboratory. Venom complexity in composition and function will then be modeled phylogenetically to test the hypothesis that higher venom diversity is a prerequisite for rapid speciation in particular lineages of these snakes.

The second part of the study will focus on the evolution of venom in different species. Closely related species pairs that show substantial differences in how their venom affects prey will be identified, allowing researchers to determine whether the molecular mechanisms by which differences in venom are generated are the same or different across species.

The broad significance of this research program is that traits that are key innovations have long been argued to play a key role in adaptive radiations. The precise details of how this occurs are unknown as is whether these details influence large-scale patterns of diversity. Venom is one of the few traits that is both readily identifiable as a key innovation and also genetically tractable, such that the precise molecular pathways to species diversification in this trait can be ascertained. The project will not just describe the large-scale evolutionary patterns of how venom impacts snake diversification, but will also identify the small-scale evolutionary processes underlying those patterns. The project will promote undergraduate and graduate student research in the US and Brazil. Public outreach will be accomplished by means of an interactive traveling display, educational pamphlets about snake diversity and evolution, and online presentations in both English and Portuguese based on the project.

Arizona Black Rattlesnake, *Crotalus cerberus*, in upland pinyon-juniper woodland habitat.

CREDIT: GREGORY TERRITO, UNIVERSITY OF CENTRAL FLORIDA

Ridge-nosed Rattlesnake, *Crotalus willardi willardi*, in montane forest habitat.

CREDIT: CHRISTOPHER L. PARKINSON

A palm-pitviper, *Bothriechis nubestris*, that was first described in 2016. This species is found only in the highlands of the Talamancan Cordillera of Costa Rica.

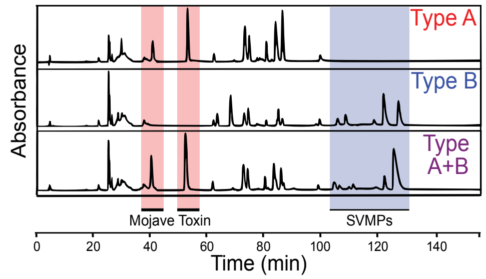
CREDIT: CHRISTOPHER L. PARKINSON

A higly arboreal rear-fanged snake, *Oxybelis brevirostris*, from Nuqui, Colombia.

CREDIT: CHRISTOPHER L. PARKINSON

A research team from Florida State University collecting rattlesnake specimens in West Texas.

CREDIT: MIKE HOGAN, FLORIDA STATE UNIVERSITY



Chromatography profiles of three major venom types found in Mojave Rattlesnakes, *Crotalus scutulatus*. Mojave Toxin is neurotoxic while Snake Venom Metalloproteases (SVMPs) are partially responsible for hemorrhagic effects of snakebites.

CREDIT: JASON STRICKLAND, UNIVERSITY OF CENTRAL FLORIDA

Graduate students Mark Margres (left) and Micaiah Ward (right) inspect an adult Ornate Blacktail Rattlesnake (*Crotalus ornatus*).

CREDIT: MIKE HOGAN, FLORIDA STATE UNIVERSITY

Fresh venom (yellow liquid) is collected from a Mojave Rattlesnake, *Crotalus scutulatus* by allowing it to crawl out of a clear plastic tube and encouraged to bite the collection cup.

CREDIT: CHRISTOPHER L. PARKINSON

Proj. 4 / 11

The evolution of novel interactions within a network of plant, insect and microbial biodiversity

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This project investigates the relationship between multiple components of biodiversity and the evolution of novel interactions among plants, insects, and microbes, to answer the fundamental question: what role does biodiversity play in the evolution and maintenance of novel interactions?

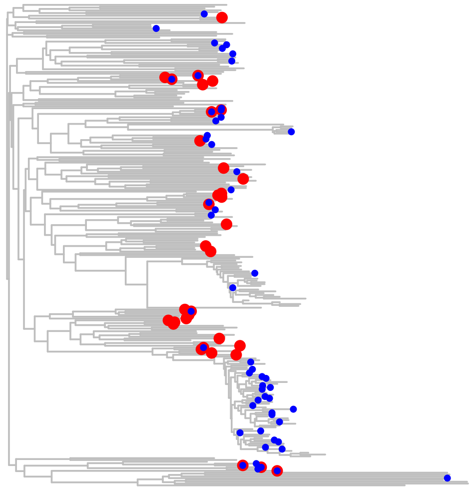
A majority of earth's biodiversity exists in networks of interacting species that include insects, plants, and microbes. Interactions in these networks have long fascinated biologists for the specificity of the relationships, and for their contribution to the evolution and maintenance of biodiversity. For example, most insects that eat plants consume only a few types of plants in any one location. Additionally, many of these insects harbour specialized fungi, or are inhabited by beneficial bacteria. Despite their significance, there is limited scientific knowledge regarding how and why these highly specialized interactions arise. This project will investigate the evolutionary origin of novel biological interactions among insects, microbes and an introduced plant, alfalfa, in western North America. By identifying the key factors that influence the existence of novel plant-insect-microbe interactions, the research will fill a substantial gap in our understanding of the diversity of life, and enhance our ability to predict how environmental change affects biological diversity and ecosystem function. Researchers will also engage and collaborate with the public through a discovery-based citizen science program, and develop new analytical tools to help other scientists.

Research into interactions among organisms and the evolution and maintenance of organismal diversity has typically focused on relatively simple pairwise interactions between a small number of interacting species or a few genetic elements, and has commonly ignored microorganisms. Given technological advances in genomics, new analytical methods, recognition of the potential roles of microorganisms, and the development of study systems that are likely representative of typical natural interactions, we can now readily fill this gap in our understanding of biodiversity dynamics. This project takes advantage of a well-studied plant-insect-microbe system (alfalfa, the Melissa blue butterfly, and symbiotic microbes) to investigate the importance of multiple components of diversity in predicting the evolution of novel interactions between species. Ultimately, the goal is to answer the fundamental question: what role does biodiversity play in the evolution and maintenance of novel interactions?

The project combines diverse observations of biological complexity with experimental manipulations to better understand the factors that shape novel species interactions. Specific approaches include: genomic variation within and among populations of interacting plants and insects; phylogenetic diversity of gut bacteria in insects and microbial diversity in plants; functional variation in plant chemistry; caterpillar survival and female butterfly egg-laying preference on host plants. This study will advance the standard model of the evolution of insect and microbe host, and will develop and validate a mechanistic model for the evolution of novel interactions that will be an important point of reference for research in other systems. Observations in natural communities and experiments from this research will build knowledge of the consequences of genomic variation for organismal traits, and the ecology and evolution of the biodiversity networks in which the organisms interact.

Matthew Forister collecting data from an experimental alfalfa garden at the University of Nevada, Reno.

CREDIT: MATTHEW FORISTER



A phylogenetic tree comparing fungal endophytes found in *Astragalus letiginosus* (red dots) and one alfalfa population (blue dots). Microbial communities associated with each plant species are clumped compared to a random expectation.

CREDIT: JAMES FORDYCE

A male Melissa blue butterfly on its host plant, alfalfa, at a field site near Hardware Ranch, Utah.

CREDIT: LAUREN LUCAS, UTAH STATE UNIVERSITY

Melissa blue caterpillars feeding on alfalfa near Victor, ID while being tended by beneficial ants.

CREDIT: LAUREN LUCAS, UTAH STATE UNIVERSITY

Matthew Forister using a backpack-vacuum to sample insect communities from an alfalfa field in Ragtown, Nevada.

CREDIT: MATTHEW FORISTER

Alfalfa commonly grows along roadsides in the western US, as shown by these flowering alfalfa plants at a field site near Dubois, Wyoming.

CREDIT: LAUREN LUCAS, UTAH STATE UNIVERSITY

A Melissa blue caterpillar feeding on lupine as part of an experiment investigating the effect of host plant species on insect gut microbiome.

CREDIT: LAUREN LUCAS, UTAH STATE UNIVERSITY

Zach Gompert adding fresh plant material to petri dishes for caterpillars as part of an experiment examining how host plant species affects larval gut microbiome, growth and survival.

CREDIT: LAUREN LUCAS, UTAH STATE UNIVERSITY

Proj. 5 / 11

Evolutionary ecology of sponges and their microbiome drives sponge diversity on coral reefs

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The goal of this project is to investigate the symbiosis between marine sponges and their microbiome, and understand how these relationships drive the evolution and ecology of sponge diversity on coral reefs across the Caribbean basin.

Coral reefs, the tropical rain forests of the marine environment, are under significant threat from a variety of stressors such as pollution, overfishing, coastal development and environmental change. Because of continuing reef degradation the phylogenetic, genetic, and functional diversity of coral reefs will increasingly be found in taxa other than scleractinian corals, such as sponges. Sponges are an ancient group of organisms essential to reef health because of their roles in nutrient cycling, providing food and homes for many other reef organisms, and their ability to synthesize diverse chemical compounds of ecological importance, and interest to the biomedical community. Many of these important ecosystem functions would not be possible without the sponge's symbiotic microbes (e.g., bacteria) known as the microbiome. In this project, researchers will examine important questions about the relationship between the sponge host and its microbiome, as the key to understanding their ecology and biodiversity.

The goal of this study is to examine the phylogenetic, genetic, and functional biodiversity of coral reef sponges across the Caribbean basin. Many marine sponges host a diverse assemblage of symbiotic microorganisms that play critical ecological roles in nutrient transfer and cycling between the water column and coral reef communities. To do this, researchers will use a combination of ecological approaches combined with biochemical and molecular analyses to unravel the role of the microbiome in the ecology and evolution of sponges. Through this integrative project researchers will provide important insights into the drivers of sponge biodiversity on coral reefs, and enhance understanding of the ecology and evolution of this understudied group of marine organisms. The co-evolution of the sponge host and its microbiome is hypothesized to produce emergent functional properties that result in increased sponge biodiversity. To assess this, researchers will quantify two fundamental functions of sponges in the Caribbean; their trophic strategy and the production of chemical defenses to deter predators from consuming them. These functions will be analyzed in the context of the taxonomic composition of the sponge hosts and their microbiomes, and the functional activities of the host and symbionts at the genetic level. These data will reveal patterns of co-evolution between sponges and their microbiomes, and how these symbioses influence the functional attributes of sponges within coral reef communities.

Diverse sponge community showing several species on a reef with low coral and high algal/cyanobacterial mat coverage near St. Croix, US Virgin Islands.

CREDIT: DEBORAH J. GOCHFELD

High density of the giant barrel sponge *Xestospongia muta*, among other sponges, on pinnacles close to Dominica.

CREDIT: DEBORAH J. GOCHFELD

Diverse community of at least six sponge species of different colors and morphologies near St. Croix, US Virgin Islands.

CREDIT: DEBORAH J. GOCHFELD

High density of the yellow tube sponge *Aplysina fistularis* at tops of pinnacles close to Dominica.

CREDIT: DEBORAH J. GOCHFELD

Dr. Deborah Gochfeld preparing vials to sample sponges in Little Cayman; *Mycale laxissima* shown in foreground.

CREDIT: MARIA CRISTINA DIAZ, NOVA SOUTHEASTERN UNIVERSITY

Proj. 6 / 11

Genetic, functional, and phylogenetic diversity determines marine phytoplankton community responses to changing temperature and nutrients

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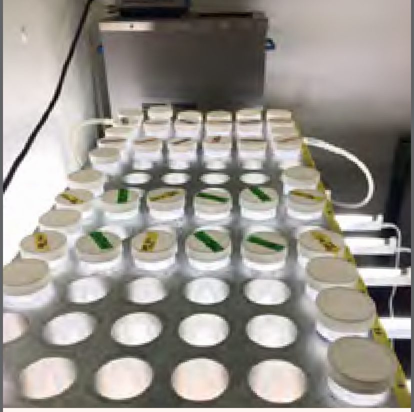
The project will combine field sampling, experiments, and mathematical models to understand and predict how marine phytoplankton communities will respond to changing temperature and nutrient regimes.

Photosynthetic marine microbes, phytoplankton, contribute half of primary production on Earth. Phytoplankton form the base of most aquatic food webs and are also major players in global biogeochemical cycles. They are also sensitive to environmental change. Understanding how phytoplankton community composition responds to changing environmental conditions is crucial because it affects higher trophic levels, from zooplankton to fish, carbon sequestration and the cycling of energy and elements. This project will investigate how phytoplankton communities respond to two major stressors in aquatic ecosystems: warming and changes in nutrient availability. The researchers will work in two marine systems with a long history of environmental monitoring, the temperate Narragansett Bay estuary in Rhode Island and a subtropical North Atlantic site near Bermuda, thus comparing two major ecosystem types, coastal areas and open ocean. Field sampling and laboratory experiments with multiple species and varieties of phytoplankton will be used to assess the diversity in responses to different temperatures under high and low nutrient concentrations. The evolutionary potential of different taxa will be investigated in laboratory experiments. Researchers will also incorporate information on phytoplankton diversity and eco-physiological responses into mathematical models to predict how phytoplankton assemblages would reorganize under future environmental scenarios. Model predictions will be tested with field data, including the long-term data series available in Rhode Island and Bermuda, and in community temperature manipulation experiments. The project will contribute new data on phytoplankton diversity and characterize the interaction of warming and changing nutrient concentrations in determining future phytoplankton composition and dynamics. In addition, the project will develop novel modeling approaches that will be broadly applicable to understanding how other types of complex ecological communities may adapt to changing environmental conditions.

Graduate students and postdoctoral associates will be trained in diverse scientific approaches and techniques such as shipboard sampling, laboratory experiments, genomic analyses and mathematical modeling. The results of the project will be incorporated into K-12 teaching, including an advanced placement environmental science class for underrepresented minorities in Los Angeles and data exercises for rural schools in Michigan. Results from the project will also be disseminated to the public through an environmental journalism institute based in Rhode Island.

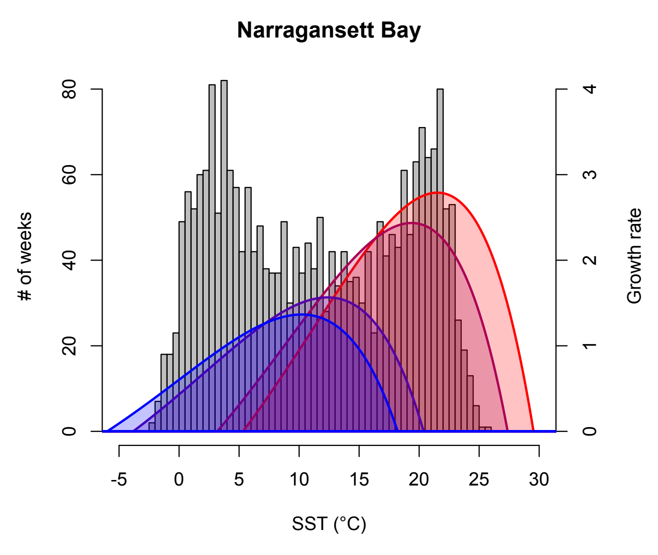


An experiment to measure thermal performance curves in phytoplankton.

CREDIT: DAVID HUTCHINS,
UNIVERSITY OF SOUTHERN CALIFORNIA

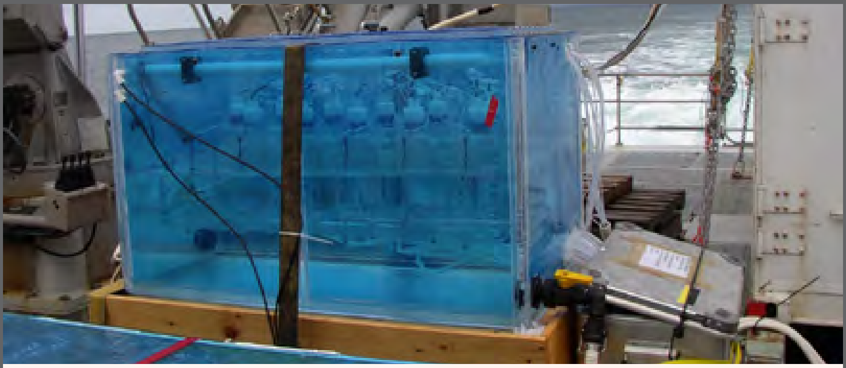
Trichodesmium sp., a colony forming, nitrogen-fixing cyanobacterium. One of the phytoplankton groups that will be used in laboratory and field warming and nutrient limitation experiments.

CREDIT: DAVID A. HUTCHINS



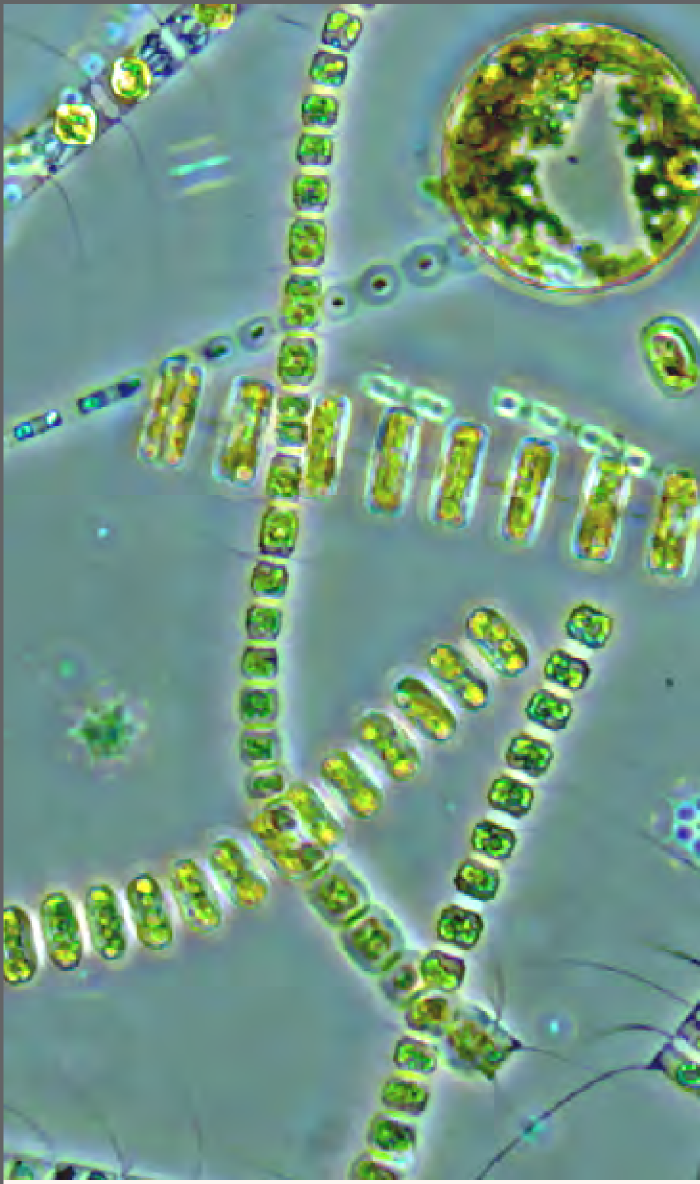
An illustration of how seasonal ocean temperature variation can permit four different species of marine phytoplankton to coexist, despite competing for shared resources.

CREDIT: COLIN T. KREMER, YALE UNIVERSITY



Incubation experiments in ecostat enclosures to examine how the interactive effects of warming and nutrient availability affect natural phytoplankton communities from estuaries and open ocean environments in the Atlantic Ocean.

CREDIT: DAVID A. HUTCHINS



A diverse phytoplankton community from Narragansett Bay, RI.

CREDIT: STEPHANIE ANDERSON, UNIVERSITY OF RHODE ISLAND,
GRADUATE SCHOOL OF OCEANOGRAPHY

Proj. 7 / 11

Predicting biodiversity vulnerability to climate change: Integrating phylogenetic, genomic, and functional diversity in river floodplains

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River floodplains are among the most biodiverse, yet endangered, landscapes on earth. This study will advance understanding of biodiversity of arthropod communities (insects and crustaceans) in river floodplains (and the interconnected aquifers) using innovative modeling and conceptual frameworks.

River floodplains are among the most diverse and productive landscapes on Earth, yet they are also among the most endangered because of damming, development, channelization, and environmental change. Unaltered floodplains are particularly important because they typically have extensive exchange between surface water and ground water in underground aquifers that often extend kilometers away from the river channel. This connectivity creates dynamic habitats that support thousands of plant, animal, and microbe species while also providing critical habitats for insects and crustaceans (a major source of food for fish), water purification, and buffering against flooding. Understanding how biodiversity varies with climate variation in a novel landscape like the aquifer (and adjacent river reaches) will help identify 'indicator species' in understudied invertebrate communities that have high vulnerability to environmental change.

Relatively little is known about the diversity and vulnerability of aquifer and river communities in a floodplain landscape context, especially the role of adaptive capacity (e.g., adaptation to local environments) in reducing vulnerability to negative effects of environmental change. This research project will test whether river species residing in the channel network are more vulnerable to warming because of the greater exposure to hydrologic (flow) and thermal variation than the aquifer species (below ground) that are buffered by the winter-warm and summer-cool ground water inputs typical of gravel bed floodplains.

This project will fill important gaps in the understanding of biodiversity by: 1) quantifying phylogenetic (species) diversity among aquifer and river floodplain species while identifying new species in six floodplains, 2) measuring sensitivity to environmental change of 12 diverse indicator species sampled from aquifers and rivers along environmental gradients, 3) quantifying exposure to change conditions in the aquifer and river by measuring and modeling variation in water temperature and dissolved oxygen, 4) assessing adaptive capacity in floodplain indicator species by measuring rates of dispersal and gene flow, and genetic diversity, and 5) predicting overall vulnerability of biodiversity within and among floodplains.

This project will catalog and characterize many new species on river floodplains in Montana and Washington through bioblitz events where students and citizen scientists will work with scientists to collect and catalog as many floodplain species as possible during a 24-hour period. Additionally, this project will help educate undergraduate students in summer field courses, train graduate students and postdoctoral researchers in intensive short courses on genomic data analysis, provide novel free software for the broader scientific community, provide Native American students with valuable field and lab experiences, and produce educational outreach videos, podcasts, a web page, and numerous scientific publications.

A gas diaphragm pump and mesh net (right) being used to collect hundreds of invertebrates from multiple species from one aquifer well on the Nyack Floodplain. Several species of amphibiotic stoneflies can be collected from one well.

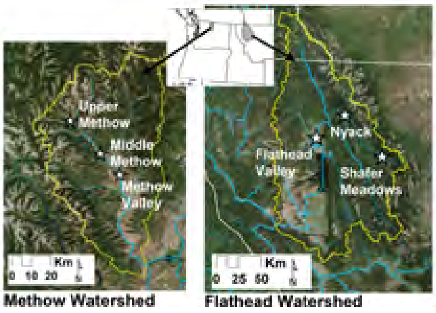
CREDIT: JACK A. STANFORD AND AMANDA DELVECCHIA

Student Chad Reynolds samples for stoneflies from the aquifer below the Nyack floodplain.

CREDIT: AMANDA DELVECCHIA, ALLEGHENY COLLEGE

The Nyack floodplain in the Middle Fork of the Flathead River in Montana during fall. One of six focal floodplains in this project, the Nyack floodplain has been at the center of 40-years of research on gravel based floodplains.

CREDIT: AMANDA DELVECCHIA, ALLEGHENY COLLEGE

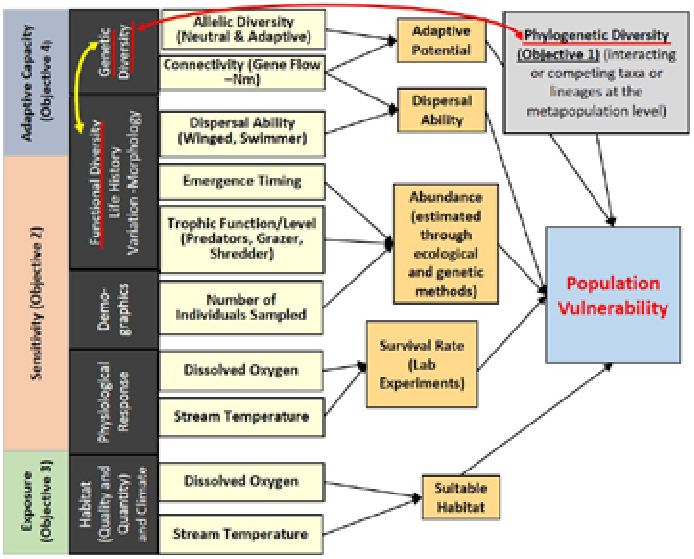


Study areas including 3 floodplains (stars) from each of 2 river drainages: the Methow in Washington, the Flathead in Montana.

CREDIT: BRIAN K. HAND, GORDON H. LUIKART AND DIANE WHITED, UNIVERSITY OF MONTANA

Student Christopher Johnson preparing to sample species from the hyporheic zone.

CREDIT: AMANDA DELVECCHIA, ALLEGHENY COLLEGE



Work-flow for assessing how interacting factors combine to affect aquatic arthropods. The project team will develop a new spatial model to assess the interactive nature of sensitivity, exposure, and adaptive capacity to investigate genetic diversity of any species, in any landscape.

CREDIT: BRIAN K. HAND AND DIANE WHITED, UNIVERSITY OF MONTANA

Proj. 8 / 11

Secondary metabolites as drivers of fungal endophyte community diversity

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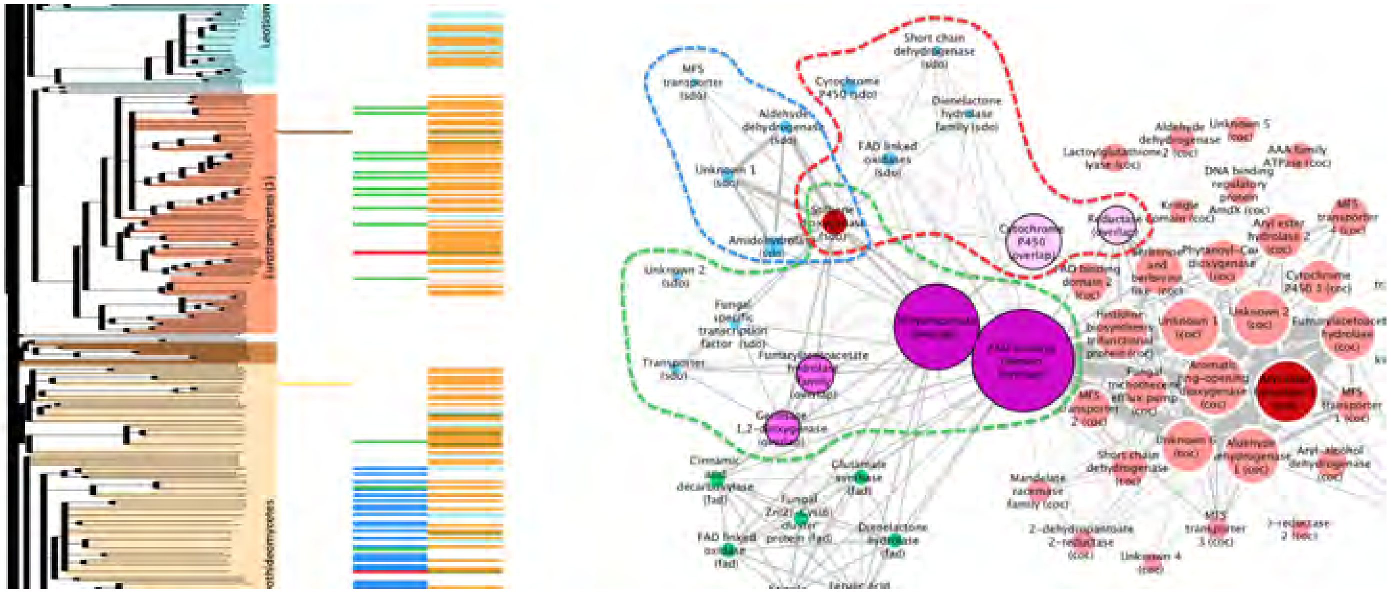
The project investigates the chemical diversity of the coffee family (Rubiaceae) and its fungal endophytes, and how this diversity impacts the composition and genome structure of plant microbiome communities.

Plants harbor fungal endophyte communities that both contribute to and are influenced by the diverse metabolome in the host. The net metabolome of plants and their fungal associates may exclude pathogens and pests, and favor beneficial communities that increase resistance to biotic and abiotic environmental stressors. Many of the medicinal and commercial compounds derived from plants result from these host-microbiome interactions. Most fungal associates of plants are acquired from the environment, but the mechanisms that allow a host to select functional microbiomes from the greater diversity of fungi are not known.

The coffee family, Rubiaceae, is hyperdiverse and abundant in the Neotropics, especially in Central America, and it has contributed several useful products to human societies, including coffee and quinine. Coffee, like many cultivated plants, is under threat from destructive pests and pathogens, and there is a growing interest in developing safe products and practices to control their severity and spread. Understanding the assembly of endophytic fungal communities that provide immunity and economic value to plant species, such as those in Rubiaceae, requires defining the genetic basis of fungal resistance to defense compounds. Fungal metabolic gene clusters encoding the mechanisms to synthesize, transform and degrade defense compounds, may play multiple roles in endophyte community assembly. Gene clusters that enable the colonization of new host plants could represent key innovations leading to fungal diversification. These gene clusters can also be horizontally propagated between divergent lineages of fungi, leading to more diverse and robust communities adapted to specific metabolomes.

This research will integrate analyses of the metabolome, community diversity, and fungal endophyte genomes to compare the leaves of coffee trees under different management practices with their wild relatives to test models of the role of chemical heterogeneity in fungal endophyte community collection/composition. Specifically, the association between metabolite combinations and fungal endophyte community diversity will be investigated. The contribution of fungal-fungal interactions to the metabolome will be studied by examining metabolites produced during interspecific competition. Novel phylogenetic methods of gene cluster discovery will be employed to develop precise understanding of genetic adaptations of fungi that allow them to survive and provide benefits in plant tissues. The broader impacts of this project include the construction of a large, integrated genome-metabolome database for a focused sample of endophytic fungi, annotated with novel biosynthetic and degradative gene clusters for use in synthetic biology and biological control. The group will further conduct workshops to train the next generation of scientists in ways to integrate genomic and metabolomic data to answer broad-scale ecological questions.



Phylogenetic and network analyses are used for the detection of endophyte gene clusters that encode the degradation of plant defense compounds.

CREDIT: EMILE GLUCK-THALER AND JASON C. SLOT

Leaf tissue is collected from different Rubiaceae species in Costa Rica.

CREDIT: PRISCILA CHAVERRI

An unknown fungal endophyte from *Coffea arabica* on agar culture awaiting DNA barcode sequencing.

CREDIT: PRISCILA CHAVERRI

Professor Chaverri isolates endophytic fungi from a sample of coffee leaves.

CREDIT: PRISCILA CHAVERRI

Graduate student Fernanda de Castro-Moretti analyzes volatile compounds from leaves using gas chromatography-mass spectrometry.

CREDIT: ANA PAULA ALONSO

Proj. 9 / 11

Desiccation and diversity in dryland mosses

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This research will investigate the links between the genes, physiology, life stages, populations, and communities of *Syntrichia* mosses that have facilited their ability to thrive in dryland ecosystems.

Mosses are the second most diverse group of land plants and they play important ecological roles in terrestrial ecosystems. Since an early divergence from other land plants some 450 million years ago, mosses took their own path to solving the challenges of survival and reproduction posed by terrestrial environments. One important survival trait in terrestrial mosses is the ability to dry out without dying, known as desiccation tolerance. This critical trait allows many mosses to survive and reproduce even in drylands, and it may be the key to their survival in the face of environmental change. *Syntrichia* is a large and diverse genus of mosses occurring worldwide and generally in dryland habitats. Despite their dominance in certain communities, such as biological soil crusts, surprisingly little is known about the drivers of biodiversity in this group. This team will integrate research from genomic, organismal, population, and community levels of organization in order to build a robust understanding of past and present dimensions of biodiversity in *Syntrichia*.

The overall goals are to elucidate evolutionary and ecological mechanisms that have produced and maintained functional diversity at these different levels of organization. The team will promote training, teaching, and understanding about dryland mosses and their soil crust communities by:
1) formal education through field and laboratory research;
2) informal education involving a classroom module, short-film series (featuring mosses and biocrusts transitioning from desiccation dormancy), a citizen science program, and series of public workshops and outreach events.

Collecting specimens of 15 North American *Syntrichia* species will require sampling of diverse microhabitats from low-elevation Mojave Desert to high-elevation plateaus and mountains throughout the United States. Specimens from environments with varying degrees of water stress will form the basis for mapping evolutionary trends and adaptive traits (e.g., desiccation tolerance), as well as a revised species classification.

CREDIT: THERESA CLARK AND KIRSTEN K. DEANE-COE

Biocrust communities are dominated by *Syntrichia* with co-occurring mosses, lichens, and cyanobacteria. Cultured clones are used to examine how diversity is linked to community resilience under climate change.

CREDIT: ANITA ANTONINKA, NORTHERN ARIZONA UNIVERSITY

Kirsten Fisher and Jenna Baughman collecting *Syntrichia* in the Mojave Desert near Phalan, CA.

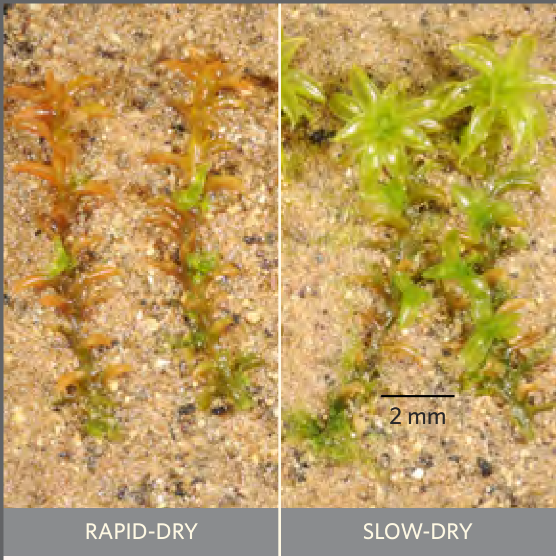
CREDIT: BRENT MISHLER

Juvenile, adult, and clonal dispersal units of *Syntrichia*.

CREDIT: LLOYD R. STARK

Dryland mosses avoid drought by drying (right) without dying, and rehydrate in rain within seconds to minutes (left). Genome sequencing of *Syntrichia ruralis* (shown here) will be used to study mechanisms of ecophysiological responses key to desiccation tolerance in this species.

CREDIT: THERESA CLARK, UNIVERSITY OF NEVADA LAS VEGAS



Laboratory experiments will test species limits of desciccation tolerance by varying factors such as drying rate. Stress-testing life stages and sexes will further understanding of hypothesized tradeoffs between reproduction and desiccation tolerance.

CREDIT: LLOYD R. STARK

Proj. 10 / 11

Landscape genomics of an adaptive radiation using ultra-high resolution genetic, morphometric, and spatial analysis

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This project will integrate genetic, morphological, and environmental data to examine how ecological heterogeneity generates different levels of biodiversity in the adaptive radiations of Anolis lizards on the Greater Antilles.

During an adaptive radiation, a group of organisms diversifies into a variety of forms specialized for different environments or ecological roles. *Anolis* lizards (anoles) on the Greater Antillean islands in the Caribbean have undergone repeated adaptive radiations, resulting in the formation of 'ecomorph' classes composed of species on different islands that have evolved similar traits for occupying similar parts of the forest habitat. This is a remarkable case of ecological divergence, in which species diversify in response to the environment, and convergent evolution, in which separate species independently evolve similar traits.

The Greater Antillean anole ecomorphs are named for the microhabitat in which they are found (trunk-ground, trunk, trunk-crown, crown giant, twig, and grass-bush), and although the species within each ecomorph share very similar characteristics (e.g., body size, limb lengths, toe-pad shapes), the physical traits of the different ecomorphs have evolved to become quite different. Moreover, many anole species inhabit a wide range of environmental conditions and populations in different environments can exhibit variation in ecologically important traits. Hence, the adaptive radiations of anoles on the Greater Antilles contain remarkable biodiversity at several different levels (within species, between species, and between ecomorphs) and present excellent opportunities to answer several important questions in evolutionary biology. For instance, what are the factors that generate diversity in the genetic and morphological traits of a species? What is the genomic basis for these traits, and are the same genes involved in the repeated evolution of particular traits in different species? When do the processes generating variation lead to speciation, in which a species diversifies into separate distinct species?

This project will examine how spatial variation in the environment leads to variation in adaptive physical traits and variation across the genome both within and between species. The researchers will use advanced methods in genomics, GIS, morphology, and spatial statistics to analyze specimens from 12 anole species collected across a broad range of environments. Whole exome sequences on each lizard will be generated, bioclimatic data will be assembled from remote sensing databases using LiDAR scanning to measure the structure of different forest habitats, and 3D morphological images will be collected from each specimen using micro-CT scanning. By examining multiple species and many specimens from each species, the researchers will be able to identify the factors that generate different levels of biodiversity during different stages of adaptive radiation.

This project will also result in the training of two postdoctoral researchers and numerous graduate and undergraduate students, including students from traditionally underrepresented backgrounds. The researchers also plan to integrate the results of the project into classroom learning modules on the ecology and evolution of adaptive radiations for K-12 students.

LiDAR scanning of two different habitats, coastal dry forest (left) and lowland rain forest (right).

CREDIT: IAN J. WANG

Hispaniolan large-headed anole (*Anolis cybotes*) from the Dominican Republic.

CREDIT: IAN J. WANG

Hispaniolan green anole (*Anolis chlorocyanus*) from the Dominican Republic.

CREDIT: IAN J. WANG

Puerto Rican crested anole (*Anolis cristatellus*) from Rincon, Puerto Rico.

CREDIT: IAN J. WANG

Proj. 11 / 11

Functional and genomic diversity in vitamin B_1 metabolism and impacts on plankton networks and productivity

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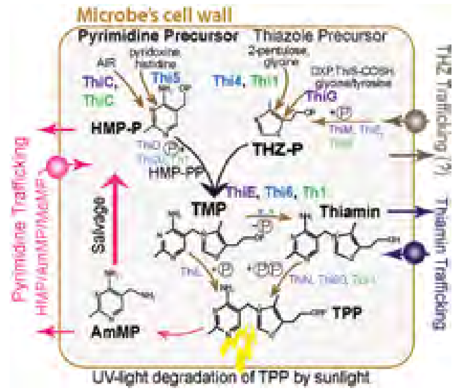
Research Institute
(1639033)
Stephen J. Giovannoni
Oregon State University
(1638928)

Research expeditions and experiments will explore the ecosystem implications of a recent discovery that ocean plankton engage in complex trafficking of component molecules, which can be assembled to make vitamin B_1. 'Omics science and advanced chemistry will be integrated to develop a new paradigm of how molecule trafficking influences microbial diversity and phytoplankton CO_2 uptake.

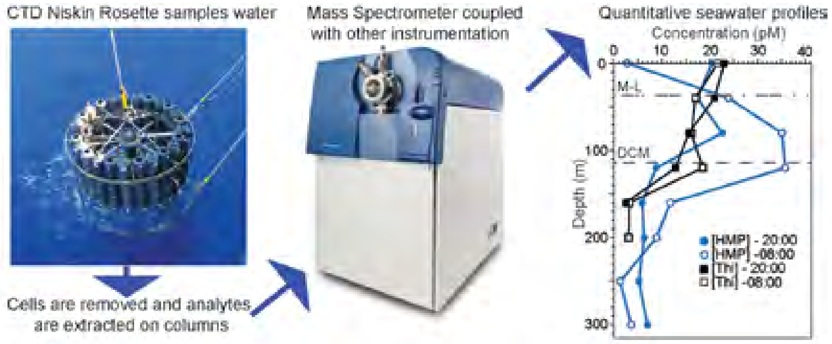
Vitamins are small organic molecules that are cofactors for essential metabolic enzymes, and therefore they have the potential to alter the health and productivity of entire ecosystems if the supply is insufficient. Many organisms, from humans to some oceanic plankton, require vitamins that are made by other organisms. Thus, in nature there is traffic in vitamins, which move from self-sufficient producers to consumers that are reliant on the surrounding community. This research explores the cycling of vitamin B_1 (thiamin) by planktonic cells at the base of the ocean food chain. Although it was once thought that all organisms either synthesize vitamin B_1, or obtain it from their environment, recent discoveries have revealed complex trafficking in B_1 components between cells, which can then be assembled to make complete vitamin B_1 molecules. Plankton has evolved diverse strategies to acquire thiamin, including salvaging thiamin component molecules from the environment. This project will study thiamin biochemistry in plankton, using comparative genomics and cell cultures, and will measure thiamin-related plankton interactions in natural and stimulated phytoplankton blooms. This investigation will join the oceanographic cruises of two major field campaigns in the North Atlantic Ocean, as well as a time-series study in the North Pacific Ocean, to measure the natural distributions and turnover of thiamin and related compounds in the oceans. This project aims to understand the role thiamin cycling plays in controlling ocean plankton biodiversity and photosynthetic productivity, and the response of plankton to changing ocean conditions. The results will be integrated using several computational approaches to interpret variations in microbial community structure, the role of biochemical, genomic and taxonomic diversity in maintaining biodiversity patterns of today's oceans and future oceans. Specific aspects of thiamin metabolism pathways and microbial networks will be explored in the context of understanding chemical interactions involving vitamin components and other scarce nutrients. These different levels of biodiversity and thiamin cycling will be investigated across transitions between productive phytoplankton blooms and the stratified, oligotrophic conditions typical of warmer oceans.

Structured collaborations between the graduate students and postdocs involved in the project will train this cohort to integrate across the three dimensions of biodiversity, with strength in bioinformatics, phylogenetics and the interdisciplinary studies needed for rigorous chemical ecology linked to evolution and diversification studies. The project also supports undergraduate research experiences and an educational module on carbon cycling by marine microorganisms for a teacher professional development program. The former prepares low-income, historically underrepresented, and other educationally underserved students from rural areas to pursue science, technology, engineering and math (STEM) careers.



Bacteria (purple), plants and green algae (green), and fungi (light blue) synthesizing vitamin B_1 (thiamin pyrophosphate, TPP) use different enzymes at several steps. Some marine phytoplankton take up B_1 precursor compounds directly by transporters (depicted as bubbles).

CREDIT: ALEXANDRA Z. WORDEN AND STEPHEN J. GIOVANNONI



The workflow for measuring thiamin-related compounds in seawater involves developing mass spectrometry techniques to quantify these compounds and their turnover along depth profiles (far right) and across the stages of phytoplankton blooms. Such data are needed to understand how much traffic in vitamins and vitamin precursors occurs between plankton species, and whether these transactions change and alter diversity and community structure over seasonal cycles.

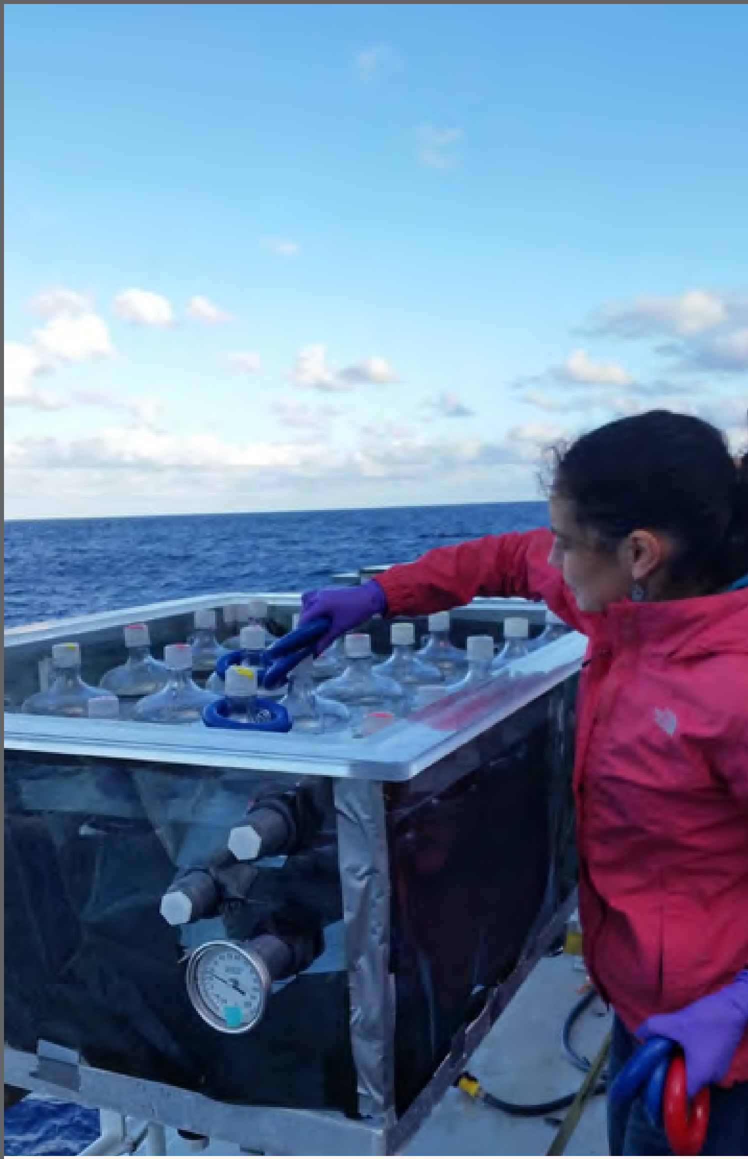
CREDIT: ALEXANDRA Z. WORDEN AND STEPHEN J. GIOVANNONI

Vitamin B_1 availability is thought to control blooms of eukaryotic phytoplankton that are important for primary production and carbon dioxide uptake, like this bloom detected from space off the French coast.

CREDIT: JACQUES DESCLOITRES, MODIS RAPID RESPONSE TEAM, NASA/GSFC

Graduate student Charlotte Eckmann collects water from a CTD Niskin Rosette in an autumn cruise to the eastern North Pacific Ocean. The water is used to study thiamin trafficking, measure compounds, and generate metagenomes and metatranscriptomes to understand genomic and physiological diversity in connection to community structure and function.

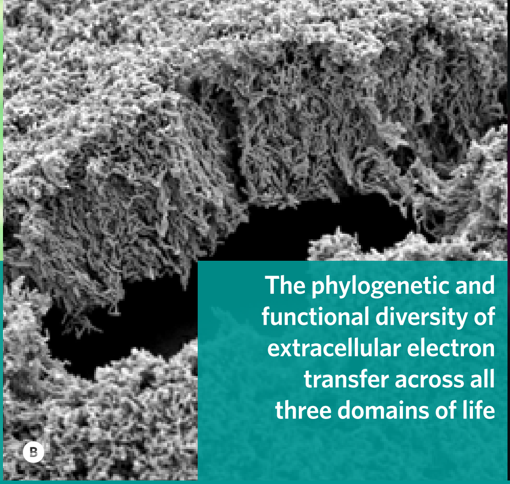
CREDIT: MARIA HAMILTON, MBARI/UNIVERSITY OF CALIFORNIA, SANTA CRUZ



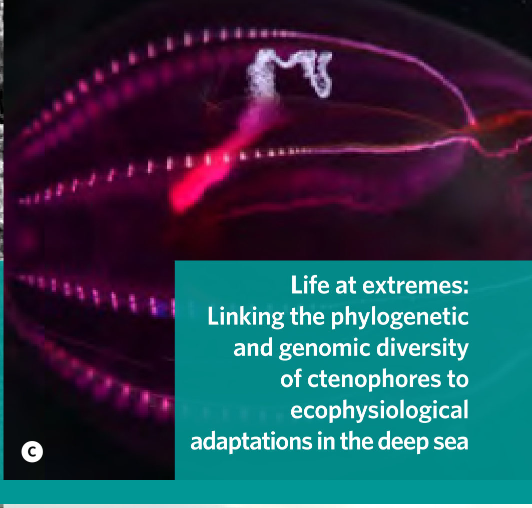
Graduate student Rachel Harbeitner checking at-sea experiments designed to test how thiamin-related compounds influence microbial interactions and biodiversity.

CREDIT: MARIA HAMILTON, MBARI/UNIVERSITY OF CALIFORNIA, SANTA CRUZ

Diversification dynamics of multitrophic interactions in tropical communities



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

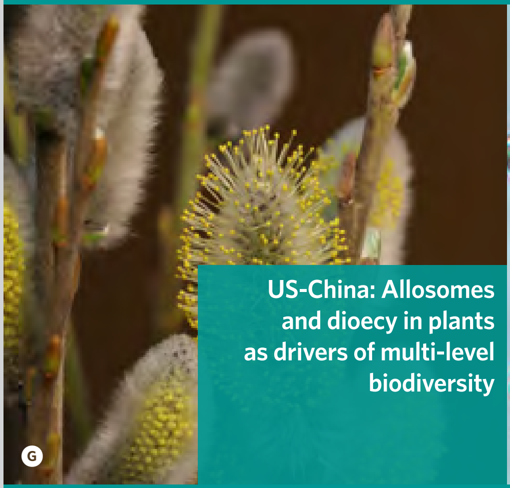


Life at extremes: Linking the phylogenetic and genomic diversity of ctenophores to ecophysiological adaptations in the deep sea

The evolution of pollination syndrome diversity in *Penstemon*

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

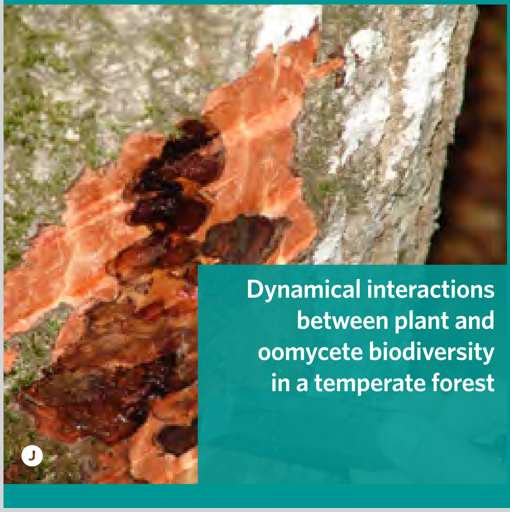
Community genomic drivers of moss microbiome assembly and function in rapidly changing Alaskan ecosystems



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 updates

IMAGE CREDIT

Ⓐ Martha A. Condon
Ⓑ Orianna Bretschger
Ⓒ Steven H. Haddock
Ⓓ Carolyn Wessinger
Ⓔ James C. Lendemer
Ⓕ Verity Salmon
Ⓖ Lawrence B. Smart
Ⓗ Steven Litaker
Ⓘ YK, Shutterstock
Ⓙ Niklaus Grünwald

Diversification dynamics of multitrophic interactions in tropical communities

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Nina A. Theis
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(1542321)

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(1542395)

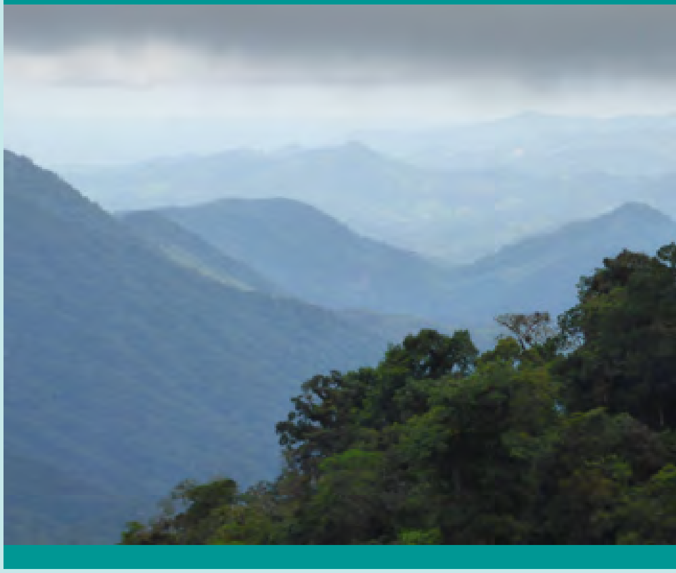
This project focuses on a species-rich tropical community of plants (Cucurbitaceae), tropical plant-feeding insects, and their predators (parasitic wasps). A major goal is to test the hypothesis that highly specific lethal interactions between herbivores and predators may explain patterns of diversity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

Update

The team assessed phenology of host-availability in seven countries (Colombia, Costa Rica, Ecuador, French Guiana, Mexico, Peru, and Trinidad). Collections of >3000 additional specimens were preserved to advance work on symbionts and both fly and parasitoid transcriptomes. Symbionts may affect patterns of lethality and reproductive isolation among parasitoid species. The team generated transcriptomes for four species of flies, and genome size was estimated in preparation for RAD-seq work. Microsatellite data revealed host-specific patterns of divergence that varied geographically. The team presented three papers on diversification at international meetings. Undergraduates were involved in all aspects of the project.

^ Andrew Rasmussen, Cornell College graduate and ace collector, is a veteran of more than a dozen expeditions — including two when he was an undergraduate. He helped collect and rear thousands of specimens.

CREDIT: MARTHA A. CONDON



^ *Top:* Fly puparium that contains a parasitoid-wasp larva. The fly can kill its predator: an adult fly (not a wasp) emerges from a puparium containing a similar-sized larval parasitoid.

Bottom: Collection site near Florencia, Colombia.

CREDIT: ANNE WEITEKAMP (TOP) AND MARTHA A. CONDON (BOTTOM)

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

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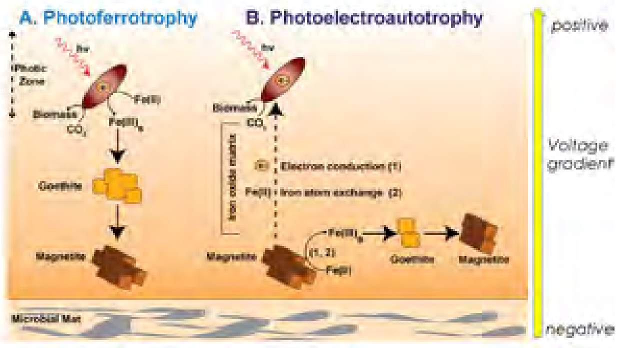
Life harnesses energy primarily through the transfer of electrons within cells. However, some microorganisms harness energy by passing electrons to the outside of the cell in a process called extracellular electron transfer (EET). This project seeks to identify and characterize the full diversity of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

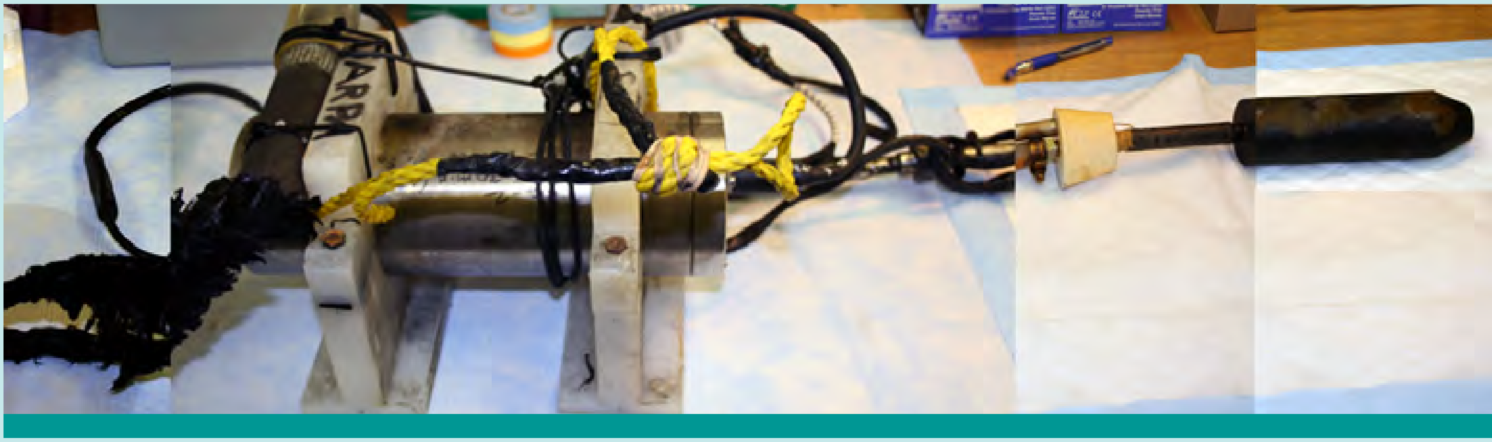
Update

All animals and many microbes harness energy by moving electrons from food (organic matter) to oxygen within the cell. We now know that some microbes can move electrons to solid compounds such as rust (iron oxides) located outside the cell. This remarkable process is called extracellular electron transfer, and is the focus of this project. We are cataloging the diversity of this capacity across all domains of life, and have already discovered new microorganisms that use such mechanisms to harness energy and fix carbon. We are also working with the Harvard museum to engage high school students in these discoveries.



> Iron oxidizing bacteria take up electrons via *extracellular electron transfer* to support carbon fixation and growth. *Rhodopseudomonas palustris* TIE-1 is a photoferrotroph, and we now know it can grow on an electrode with just sunlight, carbon dioxide, and trace minerals. We believe it grows on conductive minerals in nature.

CREDIT: PETER GIRGUIS



^ A novel incubator designed to look at extracellular electron transfer among microbes that live within hydrothermal vent walls. The wand on the right is inserted into a drill hole, which self-seals and allows the electrode within the titanium tube to be incubated in warm vent fluids for periods from days to weeks.

CREDIT: PETER GIRGUIS

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

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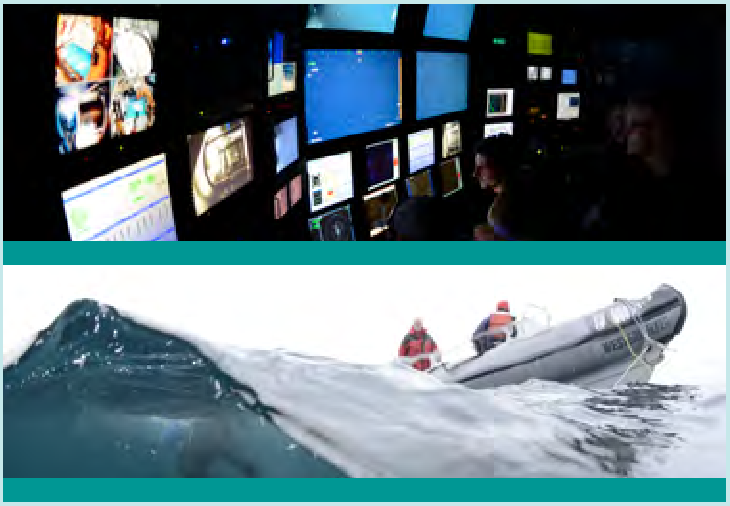
Evergreen State College
(1542673)

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.

Update

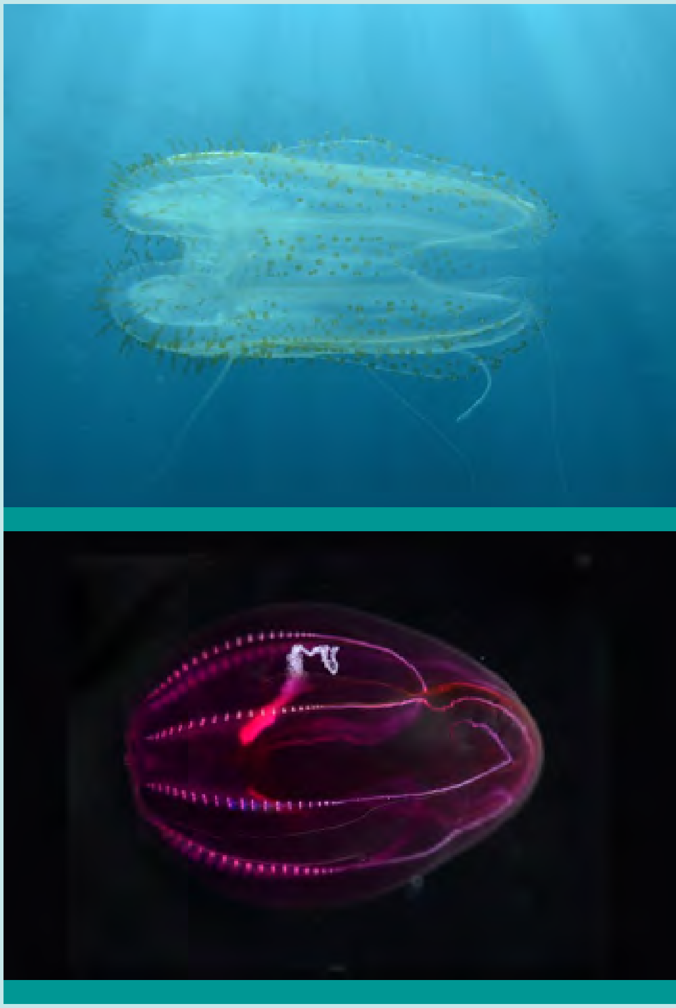
Three PhD students, a Master's student, a postdoc, and an undergraduate were recruited into the project, and our first DEEPC research expedition was carried out in June 2016 with collections down to 3600 meters depth. The effects of high hydrostatic pressure on the performance of metabolic enzymes have been investigated for 10 species of comb jellies. We have continued to process 35 pre-sequenced ctenophore transcriptomes from a range of habitat depths. We have begun identifying and aligning candidate metabolic enzymes from these transcriptomes for detailed phylogenetic/ecological analyses. Additionally, we are clustering transcripts into orthologous groups for downstream analyses, which will include a species phylogeny as well as analyses of selection and convergence. We have been engaging the general public through a television show and museum exhibit, and the scientific community through participation in a conference aimed at advancing Chicanos, Hispanics, and Native American in science.



Top: A view of the control room of MBARI's ship R/V *Western Flyer*. The remotely operated submersible *Doc Ricketts* is capable of targeted collections of organisms as deep as 4000 meters.

Bottom: Waters are not always flat calm and placid during collections. Here a team of "blue-water" scuba divers prepares to collect shallow gelatinous animals off the coast of California.

CREDIT: STEVEN H. HADDOCK



Top: *Leucothea* is one of the larger genera of ctenophores (comb jellies), reaching lengths of 25 cm. It displays several unique adaptations, including two long trailing tentacles of unknown function and the orange finger-like papillae which are thought to deter animals that may consider settling on its body.

Bottom: This young specimen of an unnamed deep-sea ctenophore will grow feeding lobes as it develops, changing its morphology and feeding strategy. Although fragile to physical contact, these juveniles are actually relatively robust and can live in the lab for several days, even after being brought up from 2000 meters deep.

CREDIT: STEVEN H. HADDOCK

The evolution of pollination syndrome diversity in *Penstemon*

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Center for Research, Inc.
(1542402)

Mark D. Rausher
Duke University
(1542387)

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.

Update

The team utilized reduced-representation genome sequencing to estimate *Penstemon* species-level relationships. Initial results confirm that floral evolution is unidirectional — hummingbird-adapted flowers evolve from bee-adapted flowers, but evolution in the reverse direction is constrained. This forms the foundation for the team to test constraints on trait evolution. To this end, the team is working with a model hummingbird-adapted species and its closest bee-adapted relative. They have generated 100s of F2 hybrid seeds for studies aimed at determining the genomic regions, genes and mutations responsible for adaptive floral evolution. To facilitate their genetic approach, the team is assembling the first *Penstemon* genome.

Publications

Wessinger CA, et al. (2016) Multiplexed shotgun genotyping resolves species relationships within the recently radiated North American genus *Penstemon*. *Am J Bot* 103: 912-922

Wessinger CA, Hileman LC (2016) Accessibility, constraint, and repetition in adaptive floral evolution. *Dev Biol* 419: 175–183

Top: PI Hileman and coPI Wessinger in the University of Kansas greenhouses where *Penstemon* genetic crosses are carried out.

Bottom: *Penstemon strictus* is a widespread species that displays the typical bee-adapted pollination syndrome.

CREDIT: LENA C. HILEMAN (TOP) AND CAROLYN WESSINGER (BOTTOM)

Penstemon barbatus is the focal hummingbird-adapted species for our genetic work.

CREDIT: CAROLYN WESSINGER

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

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Nolan C. Kane
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University of
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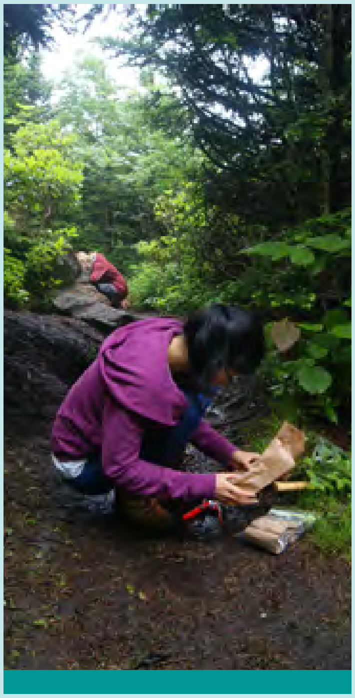
(1542387)

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.

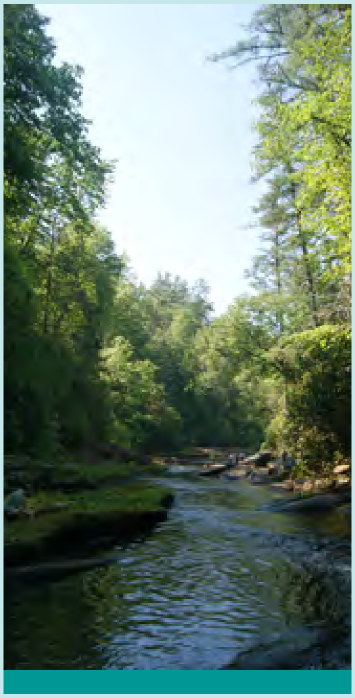
Update

The project kicked off with education and outreach components including a lichen genome assembly course, introductory lichenology course, and outreach events across the country. Permits were obtained from Alabama agencies and fieldwork was undertaken in North Carolina to test collecting strategies. Six PhD students joined the team, and in collaboration with project PIs and numerous undergraduates, made advances that yielded >250 assembled lichen metagenomes. The team began analyses of biodiversity gradient data from Great Smoky Mountains, published species new to science, and developed a workflow to vastly expand generation and capture of lichen trait data for analyses of functional diversity.



Lin Li (New York Botanical Garden) and Carly Anderson (University of Colorado) collecting lichens at Mount Mitchell State Park.

CREDIT: JAMES C. LENDEMER



Participants of the Introduction to Lichenology course studying lichens in Nantahala National Forest, North Carolina.

CREDIT: JAMES C. LENDEMER

Publications

Lendemer JC, et al. (in press) Taxonomic delimitation of the eastern North American endemic lichen *Santessoniella crossophylla* (Pannariaceae). *J Torrey Bot Soc*

Knudsen K, Lendemer JC (2016) A new perspective on *Melanophloea*, *Thelocarpella* and *Trimmatothelopsis*: species previously placed in multiple families are united within a single genus in the Acarosporaceae. *The Bryologist* 119 (3): 266–279

Stone DF, et al. (2016) A revision of the *Leptogium saturninum* group in North America. *The Lichenologist* 48 (5): 387–421

Tripp EA, et al. (2016) Biodiversity gradients in obligate symbiotic organisms: exploring the diversity and traits of lichen propagules across the United States. *J Biogeo* 43: 1667–1678

Brodo, IM, Lendemer, JC (2015) A revision of the saxicolous, esorediate species of *Ainoa* and *Trapelia* (Baeomycetaceae and Trapeliaceae, lichenized Ascomycota) in North America, with the description of two new species. *The Bryologist* 118 (4): 385–399

Hypotrachyna prolongata, one of many lichens restricted to the endangered spruce-fir forests of the southern Appalachians that has been sampled in the study.

CREDIT: JAMES C. LENDEMER

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

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Michelle C. Mack
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(1542586)

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.

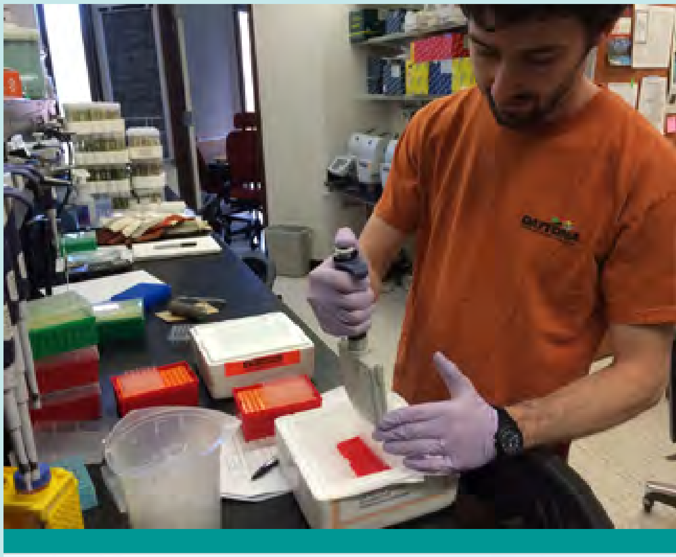
Update

The team sampled mosses and numerous environmental variables along 14 transects in the Alaskan boreal forest near Fairbanks, Alaska and in the tundra surrounding Toolik Lake Field Station during June and July, 2016. The team is now confirming the identifications of the mosses, surveying the diversity and abundance of moss-associated bacteria using amplicon sequencing, and estimating the N-fixation and methane consumption rates of the moss microbiome using a coupled $^{15}N_2$-$^{13}CH_4$ approach. The preliminary data show that the moss microbiomes fix variable amounts of N and are rich in poorly described N-fixing bacteria. A review of Arctic bryophyte biogeography is in review and other publications are in preparation.

^ *Top:* The tundra form of *Hylocomium splendens*, growing with *Ledum palustre* in acidic tundra near Toolik Lake.

Bottom: Fertile male *Aulacomnium turgidum* growing in moist acidic tundra near Toolik Lake.

CREDIT: STUART F. MCDANIEL



^ *Top:* Adam Payton prepares sequencing libraries to genotype mosses.

Bottom: Lily Lewis, Melanie Jean, and Samantha Miller surveying plant community diversity in moist acidic tundra at Toolik Lake, Alaska.

CREDIT: STUART F. MCDANIEL

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

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West Virginia University
(1542509)

Kenneth M. Keefover-Ring
University of Wisconsin, Madison
(1542479)

Lawrence B. Smart
Cornell University
(1542486)

CHINA TEAM

Jianquan Liu
Sichuan University

Tongming Yin
Nanjing Forestry University

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.

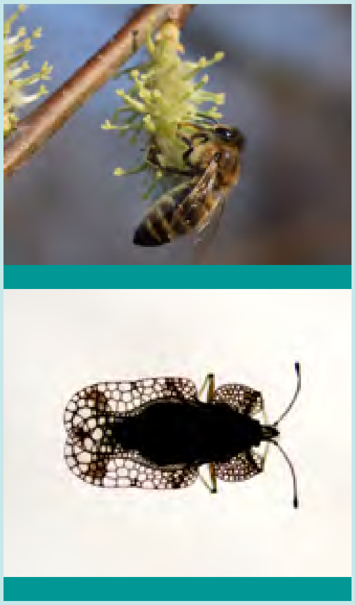
Update

During the first seven months of the project, we strengthened collaboration between our teams in the US and China, collected samples from unexplored *Salix* and *Populus* taxa, and initiated development of methods for large-scale genotyping. We discovered significant dimorphism between insect communities on males and females of *Populus trichocarpa*, completed a large-scale study to fine-map the sex determination region in *Salix purpurea*, and discovered sexual dimorphism in floral volatiles of *S. purpurea*. Broader impacts focused on outlining workshops to lower anxiety for teaching evolutionary biology and providing undergraduates with experiences in biodiversity-based research projects.

Publications

Hawley PH, et al. (in press) Declawing the dinosaurs: a workshop that lowers teacher anxiety in the biology classroom. In R Sokol-Chang, G Geher, DS Wilson, and H Head (Eds.), *Evolutionary studies: Darwin's roadmap to the curriculum*. New York, NY: Oxford University Press

Olson MS, et al. (2017) Breeding systems, mating systems, and gender determination in angiosperm trees. In: C A. Groover and Q. Cronk (Eds.) *Comparative and Evolutionary Genomics of Angiosperm Trees*. Springer Interntl Pbl



Top: Most willows produce scent to attract and nectar to reward floral visitors.

Bottom: Lace bug from the genus *Corythucha* collected on a *Populus* tree.

CREDIT: KENNETH M. KEEFOVER-RING (TOP) AND SANDRA SIMON, DEPARTMENT OF BIOLOGY, WEST VIRGINIA UNIVERSITY (BOTTOM)

Top: Graduate students, postdocs, and PIs working on the project.

Bottom: Dr. Jianquan Liu and Dr. Matthew Olson examine *Salix suchowensis* genotypes growing near Nanjing, China.

CREDIT: MATTHEW S. OLSON

Salix phelbophylla, the blood willow, sampled near Fairbanks, Alaska. These dwarf willows are characterized by their short stature and sometimes very old (>50 years) underground stems. This is contrasted with tree willows that can reach heights of >15m.

CREDIT: MATTHEW S. OLSON

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

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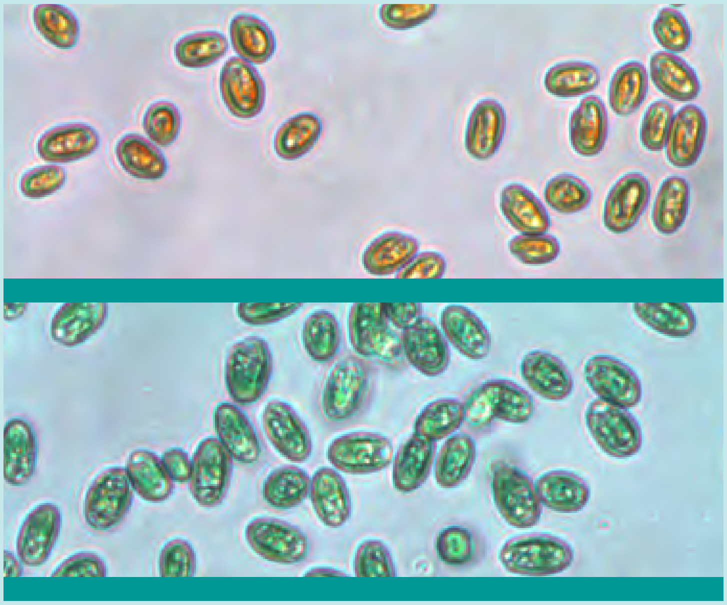
Cryptophytes are microscopic algae found in aquatic ecosystems. This project examines how color of the underwater light field influences the molecular evolution of cryptophyte light-capture genes, the spectral efficiency of their light absorption, and the taxonomic diversification and ecological distribution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

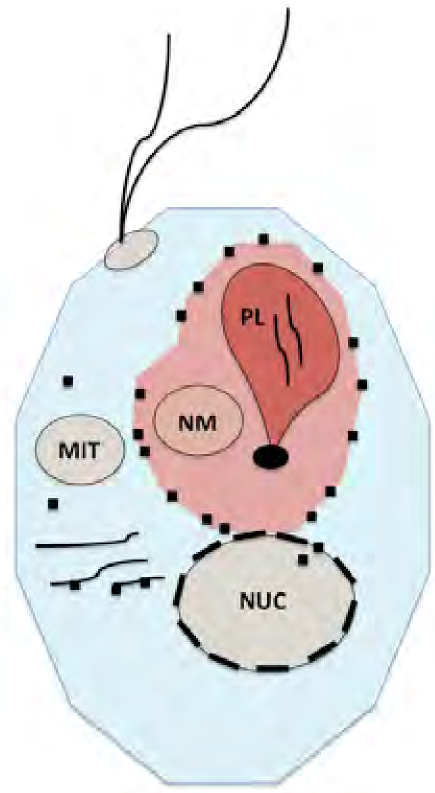
HTTP://WWW.BCO-DMO.ORG/PROJECT/655542

Update

Work in Year 1 focused on assembling and characterizing our collection of cryptophyte strains, and we have collected 47 of the 200 total strains. All 47 strains have been characterized with respect to their pigment content (types and concentrations), cell sizes, light absorption capabilities, and fluorescence excitation/emission spectra. On the molecular side, we have been isolating DNA for sequencing and archiving. Using this, and known phylogenetic markers, we have reconstructed a species phylogeny. A gene phylogeny of the phycobiliprotein subunits, which are key components of the cryptophyte photosynthetic machinery, has also been constructed.



Top: Cells of *Rhodomonas salina* under light microscopy, 40x. Individual cell length is approximately 10 micrometers.
Bottom: Cells of *Chroomonas sp.* under light microscopy, 40x. Individual cell length is approximately 20 micrometers.
CREDIT: STEVEN LITAKER, UNIVERSITY OF SOUTH CAROLINA



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

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

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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.

Update

Our major activities have focused on preparing for the first of our 3 cruises, to be conducted in year 2. To that end, we spent considerable time constructing the 4 new incubation sediment trap systems and optimizing the valves for use in water deeper than 250 meters. We have also refined our methods for specifically querying and enumerating functional genes in metagenomes. We developed a pipeline for this process that is acessible to other users and is hosted on bit bucket. The modeling sub-group has been making strides in integrating two constituent models — a novel microbial ecosystem model (DarkNite), and a size-resolved particle model (PRiSM), into an eddy-resolving ocean circulation model, and expanding the processes captured by each of these sub-models.

As part of our broader impact efforts, we hosted a summer internship program for 10 high school students, introducing them to oceanographic field and lab techniques. The students worked closely with the lab group, providing them an in-depth research experience and also giving the graduate students mentorship experience.

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

Publications

Horak RA, et al. (2016) Expansion of denitrification and anoxia in the eastern tropical North Pacific from 1972-2012. *Geophys Res Letters* 43 (10): 5252–5260

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

Dynamical interactions between plant and oomycete biodiversity in a temperate forest

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USDA-ARS
James Lutz
Utah State University
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Lewis & Clark College
David K. Oline
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(1542681)

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.

Update

Project members had a busy year launching the project. Recruitment throughout the year included a graduate student and a postdoctoral fellow as well as nine undergraduate students who particated throughout the summer in the field or laboratory research. The USU/SOU team completed a recensus of the plant species at the Wind River Forest Dynamics Plot (WRFD). The USU team updated the project tree database for the 2016 field season and developed a draft stratified sampling scheme for seedlings, including representation of rare species. At SOU, students Jessica Harper and Adam Zaky produced and sequenced clone libraries of the PR4 gene family from marked individuals of six tree species. At the WRFDP, LCC students established 30 census stations within the plot, each with a seed trap and two 1x1 m plots to census woody seedlings and assess vegetative cover of everything else. An additional 30 oomycete exclusion plots were set up ringing the WRFDP (~5-10m outside) to cover the same habitat, species, and moisture gradient as the internal plots. The USDA-ARS team conducted a pilot study using canopy rain traps during March through April and assayed oomycetes from soil samples, root samples, and waterways. Additionally, oomycetes were sampled from waterways outside of the plot for comparison.

David Oline at SOU ran the initial lab-intensive Molecular Biology research class based on the project goals, including curriculum and literature research on the molecular interactions of plant pathogenesis and resistance.

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.

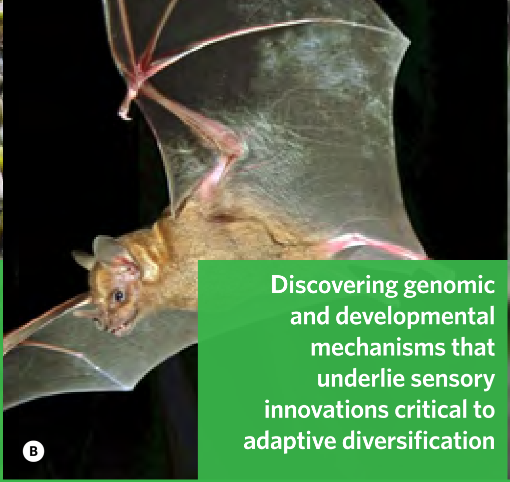
CREDIT: JAMES LUTZ

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

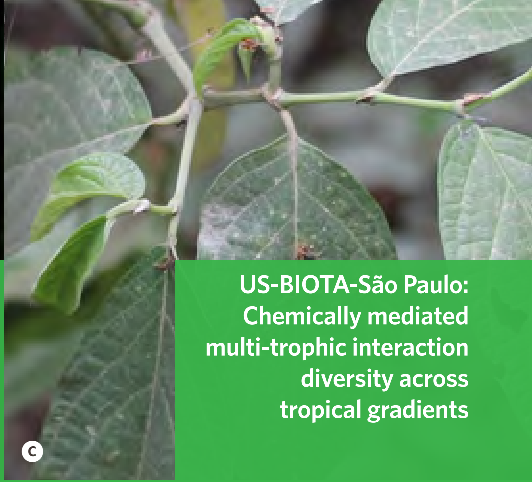
Bottom: Sudden oak death symptoms on tanoak caused by the oomycete *Phytophthora ramorum*.

CREDIT: ALLISON SIMLER (TOP) AND NIKLAUS GRÜNWALD (BOTTOM)

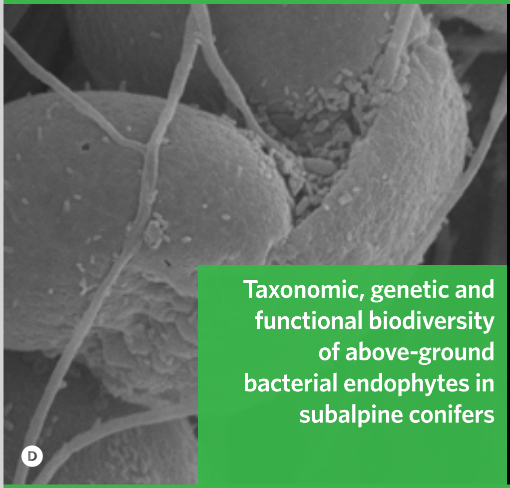
The macroalgal microbiome in space and time — maintaining primary producers in the Atlantic Rocky Intertidal Zone



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

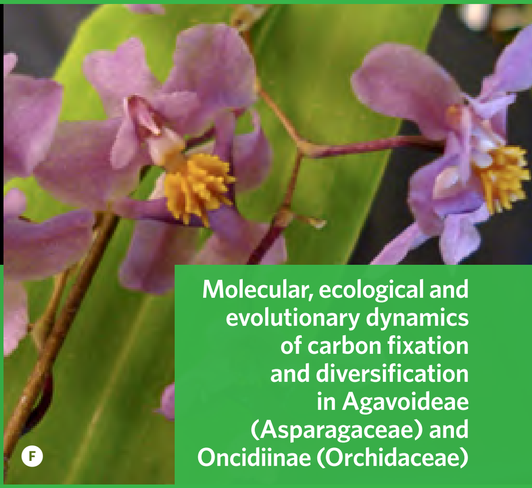


US-BIOTA-São Paulo: Chemically mediated multi-trophic interaction diversity across tropical gradients

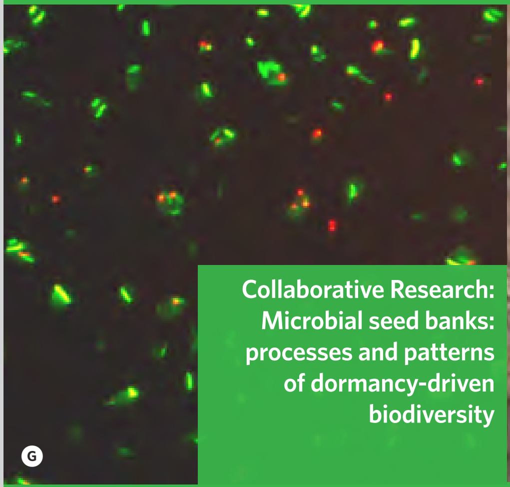


Taxonomic, genetic and functional biodiversity of above-ground bacterial endophytes in subalpine conifers

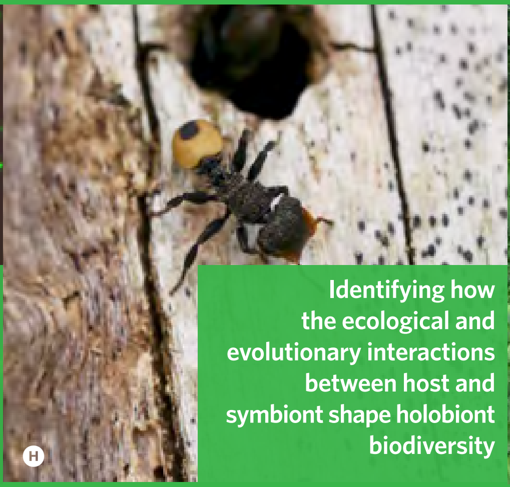
The making of biodiversity across the yeast subphylum



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



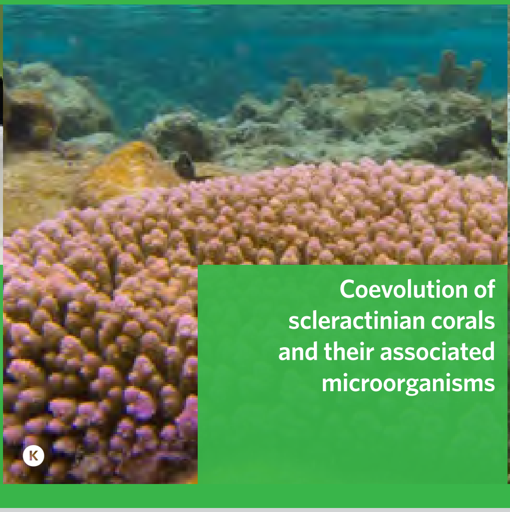
Collaborative Research: Microbial seed banks: processes and patterns of dormancy-driven biodiversity



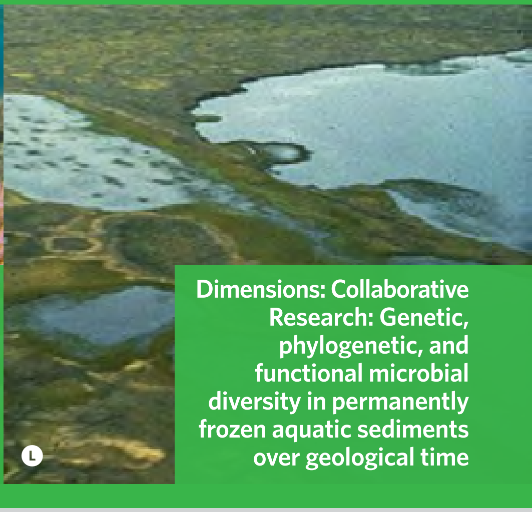
Identifying how the ecological and evolutionary interactions between host and symbiont shape holobiont biodiversity

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

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



Coevolution of scleractinian corals and their associated microorganisms



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

2014 updates

IMAGE CREDIT

Ⓐ Susan H. Brawley
Ⓑ Karen E. Sears
Ⓒ Lee Dyer
Ⓓ Paola Saldierna
Ⓔ Dana A. Opulente & Amanda B. Hulfachor
Ⓕ Katia Silvera
Ⓖ Sarah Cummins
Ⓗ Scott Powell
Ⓘ Klaus R. Nüsslein
Ⓙ Mark Whitten
Ⓚ Ryan McMinds & Jerome Payet
Ⓛ E.M. Rivkina

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

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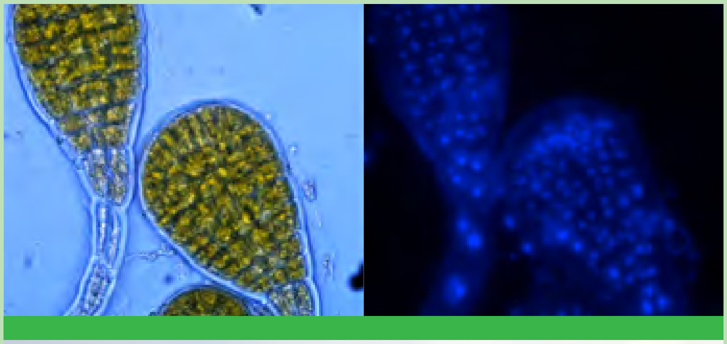
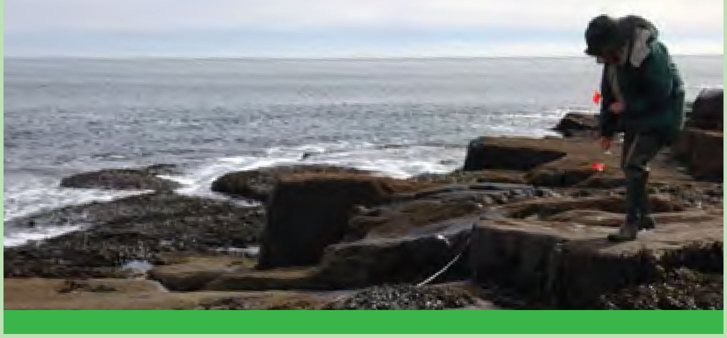
This research examines the genetic, taxonomic, and functional aspects of the bacteria associated with several macroalgae that are prominent structural "bioengineers" of the intertidal food web.

Update

The team completed most of the planned trans-Atlantic sampling of Fucus vesiculosus and *Porphyra umbilicalis*. The last field sample will be collected in early 2017, which will complete the collections needed to describe the macroalgal microbiome of these prominent rocky intertidal species over their biogeographic ranges in multiple seasons over two years. Sample preparation, sequencing, and analysis using mothur (software designed for community sequence data) and other community diversity metrics are underway.

Transplant experiments were carried out in the Maine intertidal zone, and research began to develop techniques for establishing axenic macrophytic material for reassociation experiments.





^ *Top:* Photomicrographs of *Fucus vesiculosus* embryos (brightfield) and DAPI-stained nuclei in algal cells in fluorescent photomicrograph, (right) demonstrating successful treatment to grow axenic material for reconstitution experiments. No bacteria were observed.

Bottom: Laying out a transect line to sample *Fucus* in the Maine intertidal zone.

CREDIT: SUSAN H. BRAWLEY

^ *Top:* *Porphyra umbilicalis* on the Portuguese shore showing a temperature sensor before its encapsulation at a field site. Macroalgal microbiome sampling is associated with several types of microenvironmental descriptions of the habitat.

Bottom: Processing samples on Maine shore during winter.

CREDIT: SUSAN H. BRAWLEY

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

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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.

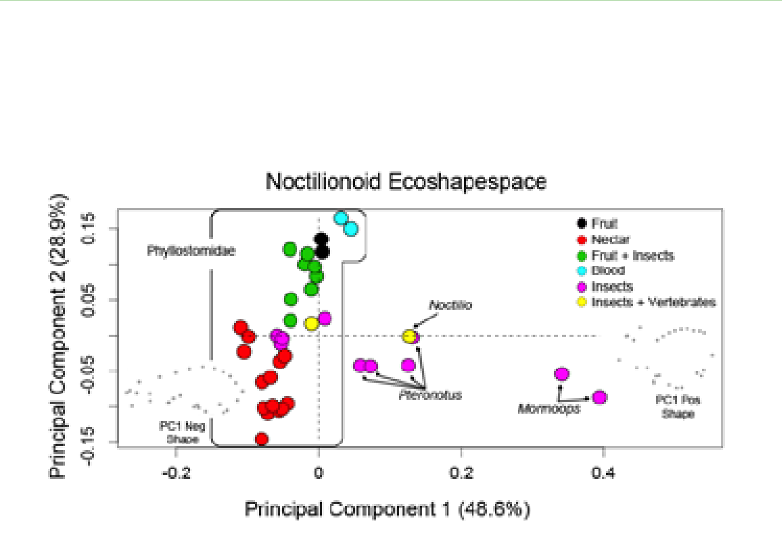
Update

We have isolated hundreds of genes of potential importance for vision and olfaction in different species. Certain olfactory receptor genes are strongly linked to frugivorous diets and may explain how bats find fruit in the dark. We have also identified and measured key sensory proteins in adults and series of individuals at different stages. Comparisons between the genes and proteins suggest there are different ways of gaining or losing specific vision cells in the retina. This research has also uncovered the major axes of variation in bat skull shape, pointing to the developmental mechanisms that generate this diversity.

Publications

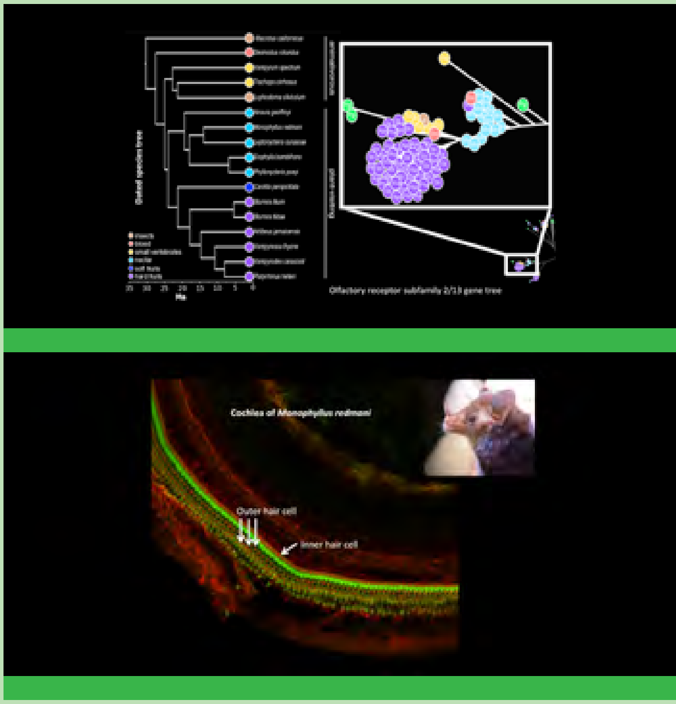
Rojas D, et al. (2016) Bats (Chiroptera: Noctilionoidea) challenge a recent origin of extant neotropical diversity. *Sys Biol* 65:432–448

Corthals A, et al. (2015) From the field to the lab: best practices for field preservation of bat specimens for molecular analyses. *PloS ONE* 10:e0118994



Analyses of the major axes of anatomical variation in bat skulls reveal the main variation in skull shape takes place through the reorganization of the skull of the Ghost-faced bat *Mormoops*, followed by change in the length of the palate associated with the evolution of nectar feeding habits at the narrow end and a specialized fig diet at the broad end.

CREDIT: BRANDON P. HEDRICK, UNIVERSITY OF MASSACHUSETTS AT AMHERST



Top: Using RNA sequences from olfactory tissue, an expansion in olfactory receptor genes has been identified associated with the evolution of a group of bats (subfamily Stenodermatinae) whose diet uniquely includes figs.

CREDIT: LAUREL R. YOHE, STONY BROOK UNIVERSITY

Bottom: Custom staining techniques have allowed us to identify actin, the protein that forms filaments in the cochlea, as well as cochlear hair cells.

CREDIT: ALEXA SADIER, UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN

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

(CO-FUNDED WITH FAPESP)

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

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Universidade de Campinas

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

Update

In the second project year, this group has continued to nurture their cross discipline collaborations with team meetings and field site visits. Common garden experiments designed to estimate heritability of secondary metabolites and genetic correlations have been initiated along a tropical latitudinal gradient of 7 sites. De novo whole genome sequencing of a *Piper arboretum* is underway and will provide a whole genome reference for rangewide population genomic analyses. New WSU graduate student, Juan Manuel Perilla Lopez, has begun establishing field sampling sites and designing experiments to study parasitoid communities in a multitrophic context. Advances have also been made in resolving *Piper* taxonomy and developing identification methods. In addition to creating reference collections for field sites and training collaborators in the identification of *Piper* species, the possibility of using spectral image data to match leaves of unknown samples collected for phytochemical analysis to a library of spectra from known specimens is being tested.

Parasitized by an unknown wasp, the *Pseudautomeris yourii* caterpillar feeds on chemically diverse host plants. Prepupal wasp larvae, now in silk cocoons (white splotches), emerged from the caterpillar after consuming its internal tissues.

CREDIT: LEE DYER

Publications

Shimbori EM, et al. (2017) A revision of the genus *Andesipolis* (Hymenoptera: Braconidae: Mesostoinae) and redefinition of the subfamily Mesostoinae. *Zootaxa* 4216: 101-152

Antigo MR, et al. (2016) Herbicides and plant growth regulators used in sugar cane and its action on adult *Trichogramma galloi* Zucchi (Hymenoptera: Trichogrammatidae). *Entomobrasilis* 9(1): 36

Bortoni M, Shimbori EM, Shaw SR (2016) A review of the genus *Orionis* Shaw (Hymenoptera: Braconidae: Euphorinae) and first records of the genus from South America and Oriental Region. *Zootaxa* 3: 249–260

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Dayany da Silva AM, et al. (2016) Bioactivity-guided isolation of laevicarpin, an antitrypanosomal and anticryptococcal lactam from *Piper laevicarpu* (Piperaceae). *Fitoterapia* 111: 24–28

Dyer LA, Forister ML (2016) Wherefore and whither the modeler: understanding the population dynamics of monarchs will require integrative and quantitative techniques. *Ann Entomol Soc Am* 109(2): 172–175

Glassmire AE, et al. (2016) Intraspecific phytochemical variation shapes community and population structure for specialist caterpillars. *New Phyt* 212(1): 208–219

CONTINUE >

Hansen AC (2016) Patterns in parasitism frequency explained by diet and immunity. *Ecography*

Inclán DJ, et al. (2016) Redefining the generic limits of *Winthemia* (Diptera: Tachinidae). *Invert Syst* 30: 274–289

Rodriguez-Castañeda G, et al. (2016) Ant predation on herbivores through a multitrophic lens: how effects of ants on plant herbivore defense and natural enemies vary along temperature gradients. *Curr Opin Insect Sci* 14: 73–80

Scherrer S, et al. (2016) Seasonal variation in diet breadth of folivorous Lepidoptera in the Brazilian cerrado. *Biotropica* 48: 491–498

Shimbori EM, et al. (2016) Eleven new species of *Athacryvac* Braet & van Achterberg from the Neotropical Region (Hymenoptera, Braconidae, Rogadinae). *Zootaxa* 4138(1): 83

Shimbori EM, et al. (2016) *Aleiodes* Wesmael (Hymenoptera, Braconidae, Rogadinae) species described by Bréthes: taxonomic clarification. *Stud Neotrop Fauna E* 51(2): 128–134

Smilanich AM, et al. (2016) Does plant apparency matter? Thirty years of data provide limited support but reveal clear patterns of the effects of plant chemistry on herbivores. *New Phyt* 210(3): 1044–1057

Stireman JO (2016) Community ecology of the 'other' parasitoids. *Curr Opin Insect Sci* 14: 87–93

Sulca L et al. (2016) Four new species of the *Aleiodes* compressor Herrich-Schaeffer species-group (Hymenoptera: Braconidae: Rogadinae) from South America. *Revista Peruana de Biologia* 23(3): 227–236

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?

Update

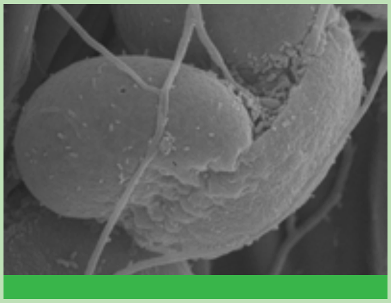
This year, the team asked if the potential to fix nitrogen is present in other sites and conifer species, and if this potential is affected by soil fertility. Using the soil chronosequence at the Ecological Staircase in Mendocino, nitrogenase activity was confirmed in Bishop- and Bolander pine, and rates of fixation were found to be independent of soil fertility. Community sequencing will reveal the organisms responsible for nitrogen fixation. Researchers also sampled limber pine and co-occurring species across the limber pine range for a biogeographic study of the pine microbiome, and established methods in microscopy and chamber-based $15N_2$ labeling of pine foliage.

Publications

Carrell AC, Carper DL, Frank C (2016) Subalpine conifers in different geographical locations host highly similar foliar bacterial endophyte communities. FEMS *Microbiol Ecol* 92:8: fiw124

Moyes AB, et al. (2016) Evidence for foliar endophytic nitrogen fixation in a widely distributed subalpine conifer. *New Phytologist* 210(2): 657

Graduate students Paola Saldierna, Dianne Quiroz, and James Kupihea working with Bishop- and Bolander pine samples from the Ecological Staircase in Mendocino, CA.



Scanning electron microscope image of a lodgepole pine pollen sac with bacteria and fungal hypae.

This bristlecone pine growing at Wheeler Peak, Great Basin National Park, NV was sampled for its foliar microbiome as part of a biogeographic study of limber pine and co-occurring conifers.

CREDIT (THIS PAGE'S IMAGES): PAOLA SALDIERNA, ENVIRONMENTAL SYSTEMS GRADUATE GROUP, UNIVERSITY OF CALIFORNIA, MERCED

The making of biodiversity across the yeast subphylum

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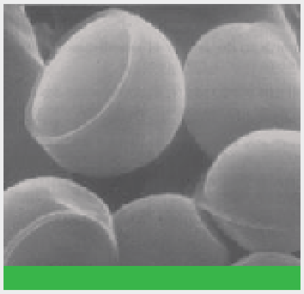
Yeasts of the ancient fungal subphylum Saccharomycotina employ many different resource utilization strategies to allow them to inhabit every continent and every major aquatic and terrestrial habitat. This project seeks to understand the diversification of yeasts by using information written in their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



Pichia membranifaciens NRRL Y-7554. Scanning electron micrograph showing placement of ledges on ascospores to be Saturn-like, hat-like, or incomplete. This micrograph demonstrates the problem of defining species and genera of yeasts from morphology of ascospores. Bar = 0.5 μm.

CREDIT: CLETE KURTZMAN, NCAUR, ARS, USDA

Update

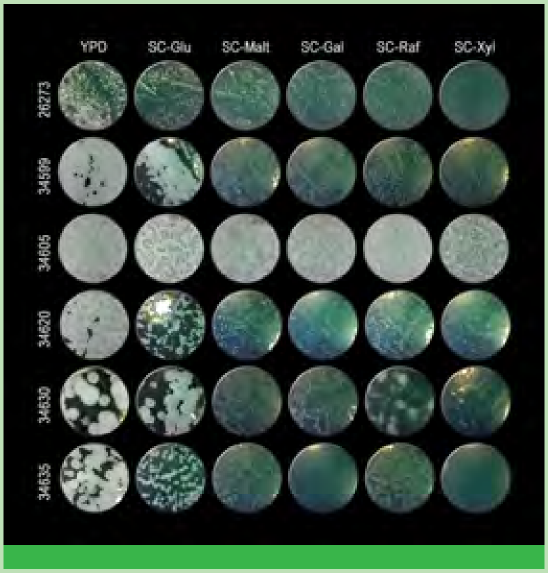
To determine how yeasts of the subphylum Saccharomycotina have diversified across their half-billion-year history, researchers are sequencing and analyzing the genomes of all known species and correlating genome content with ecologically relevant traits. More than 800 type strains have been transferred from the USDA to UW-Madison, and genome sequence data have been generated for more than 500 of these species. High-throughput phenotypic analyses have also begun. Researchers have published key computational infrastructure for the project, a genome-based phylogeny for 86 species, and a timely review article on the current state of yeast evolutionary and ecological genomics research.

Publications

Riley R, et al. (2016) Comparative genomics of biotechnologically important yeasts. *PNAS* 113(35): 9882–7

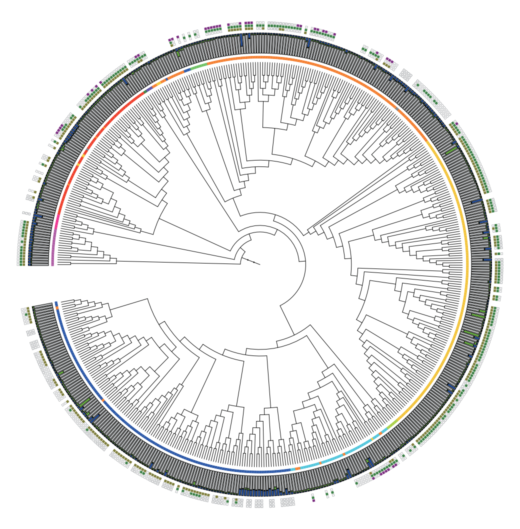
Shen XX, et al. (2016) Reconstructing the backbone of the Saccharomycotina yeast phylogeny using genome-scale data. *Genes, Genomes, Genetics* 6(12): 3927–3939

Zhou X, et al. (2016) In silico whole genome sequencer & analyzer (iwgs): a computational pipeline to guide the design and analysis of de novo genome sequencing studies. *Genes, Genomes, Genetics* 6(11): 3655–3662



Yeasts express morphological variation in response to different carbon sources.

CREDIT: AMANDA B. HULFACHOR AND DANA A. OPULENTE, LABORATORY OF GENETICS, UNIVERSITY OF WISCONSIN, MADISON



A phylogeny of 509 yeast species with taxonomic classifications, genome completeness, and phenotypic growth traits.

CREDIT: XING-XING SHEN, DEPARTMENT OF BIOLOGICAL SCIENCES, VANDERBILT UNIVERSITY

A. B. HULFACHOR AND DANA A. OPULENTE, LABORATORY OF GENETICS, UNIVERSITY OF WISCONSIN, MADISON

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

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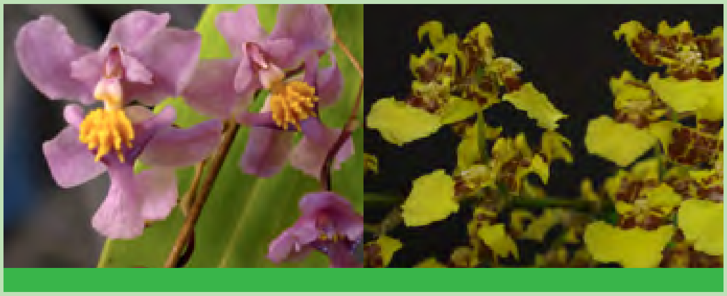
This project compares the genomic basis of physiological adaptations to water limitation in agaves, yuccas and epiphytic orchids. Researchers will identify changes in gene content and function that have enabled evolutionary shifts from typical C3/C4 photosynthesis to Crassulacean Acid Metabolism (CAM),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

Update

The research team has been characterizing physiological and genetic diversity of agaves and orchids. Specifically, in species across the Agavoideae (agaves, yuccas and relatives), they assessed variation in carbon isotope ratios, titratable acid, carbon metabolism, and leaf traits (e.g. succulence). Additionally, they conducted physiological and transcriptomic analyses of related species with differing photosynthetic pathways. Recently, efforts have focused on the hybrid facultatively CAM species, *Y. gloriosa*, with the collection of paired 24-hour physiological and transcriptomic data for 24 genotypes. For the orchids, material for experiments and assessing titratable acid has been collected from species across Oncidiinae, as well as extensive transcriptomic data for the CAM species, *Erycina pusilla* and the C3 species, *E. crista-gali*.

Towards the goal of understanding of how regulatory changes can lead to physiological and ecological diversification, anonymous informatic analyses of transcriptomes, along with regulatory network analysis, has highlighted at least one FKF family member (the FKF1 gene) as a likely regulator of CAM processes. Prof. Ming-Tsair Chan's group at Academica Sinica in Taiwan has initiated transformation experiments. They have knocked out the ZEITLUPE (ZTL) homolog sequence and attempted CRISPR/Cas9 gene editing with it in *E. pusilla* and are now experimenting to find an appropriate inducible promoter system for use with the species.



Oncidium sotoanum (left) and *Oncidium sphacelatum* (right). Both are epiphytic C_3 species.

CREDIT: KATIA SILVERA

Publications

Heyduk K, et al. (2016) Evolution of a CAM anatomy predates the origins of Crassulacean acid metabolism in the Agavoideae (Asparagaceae). *Mol Phy Evol* 105: 102–113

Honaas LA, et. al. (2016) Selecting superior de novo transcriptome assemblies: lessons learned by leveraging the best plant genome. *PloS ONE* 11(1), e0146062

McKain MR, et al. (2016) Timing of rapid diversification and convergent origins of active pollination within Agavoideae (Asparagaceae). *Am J Bot* 103(10): 1717–1729

Silvera K, Lasso E (2016) Ecophysiology and Crassulacean Acid Metabolism of Tropical Epiphytes. *Tropical Tree Physiology* 25–43. Guillermo Goldstein and Louis S. Santiago, Eds., Springer International Publishing

Yucca moths (*Tegeticula* spp.), obligate pollination mutualists to yuccas, are seen pollinating (moth on left) and injecting eggs into a yucca flower (moth on right).

CREDIT: OLLE PELLMYR, AS PUBLISHED IN SEGRAVES, KARI A. "BRANCHING OUT WITH COEVOLUTIONARY TREES." EVOLUTION: EDUCATION AND OUTREACH 3.1 (2010): 62-70. CREATIVE COMMONS LICENSE HTTP://CREATIVECOMMONS.ORG/LICENSES/BY/2.0

Microbial seed banks: Processes and patterns of dormancy-driven biodiversity

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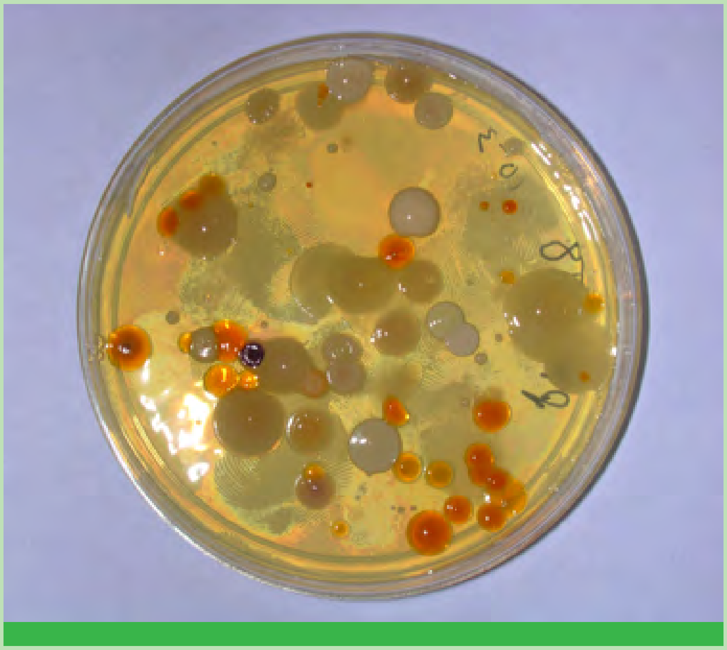
When faced with unfavorable conditions, many organisms enter a reversible state of reduced metabolic activity, or dormancy. This project focuses on how dormancy creates 'seed banks', which are important reservoirs of taxonomic, genetic, and functional biodiversity of microbial communities.

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.



^ Bacteria cultured from an agricultural soil sample.

CREDIT: JAY T. LENNON

Publications

Aanderud ZT, et al. (2016) Bacterial dormancy is more prevalent in freshwater than hypersaline lakes. *Front Microbiol* 7: 853 doi: 10.3389/fmicb.2016.00853

Hall EK, et al. (2016) Scaling relationships among drivers of aquatic respiration: from the smallest to the largest freshwater ecosystems. *Inland Waters* 6: 1–10

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LaSarre B, et al. (2016) Microbial mutualism dynamics governed by dose-dependent toxicity and growth-independent production of a cross-fed nutrient. *ISME J* 1–12

Lennon JT, et al. (2016) Microbial contributions to subterranean methane sinks. *Geobiology* 7: 853 doi: 10.1111/gbi.12214

Lennon JT, Lehmkuhl BK (2016) A trait-based approach to biofilms in soil. *Environ Microbiol* 18: 2732–2742

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Locey KJ, Lennon JT (2016) Reply to Willis: powerful predictions of biodiversity from ecological models and scaling laws. *PNAS* doi/10.1073/pnas.1609635113

Locey KJ, Lennon JT (2016) Scaling laws predict global microbial diversity. PNAS doi: 10.1073/pnas.1521291113

Muscarella ME, Jones SE, Lennon JT (2016) Species sorting along a subsidy gradient alters community stability. *Ecology* 97: 2034–2043

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 researchers to understand the rules governing a ubiquitous but poorly understood partnership—the symbiotic relationship between animals and their gut bacteria.

Update

In the 2015-2016 year, the *Cephalotes* turtle ant -holobiont biodiversity team neared completion of their massive collection efforts for the genus across its diverse geographic and habitat ranges. The team published papers naming two of the dominant, core gut symbionts and continues to pursue functional characterization through *in vitro*, *in vivo*, and genomic inferences. Nitrogen-recycling has been characterized as a major feature of *Cephalotes'* gut microbiota. This symbiotic function appears conserved throughout the genus and across a broad geographic range. Symbiotic gut bacteria have, thus, likely played a substantial role in the success of *Cephalotes* ants and their radiation into the arboreal canopy.

Publications

Russell JA, Sanders JG, Moreau CS (2017) Hotspots for symbiosis: function, evolution, and specificity of ant-microbe associations from trunk to tips of the ant phylogeny (Hymenoptera: Formicidae). *Myrmecological News* 24: 43–69

Burchill AT, Moreau CS (2016) Colony size evolution in ants: macroevolutionary trends. *Insectes Sociaux* 63(2): 291–298

Lin JY, et al. (2016) *Cephaloticoccus* gen. nov., a new genus of 'Verrucomicrobia' containing two novel species isolated from *Cephalotes* ant guts. *Int J Syst Evol Biol* 66(8): 3034–3040

Cephalotes unimaculatus, a turtle ant that is a member of an ancient lineage now found only on the island of Hispaniola. The evolutionary history and isolated geographical location of this species may have left an important signature on the diversity and function of its microbiome.

CREDIT: SCOTT POWELL

Ventosamonas gracilis isolated from *Cephalotes varians*. This isolate, along with relatives cultivated from eleven different species of ants, represent a novel family within the Pseudomonadales order of Bacteria. The family is solely comprised of *Cephalotes* and *Procryptocerus* gut symbionts that have nearly identical metabolic properties, irrespective of ant host.

CREDIT: JOHN WERTZ

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

(CO-FUNDED WITH FAPESP)

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BRAZIL TEAM

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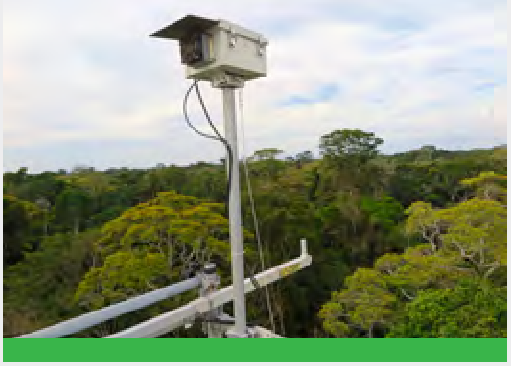
The deforestation of tropical forests for agriculture affects the production and consumption of methane, a potent greenhouse gas. The team seeks to identify the microorganisms involved in methane production and consumption, their physiologies and genetics, and their contribution to the flow of methane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



^ An overview of the Amazon rainforest canopy from the top of the eddy flux tower.

CREDIT: KLAUS RUDOLF NÜSSLEIN

Update

The research team has conducted three sampling expeditions in the Amazon. Researchers are currently developing a profile of methane emissions in different land uses, combined with approaches to analyze the genetic potential for the methane cycle in the same soil sites. Soil cores have been collected and processed for total DNA isolation and physiological-chemical analyses. Presently, the team is testing a mass spectrometer to be deployed in the field during the next sampling expedition. This will aid in determining the substrates for methane generation in soil gases and the atmosphere. In addition, researchers are also developing a technique to limit the genetic analysis of soil DNA to just the target groups of interest. Soil core samples during the last expedition were incubated with labeled substrates to identify microorganisms actively involved in the methane cycle.

^ Sampling crew moving through a soybean plantation side by side with an Amazon rainforest.

CREDIT: KLAUS RUDOLF NÜSSLEIN

Publications

Meyer KM, et al. (2017) Conversion of Amazon rainforest soil to agriculture alters community traits of methane-cycling organisms. *Mol Ecol* doi: 10.1111/mec.14011

Hamaoui GS Jr, et al. (2016) Land-use drives abundance and community structure alterations of thaumarchaeal ammonia oxidizers in tropical rainforest soils in Rondônia, Brazil. *Appl Soil Ecol* 107: 48–56

Mueller RC, et al. (2016) Land use change in the Amazon rainforest favors generalist fungi. *Funct Ecol* 30(11): 1845–1853

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.

Pylro VS, et al. (2016) A step forward to empower global microbiome research through local leaderships. *Trends Microbio* 24: 767–771

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.

Stewartia malacodendron in Talladega National Forest, Alabama; member of a genus with a disjunct distribution in eastern North America and eastern Asia.

CREDIT: MARK WHITTEN, FLORIDA MUSEUM OF NATURAL HISTORY, UNIVERSITY OF FLORIDA

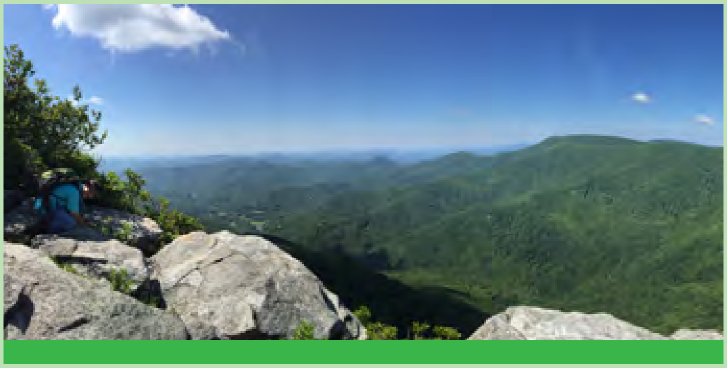
HTTP://WWW.USA-CHINA-BIODIVERSITY.ORG

Update

Fieldwork was completed, with new samples from North Carolina, Massachusetts, and New Hampshire. Soil microbial diversity is more closely associated with geography than with the habitat or tree species from which the samples were taken. Analyses of plant functional traits are underway, and tree crowns have been mapped using NEON hyperspectral data. Primers (144 loci) were developed for generating community phylogenies (in progress) for the six US and four Chinese sites. Phylogenetic analyses of 20 disjunct genera are ongoing. A course on Ecophylogenetics was given, and five graduate students, two post-docs, and three undergraduates were mentored. US and Chinese participants visited each other's labs and field sites.

Publications

Yu Y, et al. (2017) Whole-genome duplication and molecular evolution in *Cornus* L. (Cornaceae)—Insights from transcriptome sequences. *PloS ONE* 12(2): e0171361



View from Pickens Nose, Coweeta Hydrologic Lab, Coweeta, North Carolina.

CREDIT: MARK WHITTEN, FLORIDA MUSEUM OF NATURAL HISTORY

Gutianshan National Nature Reserve is also an ecotourist site, and the temple shown here is part of the entrance to the Reserve.

CREDIT: PAMELA SOLTIS

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://CORALREEFMOVIE.ORG | HTTP://MARINESTUDIES.OREGONSTATE.EDU/GLOBAL-CORAL-MICROBIOME-PROJECT

Update

Nearly all coral samples for this project are collected and their bacterial DNA has been extracted. 16S amplicon sequencing has been completed for more than a third of the coral sample collection, and 11 genomes of bacterial strains isolated from coral colonies have been sequenced.

Several mini-documentaries generated by the project's videography team during expeditions are now viewable online. In these films, the project objectives are discussed as well as the roles of fishes and coral reefs for regional communities from the perspective of both locals and scientists.

Among the many outreach activities this year, postdoc Dr. Joe Pollock founded the award winning Aboriginals and Torres Straight Islanders in Marine Science (ATSIMS) Program and postdoc Dr. Jesse Zaneveld developed a card game illustrating reef dynamics as well as a teaching module, "Perspectives on Microbial Community Change in Health and Disease".

^ Coral taxa from coral reefs in Moorea.

CREDIT: RYAN MCMINDS AND JEROME PAYET

^ Coral taxa from coral reefs in Australia.

CREDIT: RYAN MCMINDS AND JEROME PAYET

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

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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.

HTTP://CEB.UTK.EDU/PERMAFROST-MICROBIOLOGY

Update

This year, research has focused on isolation of DNA from permafrost samples collected in Siberia in August 2015, metagenome sequencing, and bioinformatics analyses. To date, ten metagenomes have been annotated and more are under construction. The team used the metagenome from a methane-producing enrichment of Late Pleistocene Antarctic permafrost to bin the genome of a methanogenic archaeon, which does not grow in pure culture but exists as a member of the microcosm community. The newly reconstructed genome is closely related to psychrotolerant methanogen *Methanosarcina lacustris*, and other *Methanosarcina* isolated from deep subsurface shell formations and Siberian permafrost-affected soils. The team produced a short video of Kolyma lowland field site to extend public knowledge on Siberian permafrost area.

Publication

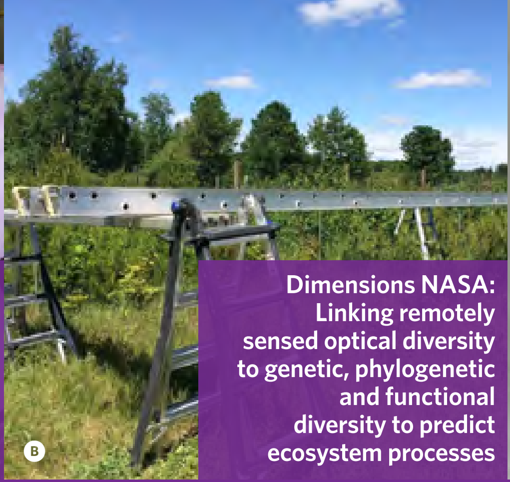
Buongiorno J, et al. (2016) Draft genome sequence of antarctic methanogen enriched from dry valley permafrost. *Genome Announce* 4(6): e01362-16

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

^ Aerial photo of study site located at Alazeya River in the northeastern Siberia.

CREDIT: TATIANA VISHNIVETSKAYA

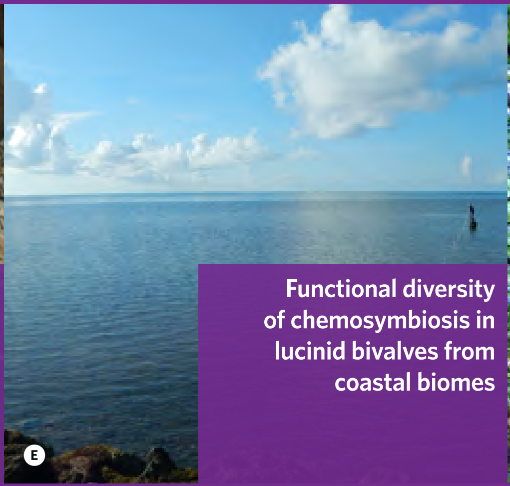
US-BIOTA-São Paulo: Improving biodiversity prediction in the Atlantic rainforest



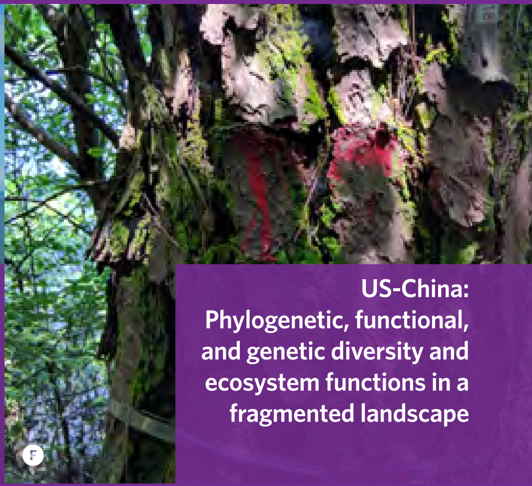
Dimensions NASA: Linking remotely sensed optical diversity to genetic, phylogenetic and functional diversity to predict ecosystem processes

Experimental adaptive radiation — genomics of diversification in bird lice

Biodiversity of the gut microbiome of herbivorous rodents

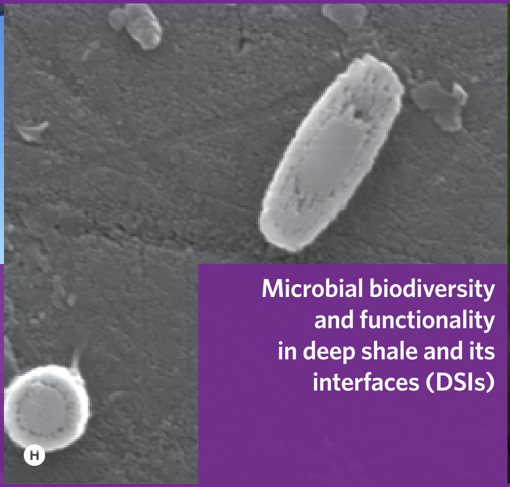


Functional diversity of chemosymbiosis in lucinid bivalves from coastal biomes

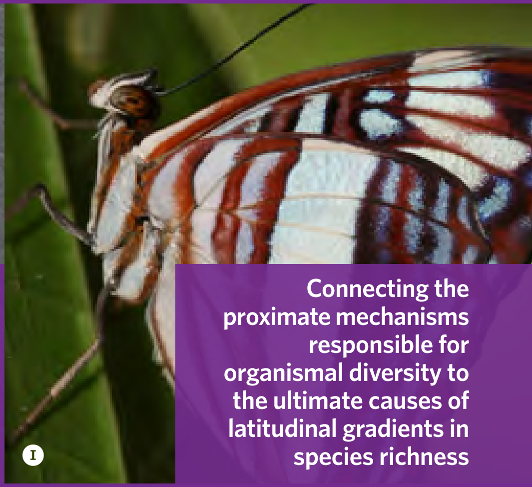


US-China: Phylogenetic, functional, and genetic diversity and ecosystem functions in a fragmented landscape

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

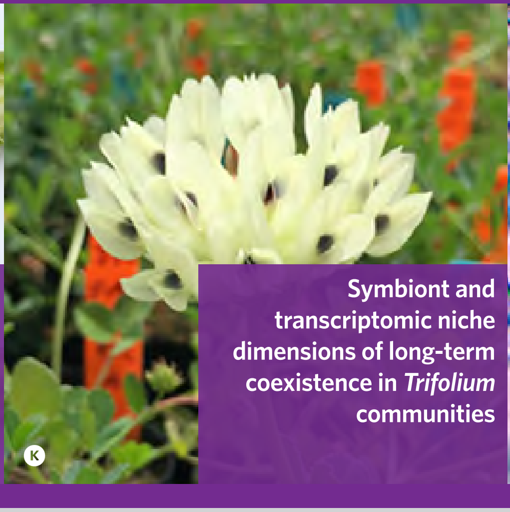


Microbial biodiversity and functionality in deep shale and its interfaces (DSIs)

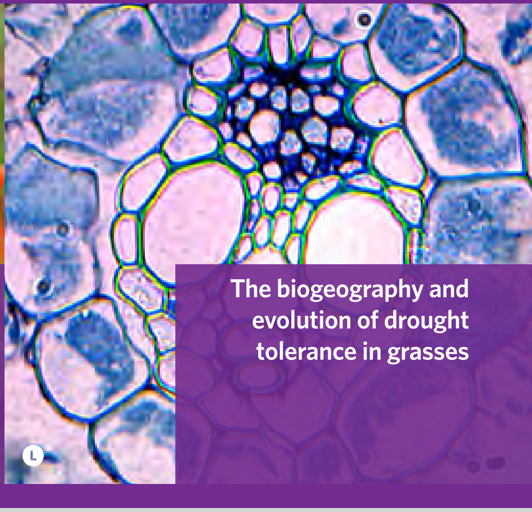


Connecting the proximate mechanisms responsible for organismal diversity to the ultimate causes of latitudinal gradients in species richness

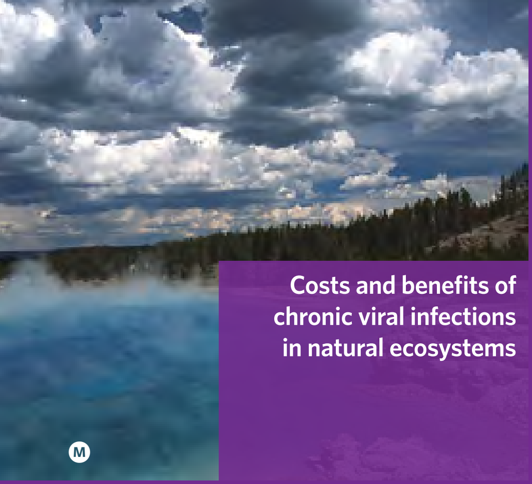
Landscapes of Linalool: Scent-mediated diversification of flowers and moths across western North America



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

Ⓐ Fabian A. Michelangeli
Ⓑ Anna K. Schweiger
Ⓒ Sydney A. Stringham
Ⓓ Denise M. Dearing
Ⓔ Annette S. Engel
Ⓕ Lin Jiang
Ⓖ Brent Nowinski
Ⓗ David Cole
Ⓘ Keith Willmott
Ⓙ Tania Jogesh
Ⓚ Andrew Siefert
Ⓛ Joe Craine
Ⓜ Mark J. Young

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

(CO-FUNDED WITH FAPESP)

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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

This year, our project 1) described the distribution and diversity of animals and plants in the Atlantic Forest, 2) identified environmental changes impacting the region during the Late Quaternary, 3) generated novel genomic data and methods to describe biological responses to past environmental shifts, 4) collected physiological, microenvironmental and ecological data from target taxa and environments, 5) generated new climatologies based on remote sensing data, and 6) developed analytical tools to predict the distribution of genetic diversity under future climates. Many new scientific articles were published and students directly associated with the project, based in the U.S., Brazil, and France, gave 40+ scientific presentations.

Our team searches for rare endemic plants at the top of the Parque Nacional da Serra dos Orgaos, in Eastern Brazil.
CREDIT: FABIAN A. MICHELANGELI

Publications

Amaral FR, et al. (2016) The "Atlantis Forest hypothesis" does not explain Atlantic Forest phylogeography. *PNAS* doi: 10.1073/pnas.1602213113

Bernal JP, et al. (2016) High-resolution Holocene South American monsoon history recorded by a speleothem from Botuverá Cave, Brazil. *Earth Planet Sci Lett* 450: 186–196

Brown JL, et al. (2016) Predicting the genetic consequences of future climate change: the power of coupling demography, the coalescent, and contemporary genetic patterns. *Am J Bot* 103: 153–163

Grohmann CH (2016) Comparative analysis of global digital elevation models and ultra-prominent mountain peaks. *ISPRS Annals of the Photogrammetry, Remote Sensing and Spatial Information Sciences*, Volume III-4, 2016 XXIII ISPRS Congress, 12–19 July 2016, Prague, Czech Republic

Harvey MS, Andrade R, Pinto-da-Rocha R (2016) The first New World species of the pseudoscorpion family Feaellidae (Pseudoscorpiones: Feaelloidea) from the Brazilian Atlantic Forest. *J Arach* 44: 227–234

Joseph T, Hickerson MJ, Alavarado-Serrano D (2016) Demographic inference under a spatially continuous coalescent model. *Heredity* 117: 94–99. doi: 10.1038/hdy.2016.28

CONTINUE >

Kaminski LA, Iserhard CA, Freitas AVL (2016) *Thisbe silvestre* sp. nov. (Lepidoptera: Riodinidae): a new myrmecophilous butterfly from the Brazilian Atlantic Forest. *Aust Entomol* 55: 138–146

Ledru MP, et al. (2016) Long-term spatial changes in the distribution of the Brazilian Atlantic forest. *Biotropica* 48

Maestri R, et al. (2016) Predictors of intraspecific morphological variability in a tropical hotspot: comparing the influence of random and non-random forces. *J Biogeo* doi: 10.1111/jbi.12815

Moquet JS, et al. (2016) Calibration of speleothem δ^{18}O records against hydroclimate instrumental records in Central Brazil. *Global Planet Change* 139: 151–164

Novello VF, et al. (2016) Centennial-scale solar forcing of the South American Monsoon System recorded in stalagmites. *Sci Rep* 6: 24762. doi: 10.1038/srep24762

Pinto-da-Rocha R, Andrade R, Moreno-González J (2016) Two new cave-dwelling genera of short-tailed whip-scorpions from Brazil (Arachnida: Schizomida: Hubbardiidae). *Zoologia* 33: e20150195

Prates I, et al. (2016) Inferring responses to climate dynamics from historical demography in Neotropical forest lizards. *PNAS* 113 (29): 7978–7985

Reginato M (2016) monographaR: An R package to facilitate the production of plant taxonomic monographs. *Brittonia* doi:10.1007/s12228-015-9407-z

Reginato M, Michelangeli FA (2016) Untangling the phylogeny of *Leandra* sensu str. (Melastomataceae, Miconieae). *Mol Phy Evol* 96: 17-32

Saiter FZ, et al. (2016) Environmental correlates of floristic regions and plant turnover in the Atlantic Forest hotspot. *J Biogeo* doi: 10.1111/jbi.12774

Talavera G, et al. (2016) One-note samba: the biogeographical history of the relict Brazilian butterfly *Elkalyce cogina*. *J Biogeo* 43: 727-737

Teixeira Jr, et al. (2016) Molecular data reveal spatial and temporal patterns of diversification and a cryptic new species of lowland *Stenocercus* Duméril & Bibron, 1837 (Squamata: Tropiduridae). *Mol Phy Evol* 94: 410-423

Top Left: *Polychrus marmoratus*, the many-colored bush anole, a lizard from South American rainforests. *Top Right:* *Behuria mouraei*, known only from two other collecting trips (the last one dating back to the 1930s), is a species restricted to the Eastern Brazilian mountains. By studying narrowly distributed species like this one, we will be able to understand the complex biogeographic patterns of the many biological groups that live in the Atlantic Forest. *Bottom:* The complex topography of Brazil's coast, where the Atlantic Forest is distributed.

CREDIT: IVAN PRATES, CITY COLLEGE OF CUNY (TOP LEFT) AND FABIAN A. MICHELANGELI (TOP RIGHT & BOTTOM)

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

(CO-FUNDED WITH NASA)

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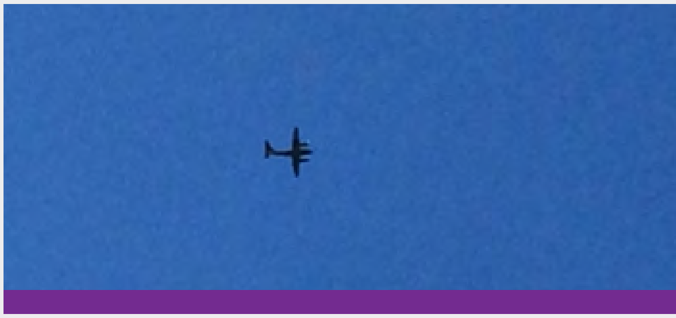
Remote sensing methods for monitoring the Earth's biodiversity are being applied to experimental manipulations of plant diversity. This allows scientists to examine the linkages between plant biodiversity, soil microbe diversity, and ecosystem function at multiple scales of spatial resolution.



> NASA AVIRIS flight over Cedar Creek Ecosystem Science Reserve.

CREDIT: ANNA K. SCHWEIGER, UNIVERSITY OF MINNESOTA

Update

We have advanced our work through new publications and leveraged initiatives 1) linking hyperspectral data to the tree of life, 2) predicting belowground processes from remotely sensed vegetation chemistry, 3) accurately detecting three tree diseases using hyperspectral data, 4) examining the scale dependency of biodiversity detection, and 5) developing a framework for detecting evolutionary legacy effects on ecosystems via remote sensing. The National Institute for Mathematical Biology and Synthesis (NIMBios) has funded our working group on remote sensing of biodiversity and linking spectra to the tree of life, and the University of Minnesota Grand Challenges program has funded our initiative for accurate detection of tree disease.

^ Post doc Anna K. Schweiger working with undergraduates Brett Frederickson and Erin Murdock to use field spectrometers to detect plant function and diversity.

CREDIT: LEWIS A. FRENCH, UNIVERSITY OF MINNESOTA

Publications

Cavender-Bares J, et al. (2016) Monitoring plant functional diversity from space. *Nat Plants* 2: 16024

Cavender-Bares J, et al. (2016) Associations of leaf spectra with genetic and phylogenetic variation in oaks: prospects for remote detection of biodiversity. *Remote Sensing* 8.3: 221

Cavender-Bares J, et al. (2016) Evolutionary legacy effects on ecosystems: biogeographic origins, plant traits, and implications for management in the era of global change. *Ann Rev Ecol Evol Sys* 47: 433–462

Couture JJ, et al. (2016) Spectroscopic determination of ecologically relevant plant secondary metabolites. *Meth Ecol Evol* 7(11): 1402–1412

Wang R, et al. (2016) Seasonal variation in the NDVI–species richness relationship in a prairie grassland experiment (Cedar Creek). *Remote Sensing* 8: 128

^ Platform for continuous monitoring of plant function and diversity using a high resolution imaging spectrometer in the Cedar Creek Forest and Biodiversity (FAB) experiment.

CREDIT: ANNA K. SCHWEIGER, UNIVERSITY OF MINNESOTA

Experimental adaptive radiation—genomics of diversification in bird lice

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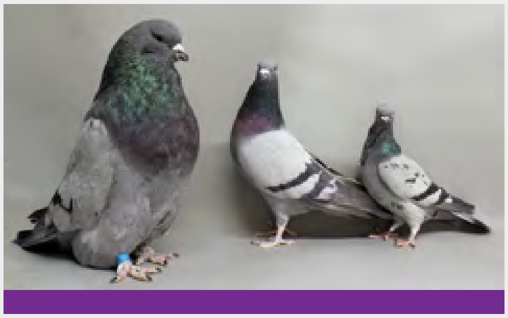
This project will expand the understanding of adaptive radiation using bird-specific ectoparasites as a model system. The researchers are conducting experimental studies that link phylogenetic, genomic, phenotypic, and functional data in order to clarify how micro-and macro-evolutionary processes influence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



< Variation in the body size of rock pigeons (*Columba livia*). Lice were transferred to giant runts (left), the largest domesticated breed of pigeon, wild-caught feral pigeons (center), and figuritas (right), the smallest domesticated breed of pigeon.

CREDIT: SYDNEY A. STRINGHAM, UNIVERSITY OF UTAH

Update

A reference genome for the pigeon louse *Columbicola columbae* has been sequenced, and we are now optimizing the assembly. We are continuing to monitor phenotypic changes in experimental lineages of *C. columbae* that have been evolving on pigeon breeds of different sizes and colors for 2.5 years. Samples of lice are periodically frozen for genomic comparisons to the reference genome. The genomes of 64 additional species of *Columbicola* have also been sequenced, and data from 1,107 single copy orthologous genes have been assembled. The team has also focused on outreach, building educational kits that have been distributed locally and internationally.

^ Variation in the size and color of lice in the genus *Columbicola*.

CREDIT: : SCOTT M. VILLA, UNIVERSITY OF UTAH

Publications

Boyd BM, et al. (2017) Phylogenomics using target restricted assembly resolves intrageneric relationships of parasitic lice (Phthiraptera: Columbicola). *Sys Biol* doi: 10.1093/sysbio/syx027

Bartlow AW, et al. (2016) Walk or Ride? Phoretic behavior of amblyceran and ischnoceran lice. *Int J Parasit* 46 (4): 221-227

Sweet AD, Johnson KP (2016) Cophylogenetic analysis of New World ground-doves (Aves: Columbidae) and their parasitic wing lice (Insecta: Phthiraptera: *Columbicola*). *Mol Phy Evol* 103: 122–132

Sweet AD, Boyd BM, Johnson KP (2016) Cophylogenetic patterns are uncorrelated between two lineages of parasites on the same hosts. *Biol J Linn Soc* 118(4): 813–28

Sweet AD, Maddox JD, Johnson KP (2016) A complete molecular phylogeny of *Claravis* confirms its paraphyly within small New World ground-doves (Aves: Peristerinae) and implies multiple plumage state transitions. *J Avian Biol* doi:10.1111/jav.01077

Villa SM, et al. (2016) Does anti-parasite behavior improve with experience: An experimental test of the priming hypothesis. *Behav Ecol* doi: 10.1093/beheco/arw032

Biodiversity of the gut microbiome of herbivorous rodents

Denise M. Dearing
Colin Dale
Robert B. Weiss
University of Utah
(1342615)

A "Belly Bugs" student displays a petri dish with microbes sampled from her hand.

CREDIT: DENISE M. DEARING

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

We have been investigating the diversity and function of microbial communities in herbivores, particularly those of woodrats, through 16S and shotgun sequencing. Our metagenomic sequencing results demonstrate that the microbial functions of the foregut and cecal chambers of the hindgut differ significantly. Specifically, the abundance of an oxalate detoxification gene (oxc) is much more abundant in the foregut compared to the cecum. Several other detoxification genes are more abundant in the cecum. For the second time we offered a summer camp opportunity aimed at teaching 7th graders about the gut microbiome via the design of video games.

Top: An image of the White-throated Woodrat, *Neotoma albigula*. Some populations of this species ingest large quantities of oxalate through their diet of cactus. Oxalate can only be degraded by gut microbes as mammals lack the ability to degrade oxalate.

Bottom: A segment of our summer cohort of 7th graders in our outreach program "Belly Bugs" geared at teaching students about the wonders of the gut microbiome through video game design.

CREDIT: DENISE M. DEARING

Publications

Kohl KD, Dearing MD (2016) The woodrat gut microbiota as an experimental system for understanding microbial metabolism of dietary toxins. *Front Microbiol* 7: 1165

Kohl KD, et al. (2016) Experimental evolution on a wild mammal species results in modification of gut microbial communities. *Front Microbiol* 7: 634

Kohl KD, et al. (2016) Microbial detoxification in the gut of a specialist avian herbivore, the Greater Sage-Grouse. *FEMS Microb Lett* 363(14)

Kohl KD, et al. (2016) Effects of fruit toxins on intestinal and microbial β-glucosidase activities of seed-predating and seed-dispersing rodents (*Acomys* spp.). *Phys Biochem Zool* 89: 198–205

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Miller AW, et al. (2016) The effect of dietary oxalate on the gut microbiota of the mammalian herbivore *Neotoma albigula*. *Appl Environ Microb* 82(9): 2669–2675

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Functional diversity of chemosymbiosis in lucinid bivalves from coastal biomes

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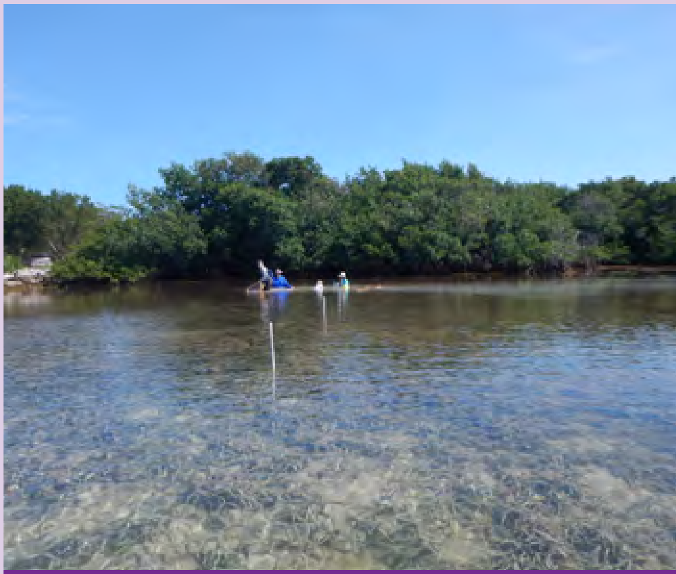
Organisms that live within another species (endosymbionts) are common within bivalves, a type of mollusk. These endosymbionts offer chemical nutrients to the host in a relationship called chemosymbiosis. This project explores uncharacterized coastal marine biomes to investigate the phylogenetic, genetic,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

Update

Fieldwork in the Bahamas and Florida has generated new ecological information and taxonomic inventories for the presence (and absence) of lucinids and their symbionts in seagrass, mangrove, and bare sand habitats. This year, anthropogenically-impacted sites were sampled to evaluate the plasticity of the lucinid-bacteria symbiotic system, including habitats modified to enhance seagrass growth. As part of thesis/dissertation research and a specialized field course, graduate and undergraduate students are characterizing lucinid host and endosymbiont diversity from metagenomes. Combined with habitat geochemistry, symbiont diversity continues to be surprisingly high. Morphometrics data are uncovering landmarks inside the shells that differentiate populations from stable seagrass versus bare sand habitats. These results may provide the potential to reconstruct habitat changes in the fossil record. Lastly, some of the field areas have been impacted by Hurricanes Joaquin and Matthew. Sampling before and after these disturbances provides information about the long-term health of these coastal systems.

As part of the UTK-SDSMT collaborative summer course, "Field Studies in Coastal Biomes," students sampled seagrass and bare sand habitats around the island of San Salvador, The Bahamas. The group met each week (virtually) to discuss laboratory results.

CREDIT: ANNETTE S. ENGEL



Top: All three institutions collected lucinid population and geochemistry data from an anthopogenically-impacted tidal flat in the Florida Keys. This site was modified 10 years ago to facilitate seagrass habitat expansion. Diverse lucinid populations were encountered, as well as many indicators of human occupation (e.g., concrete, asphalt, wood, plastic).

Bottom: Sampling water chemistry associated with a lucinid bivalve population at a marine inland pond, San Salvador, The Bahamas, during the summer 2016 field course.

CREDIT: ANNETTE S. ENGEL

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

(CO-FUNDED WITH NSFC)

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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.

Update

The team continued the collection and analyses of data on plants, arthropods, and soil microbes on the TIL islands. The first plant survey was completed and data are being analyzed to understand community assembly mechanisms. Functional traits and growth of common woody plant species are being measured. Population genetic analyses were conducted for several species. Habitat diversity was quantified for each island. The first phase of litter decomposition experiments was completed. Soil bacteria and fungi were sampled again to gauge their temporal and spatial variation. Tens of thousands of insect individuals were collected; identification through morphological and genetic tools is ongoing.

Publications

Ojima MN, Jiang, L (2017) Interactive effects of disturbance and dispersal on community assembly. *Oikos* 10.1111/oik.03265

Pu Z, Cortez MH, Jiang L (2017) Predator-prey coevolution drives productivity-diversity relationships in planktonic systems. *Am Nat* 189(1): 28–42

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Yang Z, et al. (2017) Daytime warming lowers community temporal stability by reducing the abundance of dominant, stable species. *Global Change Biol* 23(1): 154–163

Chen D, et al. (2016) Effects of plant functional group loss on soil biota and soil carbon sequestration: A plant removal experiment in the Mongolian grassland. *J Ecol* 104: 734–743

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Li SP, et al. (2016) Convergence and divergence in a long-term old-field succession: the importance of spatial scale and species abundance. *Ecol Lett* 19: 1101–1109

Ma C, et al. (2016) Different effects of invader-native phylogenetic relatedness on invasion success and impact: a meta-analysis of Darwin's naturalization hypothesis. *Proc R Soc B* 283 (1838): 20160663

Ma YJ, et al. (2016) Water loss by evaporation from China's South North Water Transfer Project. *Ecol Eng* 95: 206–215

Pan Q, et al. (2016) Effects of functional diversity loss on ecosystem functions are influenced by compensation. *Ecology* 97: 2293–2302

Tan J, et al. (2016) Phylogenetic context determines the role of competition in adaptive radiation. *Proc R Soc B* 283: 20160241

Wilson MC, et al. (2016) Habitat fragmentation and biodiversity conservation: key findings and future challenges. *Landscape Ecol* 31: 219–227

Wilson MC, Wu JG (2016) The problem of weak sustainability and associated indictors. *Int J Sustain Dev World Ecol* 24(1): 44–51

Zhang W, et al. (2016) Fate of engineered cerium oxide nanoparticles in an aquatic environment and their toxicity toward 14 ciliated protist species. *Environ Pollut* 212: 584–591

Top: A *Pinus massoniana* tree marked with a numbered tag and dendroband. *Bottom:* A litter trap for collecting fallen leaves on one of the TIL islands.

CREDIT: LIN JIANG

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

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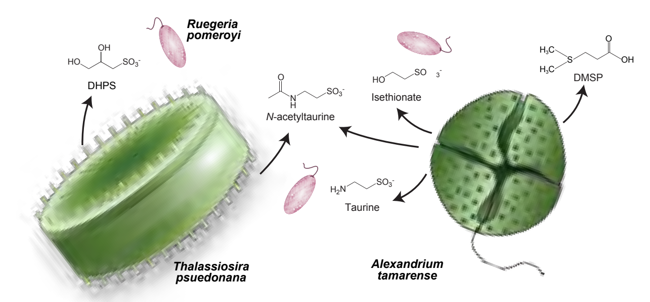
This project seeks to understand how the regulation of dimethylsulfoniopropionate (DMSP) metabolism in marine bacteria affects the climate-relevant sulfur cycle between the ocean and the atmosphere. The goal is to understand how the diversity and community structure of microbial life impacts the fate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

Update

Our studies of the ecology and physiology of DMSP-degrading bacteria focus on laboratory model systems and natural bacterioplankton communities. In model organism studies, bacterial co-cultures with phytoplankton that differ in their DMSP production levels revealed that a broad suite of novel organic sulfur compounds serve as sources of carbon and sulfur for the ocean microbiome. The demand for reduced sulfur for biosynthesis, the availability of osmolytes (of which DMSP is one), and the need to manage bacterial oxidative stress, affects bacterial DMSP degradation strategies. In field studies, DMSP gene abundance was tracked in coastal California surface waters during a month-long study in which the Environmental Sample Processor (ESP) autonomously archived microbial samples. Analysis of these samples showed that bacteria carrying DMSP genes account for up to 40% of the community. The distribution of genes mediating the two competing pathways for DMSP degradation differed taxonomically, with the majority of demethylation genes harbored by SAR11 members and the majority of cleavage by Roseobacter group members. Ongoing studies are focusing on the biological and physical factors that determine the fate of DMSP in the ocean.



A three-member microbial model system revealed five organic sulfur compounds (including DMSP) that are released by marine phytoplankton and serve as carbon and sulfur sources for heterotrophic bacteria.

CREDIT: MARY ANN MORAN

Publications

Burns AS, et al. (2016) sRNAs expressed during DMSP degradation by a model marine bacterium. *Environ Microbiol Rep* 8: 763–773

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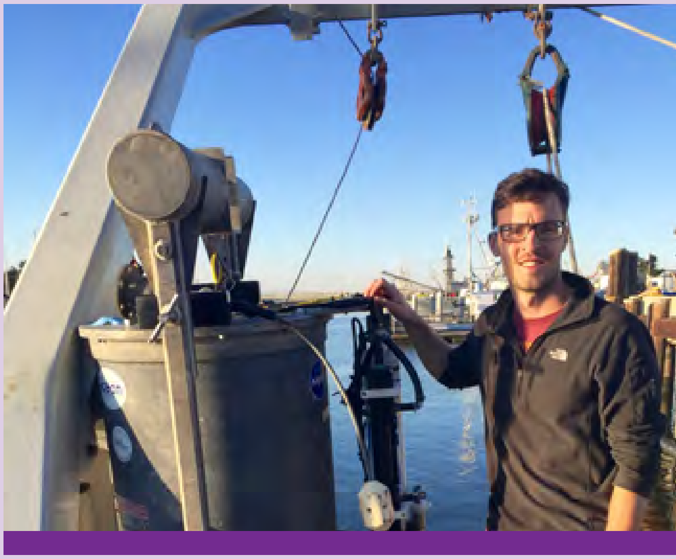

The Environmental Sample Processor on the morning of a 45-day deployment to study DMSP-degrading bacteria in Monterey Bay, CA, pictured with Ph.D. student Brent Nowinski.

CREDIT: BRENT NOWINSKI, UNIVERSITY OF GEORGIA

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

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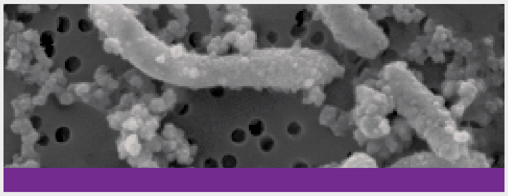

This project will characterize the diversity of microbes living at deep shale interfaces, identify the origin of these microbes within geologic time, and assess how this community is adapting to changing environments. With increased hydraulic fracturing, these deep shale environments may be particularly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

< Scanning Electron Microscopy (SEM) image of salt-loving bacteria closely related to *Marinobacter* sp. isolated from fluids produced from hydraulically fractured wells in the Utica shale, Ohio.

CREDIT: SUE WELCH, OHIO STATE UNIVERSITY SUBSURFACE ENERGY MATERIALS CHARACTERIZATION AND ANALYSIS LABORATORY (SEMCAL)

Update

In September 2015 we collected sidewall cores from ~2,200 m below ground surface at the Marcellus Shale Energy and Environmental Laboratory site in Morgantown, WV. Additionally, two wells were hydraulic fractured at the site and our team is sampling these fluids through time. We have cultivated a dozen salt-loving taxa from Marcellus and Utica shale wells and have sequenced their genomes. Preliminary results have revealed that shale microbial populations are not diverse and are conserved regardless of geography, formation age, well depth, and site operator. Shale microbial metabolisms include the ability to live at high pressures, the capability to generate methane from osmoprotectants, and the ability to ward off viral attacks.

^ Prof. Shikha Sharma (sunglasses) inspecting sidewall rock cores collected from 2,200 m below ground surface at the Marcellus Shale Energy and Environmental Laboratory (MSEEL) in Morgantown, WV in September, 2015.

CREDIT: SHIKHA SHARMA

Publications

Chen R, Sharma S (2017) Linking the Acadian Orogeny with organic-rich black shale deposition: Evidence from the Marcellus Shale. *Mar Petrol Geol* 79: 149–158

Chen R, Sharma S (2016) Role of oscillating redox conditions in the formation of organic-rich intervals in the Middle Devonian Marcellus Shale, Appalachian Basin, USA. *Palaeogeogr Palaeocl Paleoecol* 446: 85–97

Daly RA, et al. (2016) Microbial metabolisms in a 2.5-km-deep ecosystem created by hydraulic fracturing in shales. *Nat Microbiol* 1: 16146

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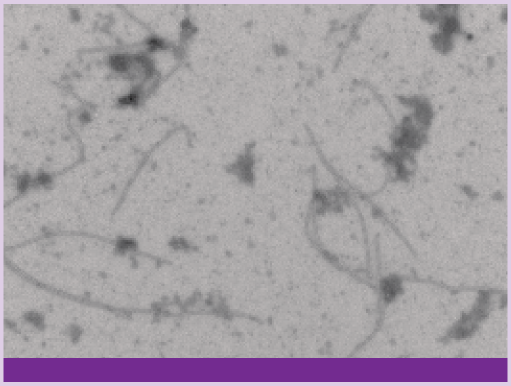

^ Bacteriophage (filament-like structures) associated with a *Geotoga* species isolated from the Utica Shale.

CREDIT: MICHAEL D. JOHNSTON, OHIO STATE UNIVERSITY

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.

Update

Over the past 12 months, our team has conducted extensive fieldwork in the western United States, Costa Rica, and on both slopes of the Ecuadorian Andes. As a result, we have 1) collected and cataloged hundreds of butterfly samples for genomic analyses, 2) used mark-recapture data to estimate species abundance and longevity among sites, 3) assessed niche breadth within communities, and 4) generated new host-plant records and larval life-history descriptions for multiple species. Collectively, these data, along with the results of ongoing predation studies, will be used to directly test our hypothesis that biotic interactions are stronger in tropical communities.

Publications

Finkbeiner SK, Briscoe AD, Mullen SP (2017) Complex dynamics underlie the evolution of imperfect wing pattern convergence in butterflies. *Evolution* doi:10.1111/evo.13165

Willmott KR, Mielke OHH, Freitas AVL (2016) A new subspecies and validation of the enigmatic species *Adelpha herbita* Weymer endemic to the Brazilian Atlantic forest (Nymphalidae: Limenitidinae). *Trop Lepid Res* 26(1): 32

Zhang W, et al. (2016) Genome-wide introgression among distantly related *Heliconius* butterfly species. *Genome Biol* 17

^ Ultimate instar of *Adelpha naxia naxia*. Observations in southwest Costa Rica have added significantly to the information of this little known species. Our descriptions of the immature stages and knowledge of their food plants will help in understanding species groups and interpreting patterns of evolution within the genus.

CREDIT: R.I. HILL AND C.E. RUSH, UNIVERSITY OF THE PACIFIC

^ Ultimate instar of *Adelpha nea nea*. This rare species was previously known from very few specimens in Costa Rica. We have discovered new populations in multiple locations and described the complete life history. This discovery has added a new food plant family that was previously unknown for the genus.

CREDIT: R.I. HILL AND C.E. RUSH, UNIVERSITY OF THE PACIFIC

Landscapes of Linalool: 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

We have collected extensive ecological data from 65 populations of 16 species and population genetic data (GBS) on 5 species. We conducted a linalool augmentation experiment to understand the ecological basis of floral scent polymorphisms in *Oenothera harringtonii* and initiated a phenotypic selection study. A backbone phylogeny of family Onagraceae is underway and includes data from 322 targeted loci for over 300 samples. In the coming year we aim for complete taxon sampling in the Tribe Onagraceae. Four graduate students (1 PhD, 3 Masters; 2 defended) and three undergraduates (2 honors theses) have conducted independent research in this system.

Oenothera primiveris flowering in Eureka dunes, Death Valley National Park. Flowers in California are large and hawkmoth-pollinated, whereas flowers east of Nevada are smaller and self-compatible. *O. primiveris* is one of 16 taxa where we have measured intraspecific floral trait variation in relation to biotic interactions.

CREDIT: TANIA JOGESH, CHICAGO BOTANIC GARDEN

Publications

Arceo-Gomez G, Raguso RA, Geber MA (2016) Can plants evolve tolerance mechanisms to heterospecific pollen effects? An experimental test of the adaptive potential in *Clarkia* species. *Oikos* 125: 718–725

Lewis EM, et al. (2016) Microsatellites for *Oenothera gayleana* and *O. hartwegii* subsp. *filifolia* (Onagraceae) and their utility in section *Calylophus*. *Appl Plant Sci* 4(2): 1500107

Pichersky E, Raguso RA (2016). Why do plants produce so many terpenoid compounds? *New Phytol* doi:10.1111/nph.14178

Raguso RA (2016) More lessons from linalool: insights gained from a ubiquitous floral volatile. *Curr Opin Plant Biol* 32: 31–36

Rusch C, et al. (2016) Olfaction in context — sources of nuance in plant-pollinator communication. *Curr Opin Insect Sci* 15: 53–60

Skogen KA, et al. (2016) Land-use change has no detectable effect on reproduction in a disturbance-adapted plant pollinated by long-distance dispersing hawkmoths. *Am J Bot* 103(11): 1950–1963

The flowers of *Oenothera psammophila*, an evening primrose species endemic to the St. Anthony Sand Dunes in Idaho, begin to open as the sun sets in the distance. Floral scent is being collected using dynamic headspace methods from the flower enclosed in the plastic bag.

CREDIT: ANDREA GRUVER, CHICAGO BOTANIC GARDEN

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

This year the team conducted several large field and greenhouse experiments, and collected extensive field data on *Trifolium* species and their associated soil microbial communities. Greenhouse experiments tested the interactive effects of plant-soil feedbacks and plant competition on *Trifolium* performance, functional traits, and transcriptomes. Field data collection extended a long-term dataset of *Trifolium* co-occurrence in natural communities and added extensive data linking plant fitness, functional traits, transcriptomes, rhizosphere and phyllosphere microbiomes, and soil chemistry. Results show that plant-soil feedbacks mediated by rhizobial mutualists cause *Trifolium* species to have an advantage when rare, the key signature of stable coexistence.

Publications

Barker JL, et al. (2017) Synthesizing perspectives on the evolution of cooperation within and between species. *Evolution* doi:10.1111/evo.13174

Bowsher et al. (2017) Transcriptomic responses to conspecific and congeneric competition in co-occurring *Trifolium*. *J Ecol* 105 (3): 602–615

^ *Top:* Surveying *Trifolium* species co-occurrence in long-term plots at Bodega Bay, CA.

Bottom: Planting *Trifolium* seedlings in a field experiment at Bodega Bay, CA.

CREDIT: ANDREW SIEFERT, UNIVERSITY OF CALIFORNIA, DAVIS

^ *Trifolium fucatum* and relatives flowering in a greenhouse experiment examining interactive effects of plant-soil feedbacks and competition on plant fitness.

CREDIT: ANDREW SIEFERT, UNIVERSITY OF CALIFORNIA, DAVIS

The biogeography and evolution of drought tolerance in grasses

(CO-FUNDED WITH NASA)

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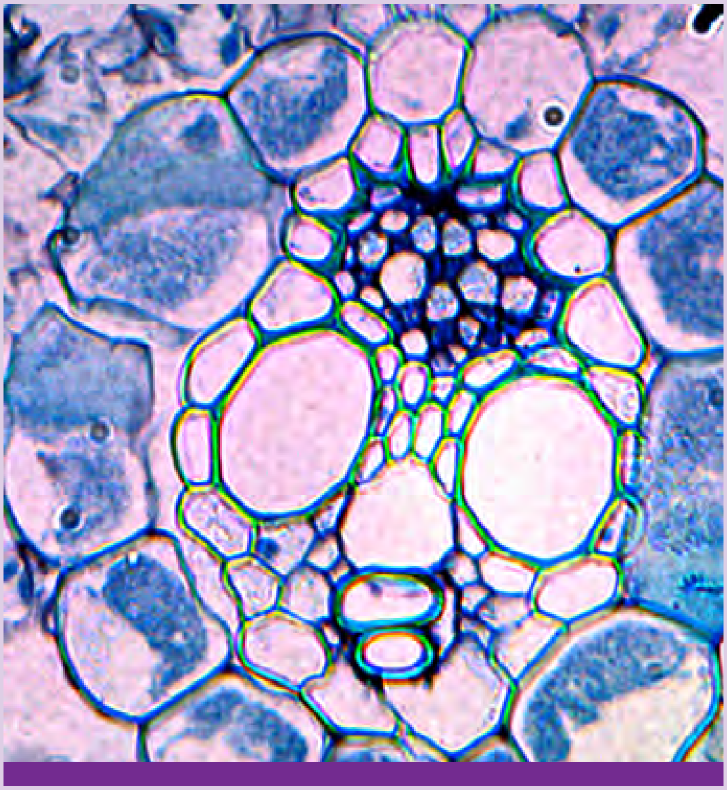
The goal is to understand the dimensions of biodiversity of drought tolerance in grasses. This project examines interspecific variation in drought tolerance among related species, intraspecific variation in drought tolerance of geographically widespread species, and physiological and genomic aspects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

Update

Multiple dry-down experiments were conducted for selected grass species that exhibit variable levels of tolerance and susceptibility to water stress and that utilize both the C3 and C4 photosynthetic pathways. These dry-down experiments combined intensive daily physiological measures, thermography, and multi-interval transcriptomic analyses, and will be complemented by leaf and root anatomy data and plastome sequence information generated in parallel. The team developed an evolutionary framework for linking gene expression, through ecophysiological responses, to the global ecology of grasses. This framework was used to identify additional species with contrasting climate-associations for further analyses.



^ Xylem within these vascular bundles undergoes strong selection for physiological drought tolerance.

CREDIT: JOE CRAINE, KANSAS STATE UNIVERSITY

Publications

Attigala L, et al. (2016) Phylogenetic estimation and morphological evolution of Arundinarieae (Bambusoideae: Poaceae) based on plastome phylogenomic analysis. *Mol Phy Evol* 101: 111-121

Clark LG (2016) Phylogenomics and plastome evolution of tropical forest grasses (*Leptaspis, Streptochaeta*: Poaceae). *Front Plant Sci* 7: 1–12

Duvall MR, et al. (2016) Phylogenomics and plastome evolution of the chloridoid grasses (Chloridoideae: Poaceae). *Int J Plant Sci* 177(3): 1–12

Orton LM, et al. (2016) Plastid phylogenomic study of species within the genus *Zea*: rates and patterns of three classes of microstructural changes. *Curr Genet* 2016: 1–13

Wysocki WP, et al. (2016) The first complete plastid genome from Joinvilleaceae (*J. ascendens*; Poales) shows unique and unpredicted rearrangements. *PloS ONE* 11.9: e0163218

Wysocki WP, et al. (2016) The floral transcriptomes of four bamboo species (Bambusoideae; Poaceae). *BMC genomics* 17: 384

Costs and benefits of chronic viral infections in natural ecosystems

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Microbial communities in the hot springs of Yellowstone National Park are prone to chronic viral infections, and this project investigates the genetic and functional basis of those infections. 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-mediated dormancy, are advancing our understanding of this ecosystem.

Publications

Gudbergsdottir SR, et al. (2016) Novel viral genomes identified from six metagenomes reveal wide distribution of archaeal viruses and high viral diversity in terrestrial hot springs. *Environ Microbiol* 18(3): 863–874

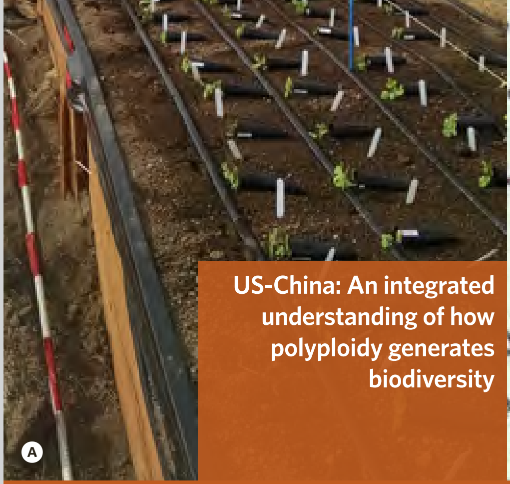
Gulbudak H, Weitz JS (2016) A touch of sleep: Biophysical model of contact-mediated dormancy of Archaea by viruses. *Proc R Soc B* 283(1839): 1037

Hochstein R, et al. (2016) *Acidianus* tailed spindle virus: a new archaeal large tailed spindle virus discovered by culture-independent methods. *J Virol* 90(7): 3458–3268

Menzel P, et al. (2015). Comparative metagenomics of eight geographically remote terrestrial hot springs. *Microb Ecol* 70: 411

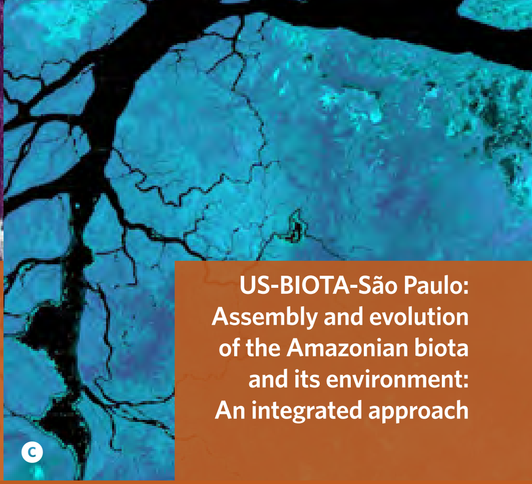
A boiling Yellowstone mud hot spring sampled for this project.
CREDIT: MARK J. YOUNG

Typical high temperature Yellowstone hot spring.
CREDIT: MARK J. YOUNG

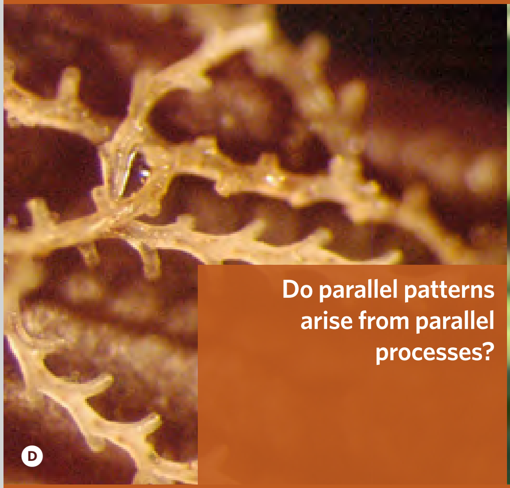


US-China: An integrated understanding of how polyploidy generates biodiversity

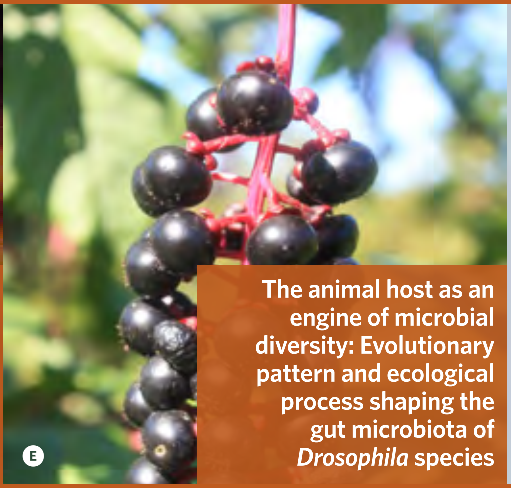
Research on Airborne Ice Nucleating Species (RAINS)



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



Do parallel patterns arise from parallel processes?



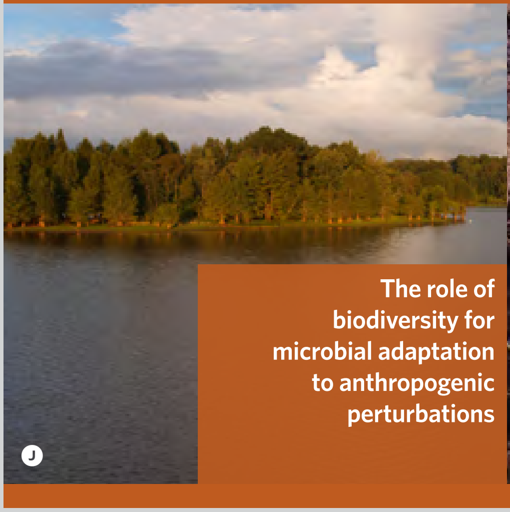
The animal host as an engine of microbial diversity: Evolutionary pattern and ecological process shaping the gut microbiota of *Drosophila* species

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

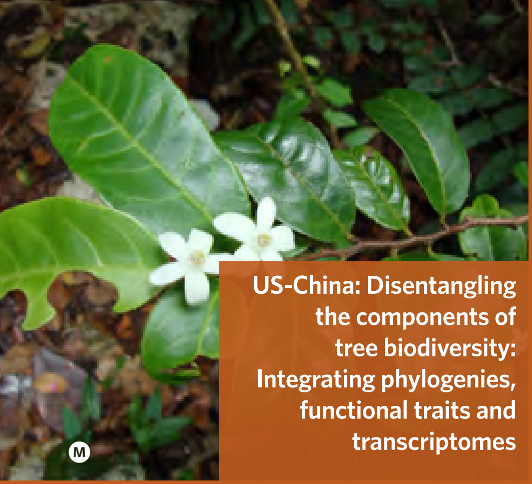
The role of taxonomic, functional, genetic, and landscape diversity in food web responses to a changing environment



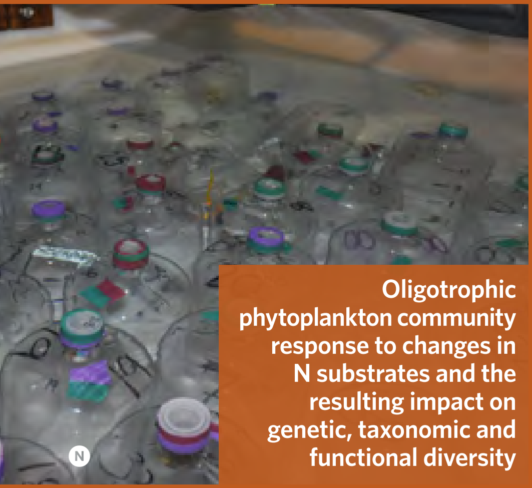
The role of biodiversity for microbial adaptation to anthropogenic perturbations

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

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

- Ⓐ Aaron Liston
- Ⓑ Brent Christner
- Ⓒ Joel Cracraft
- Ⓓ Michael N. Dawson
- Ⓔ Gabrielle Brind 'Amour
- Ⓕ Astrid Hersilia Ferrer Correa
- Ⓖ Karl Magnacca
- Ⓗ Paul Dijkstra
- Ⓘ Anthony Ives
- Ⓙ K. Konstantinidis & D. Tsementzi
- Ⓚ Thomas E. Martin
- Ⓛ Hans Paerl
- Ⓜ Nathan Swenson
- Ⓝ Gert van Dijken

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

(CO-FUNDED WITH NSFC)

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CHINA TEAM	**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 as models. The strawberry genus, Fragaria, with generally small genomes and cytogenetic compatibility, is ideal for exploring patterns of genetic diversity arising from polyploidization.

HTTP://WILDSTRAWBERRY.ORG

Update

The team extended their elucidation of polyploidization history in *Fragaria* to the decaploid (2*n*=70) *Fragaria cascadensis*. They discovered that ancient hybridization, and not current sympatry, best explained the origin of this species. In addition, the fitness and phenotypic responses in functional traits to climate differences were studied in over 3000 clones of 284 genotypes from 11 species grown in three geographically separate "common gardens". This detailed study was paired with gene expression responses for 40 genotypes, linking phenotype to genotype and fitness consequences. Major progress has been made in deciphering the taxonomy, phylogeny and biogeography of the Chinese strawberry species.

Publications

Glick L, et al. (2016) Polyploidy and sexual system in angiosperms: Is there an association? *Am J Bot* 103: 1223–1235

Tennessen J, et al. (2016) Homomorphic ZW chromosomes in a wild strawberry show distinctive recombination heterogeneity but a small sex-determining region. *New Phytol* 211: 1412–1423

Geographic distribution of *Fragaria cascadensis* and its potential ancestors.

CREDIT: NA WEI, UNIVERSITY OF PITTSBURGH

Planting the strawberry common garden in Bend, Oregon.

CREDIT: AARON LISTON

Research on Airborne Ice Nucleating Species (RAINS)

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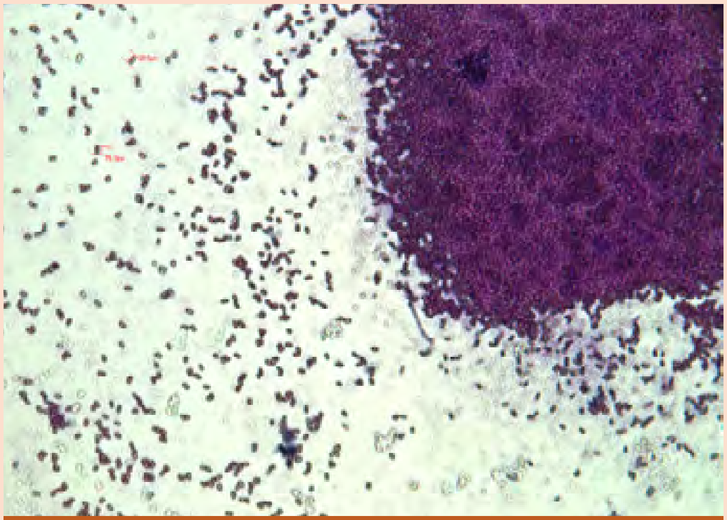
This project examines the diversity and activity of airborne microbes that catalyze the formation of ice crystals in the atmosphere. RAINS seeks to understand the role of microbial ice nucleation in atmospheric microbial dispersal, and ultimately, precipitation generation.

Update

RAINS PIs at Virginia Tech completed their identification and systematic study of culturable ice nucleation active bacteria isolated from precipitation. Additionally, they identified a new Lysinibacillus bacterium using genome sequencing and characterized it for heat and proteinase resistance, secretability, and size. MSU and UC-Davis researchers developed a protocol to screen plant material for the abundance of microbial ice nucleators in wheat and alfalfa. Short-term ancillary RAINS projects were initiated in 2016 by the Idaho team in alpine and sage steppe ecosystems of the Central Rocky Mountains.

Outreach activities by RAINS PIs this year include a 3-day workshop with middle school teachers, developing and executing an engaging lesson plan that showcases various aspects of the RAINS project research and a workshop aimed at mentoring early career scientists investigating bioaerosols and land-atmosphere feedbacks, while introducing them to RAINS project activities.



^ 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

Publications

Pietsch RB, Vantzer BA, Schmale DG (2017) Diversity and abundance of ice nucleating strains of *Pseudomonas syringae* in a freshwater lake in Virginia, USA. *Front Microbiol* 8(318): 1–11

Striluk ML, Aho K, Weber CF (2017) The effect of season and terrestrial biome on the abundance of bacteria with plant growth-promoting traits in the lower atmosphere. *Aerobiologia* 33: 137–149

Morris CE, et al. (2016) Mapping rainfall feedback to reveal the potential sensitivity of precipitation to biological aerosols. *Bull Amer Meteorol Soc* doi.org/10.1175/BAMS-D-15-00293.1

Pietsch RB, et al. (2016) Turning into ice: teaching biological ice nucleation and the global water cycle. *Sci Teacher* 83(9): 37–42

Weber, CF (2016). Beyond the cell: using multiscalar topics to bring interdisciplinarity into undergraduate cellular biology courses. *CBE-Life Sciences Education* 15(2): 1–11

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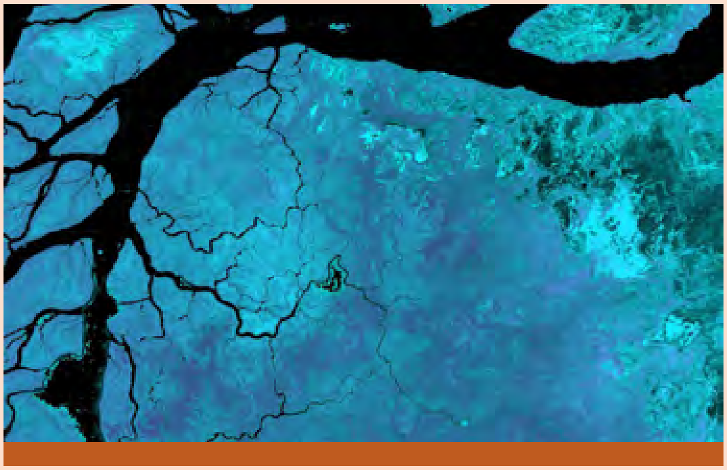
This project seeks to understand the evolutionary and ecological history of Amazonia, the most diverse ecosystem on Earth. A goal is to build a comprehensive database of plants, birds and primates, which, together with phylogenetic, population genetic, remote sensing, geology, and Earth-systems modeling,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

Update

Species pages and detailed maps are being constructed for all neotropical Lecythidaceae from the over 17,000 georeferenced specimens to date, at more than 12,500 collecting sites. Researchers have also been focusing efforts on understanding the biogeographic history of the Amazon basin through extensive phylogeographic studies avifauna, geologic data, and satellite imagery. Lastly, a genetic study of the *Heliconia* butterfly system is being used to test the Pleistocene Refugium hypothesis, while another, on woody plants, will test Wallace's Riverine Barrier hypothesis.



^ This image depicts the Amazon basin and was created with data from NASA's Shuttle Radar Tomography Mission combined with imagery from the Japanese Space Agency's Advanced Land Observing System (ALOS) Phased Array type L-band Synthetic Aperture Radar (PALSAR).

CREDIT: JOEL CRACRAFT

Publications

Brower AVZ (2016) Rethinking tree-thinking: cladograms, ancestors and evidence. *Am Biol Teacher* 78: 380

Brower AVZ (2016) Are We All Cladists? In: *The Future of Phylogenetic Systematics: The Legacy of Willi Hennig.* (Williams DM, Wheeler QD, Schmitt M, eds.), Cambridge Univ Press, Cambridge.

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Patitucci KF, Tkach VV, Bates JM (2016) *Mosesia ovalis n. sp.* (Digenea: Phaneropsolidae) from the green manakin *Xenopipo holochlora* from Peruvian Amazon with notes on morphology of *Mosesia mosesi* Travassos, 1921. *Comp Parasitol* 83(1): 49–53

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Smith NP, et al. (2016) Conservation assessment of Lecythidaceae from eastern Brazil. *Kew Bulletin* 71: 14 doi: 10.1007/S12225-016-9627-8

Ribeiro M, et al. (2016) A new species of *Eschweilera* (Lecythidaceae) from the Brazilian Atlantic Forest. *Phytotaxa* 255(3): 267

Weeks BC, Claramunt S, Cracraft J (2016) Integrating systematics and biogeography to disentangle the roles of history and ecology in biotic assembly. *J Biogeo* 43: 1546

Do parallel patterns arise from parallel processes?

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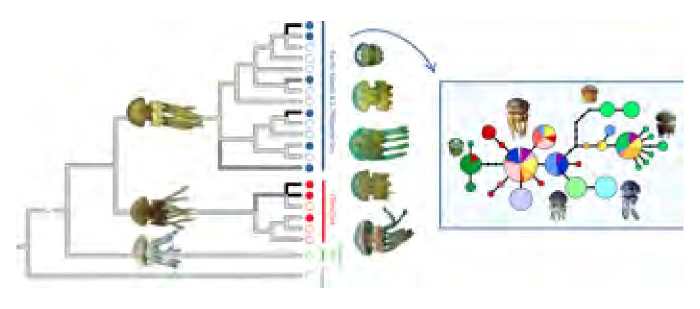
This project is to survey the dimensions of diversity of the organisms found in marine lakes, and investigate the processes that cause gains and losses in this biodiversity. Marine lakes formed as melting ice sheets raised sea level after the last glacial maximum and flooded hundreds of inland valleys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



Nested phylogenetic and population genetic analyses coupled with morphometrics illustrate three routes to crypsis in the scyphozoan jellyfish *Mastigias papua*: stasis during ancient speciation, convergent evolution when multiple species colonize similar habitats, and parallelism when multiple conspecific populations colonize similar habitats.

CREDIT: HOLLY F. SWIFT, UNIVERSITY OF CALIFORNIA, MERCED

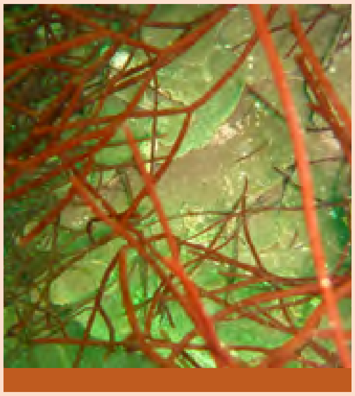
MARINE LAKES: EXPERIMENTS IN ECOLOGY AND EVOLUTION | HTTP://MARINELAKES.UCMERCED.EDU
PAPAPRO : DO PARALLEL PATTERNS ARISE FROM PARALLEL PROCESSES? | HTTP://WWW.BCO-DMO.ORG/PROJECT/2238

Update

Since 2013, the team has spent 9 months conducting fieldwork in Palau. We surveyed and collected modern marine microbes, invertebrates, fishes, and algae and recovered sediment cores up to 11 m deep and 10,000 years old. Over 15 lakes were surveyed for species diversity—with a total of 14,726 geolocated datapoints describing invertebrate and algae species distributions—and ~1500 specimens barcoded for comparative phylogeographic analyses. Experiments with microbial communities explored how functional diversity is shaped by, and shapes, environmental variation, with potential knock-on effects for macrobiota. We are now integrating these data to discover how communities have changed through time, leading to today's distributions of functions, genes and species.

Benthic point intercept transects are used to quantify species abundance, cover, and richness.

CREDIT: MICHAEL N. DAWSON



Dead coral under a bed of branching red alga may indicate a prior tipping point in the lake ecosystem.

CREDIT: MICHAEL N. DAWSON

Publications

Ladd SN, Sachs JP (2017) 2H/1H fractionation in lipids of the mangrove *Bruguiera gymnorhiza* increases with salinity in marine lakes of Palau. *Geochimica et Cosmochimica Acta* 204: 300

Dawson MN, et al. (2016) The Evolutionary Biogeography of Islands, Lakes, and Mountaintops. In: *The Encyclopedia of Evolutionary Biology.* (R. Gillespie, ed.), Elsevier, Oxford.

Meyerhof MS, et al. (2016) Microbial community diversity, structure and assembly across oxygen gradients in meromictic marine lakes, Palau. *Environ Microbiol* 18(12): 4907–4919

Richey JN, Sachs JP (2016) Precipitation changes in the western tropical Pacific over the past millennium. *Geology* 44 (8): 671–674

Schiebelhut LM, et al. (2016) A comparison of DNA extraction methods for high-throughput DNA analyses. *Mol Ecol Resour* doi:10.1111/1755-0998.12620

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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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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 are investigating host-microbe interactions in *Drosophila* flies, specifically to determine how the animal host may shape microbial diversity; and to establish how interactions with microorganisms affect various traits of the animal host, including food processing, habitat choice, competition, and interactions with parasites, all of which can potentially drive animal diversification. We have now demonstrated that a key trait of the gut habitat, pH, is a major determinant of the abundance and composition of the microbial community, complementing our demonstration (also in this project) that *Drosophila* is a key driver of the microbial communities in the immediate environment. Furthermore, the composition of the microbiota varies with host species and with environmental factors, especially diet, with consequences for the ecologically-important traits and fitness of the animal. The research team has had multiple interactions with various audiences to promote an appreciation and understanding of biodiversity, at scales from an individual human body to the global biosphere. These include the successful photographic exhibition "Shifting Paradigms: Microbes as Animal-Helpmates", now on permanent display at Cornell University, hands-on training sessions on *Drosophila* taxonomy and field monitoring, and workshops on genomics for students from local undergraduate colleges.

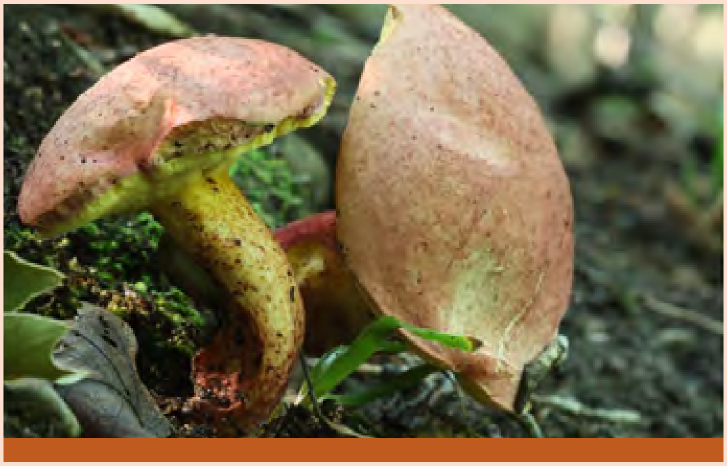
Publications

Martinson VG, Douglas AE Jaenike J (2017) Community structure of the gut microbiota in sympatric species of wild *Drosophila*. *Ecol Lett* 20(5): 629–639

Adair KL, Douglas AE (2016) Making a microbiome: the many determinants of host-associated microbial community composition. *Curr Opin Microbiol* 35: 23–29

Douglas AE, Werren JH (2016) Holes in the hologenome: why host-microbial symbioses are not holobionts. *mBio* 7(2): e02099-15

Overend G, et al. (2016) Molecular mechanism and functional significance of acid generation in the *Drosophila* midgut. *Sci Rep* 6: 27242



^ Wild mushrooms of the order Boletales are a food source of *Drosophila falleni* as well as several other mushroom-feeding drosophilids found in central NY.

CREDIT: VINCE MARTINSON, UNIVERSITY OF ROCHESTER

^ Microbes cultured from the guts of *Drosophila melanogaster*.

CREDIT: KAREN ADAIR, CORNELL UNIVERSITY

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

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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.

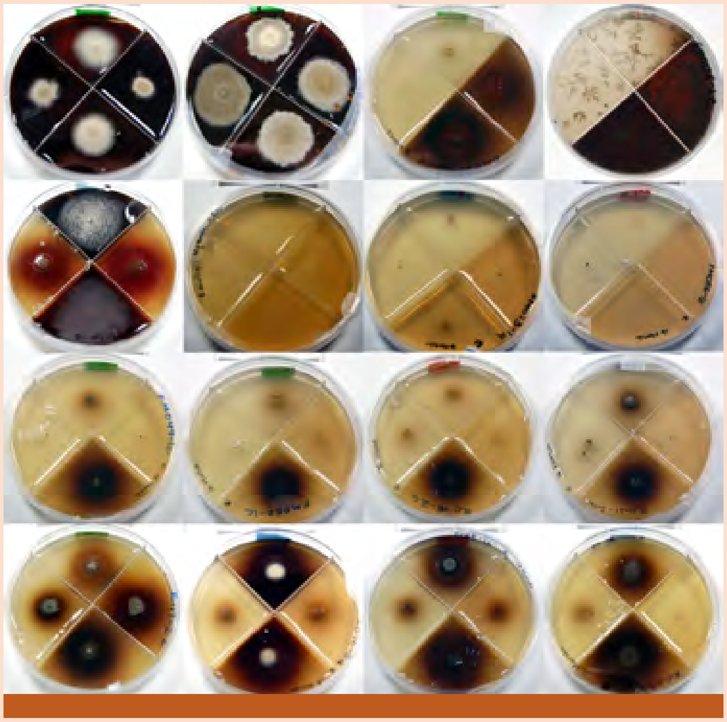
HTTP://PUBLISH.ILLINOIS.EDU/AQUATICFUNGI

Update

Using environmental sequencing we find that salinity strongly structures fungal, bacterial and archaeal communities that colonize wood blocks placed in water, but that stage of decay only impacts fungal communities. Assays of fungi cultured from the same wood blocks shows that both pH and salinity affect lignocellulolytic enzyme activity, with pH effects dependent on the isolate's environmental origin. pH may therefore be as important as salinity in determining fungal distributions. Analysis of the wood substrate shows that decay is faster in brackish and marine environments than in freshwater, and is associated with a greater loss of the breakdown products of lignin.

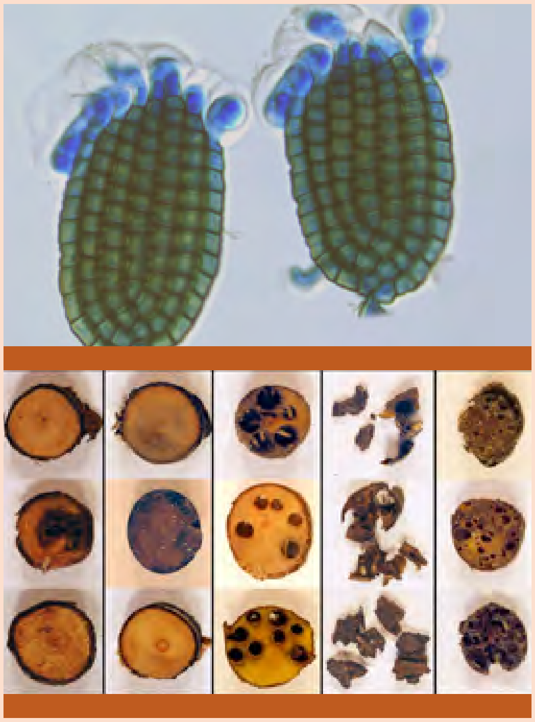
Publication

Brown SP, et al. (2016) Don't put all your eggs in one basket: a cost-effective and powerful method to optimize primer choice for rRNA environmental community analyses using the Fluidigm Access Array. *Mol Ecol Resour* 16: 946–956



Individual fungal isolates grown under different salinity and pH conditions. The four quadrants of the dish contain media with pH and salinity conditions reflecting freshwater and marine habitats. Those producing the cellulose degrading enzyme β-glucosidase turn the media dark. The image shows that fungi differ in the environmental conditions under which this enzyme is active.

CREDIT: ASTRID HERSILIA FERRER CORREA



Top: Spores of the ascomycete fungus *Dictyosporium* sp. isolated from wood samples submerged in low salinity brackish water. Spores are used to obtain pure fungal cultures for experimental work.

Bottom: Samples of wood incubated on land and under various salinities (low to high, left to right) along the Playa Hermosa river on Coiba Island, Panama.

CREDIT: ASTRID HERSILIA FERRER CORREA

A community level approach to understanding speciation in Hawaiian lineages

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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

To date this diverse and dynamic team has trained 5 postdocs, 10 graduate students, and 20 undergraduates. They finished up the major portion of collecting and continue to sort and identify specimens to order at UM and UC Berkeley, exchanging data and photos. Among the many ongoing lab activities, students are developing protocols for population genetics analyses using next generation sequencing and for studying species composition in arthropod samples with metabarcoding. Additionally, some members of the team have been using isotopes to assess trophic relationships and the extent to which organisms track the chemical stoichiometries of their habitat through time, while others are assessing gut microbial diversity, species diversification, and host switching through time.

Publications

Krehenwinkel H, et al. (2017) A cost efficient and simple protocol to enrich prey DNA from extractions of predatory arthropods for large scale gut content analysis by Illumina sequencing. *Meth Ecol Evol* 8(1): 126–134

Patiño J, et al. (2017) A roadmap for island biology: 50 fundamental questions after 50 years of The Theory of Island Biogeography. *J Biogeo* doi:10.1111/jbi.1298

Gillespie RG (2016) Island time and the interplay between ecology & evolution in species diversification. *Evol App* 9(1): 53–73

Rominger AJ, et al. (2016) Community assembly on isolated islands: macroecology meets evolution. *Global Ecol Biogeogr* 25: 69

Shaw KL, Gillespie RG (2016) Comparative phylogeography of oceanic archipelagos: hotspots for inferences of evolutionary process. *PNAS* 113(29): 7986–2993

^ 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', where a pulse increase of carbon causes an acceleration in microbial-mediated soil organic matter degradation.

Update

The team has continued moving forward with quantitative approaches to assessing the functional significance of microbial biodiversity, primarily through their newly-developed technique, quantitative stable isotope probing (qSIP). This work, involving experiments and models, is pushing the frontiers of microbial ecology: providing power for determining ecological processes in intact microbial communities and in probing for the quantitative significance of specific microbial taxa for indirect effects. Among many interesting results, they found bacteria demonstrate quantitatively distinct growth rates on decomposing leaves in aquatic ecosystems, substantially distinct from their relative abundances. Furthermore, they completed *in situ* work revealing phylogenetic signals of growth rate on a substrate.

Publications

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Morrissey EM, et al. (2017) Bacterial carbon use plasticity, phylogenetic diversity, and the priming of soil organic matter. *ISME J* 43: 1–10

Ember M, et al. (2016) Phylogenetic organization of bacterial activity. *ISME J* 10: 2336–2340

Hayer M, et al. (2016) Identification of growing bacteria during litter decomposition in freshwater through H218O quantitative stable isotope probing. *Environ Microbiol Rep* 8(6): 975–982

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Schwartz E, et al. (2016) Stable isotope probing with 18O-water to investigate microbial growth and death in environmental samples. *Curr Opin Biotech* 41: 14–18

^ Collecting soil for microbial diversity analysis.

CREDIT: PAUL DIJKSTRA

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

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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

Our most recent experiment investigated whether evolution of pea aphids could occur rapidly enough to affect their ecological interactions with a parasitic wasp, one of their main predators. In large cages (7 x 30 m), we used alfalfa harvesting regimes that either discouraged (harvesting all alfalfa) or favored wasps (leaving some alfalfa standing). In cages where wasps were favored, there was rapid evolution of aphids containing symbionts that confer resistance to wasps. The following year, the now-resistant aphid populations escaped control by the wasps and exploded, showing how rapid evolution can affect populations on a yearly time scale.

Top: The parasitic wasp *Aphidius ervi* attacking a pea aphid. She will inject an egg into the aphid that hatches and consumes the still-living aphid. The aphid is trying to defend herself with a droplet of gluey substance that she secretes from her cornicles.

Bottom: Ian Chen, Pat Uphues, Maya Banks, and Mike Bosch (left to right), the aphid field crew for 2016.

CREDIT: ANTHONY IVES

Publication

Martinez AJ, et al. (2016) Specificity of multi-modal aphid defense against two parasitic wasps. *PloS ONE* 11(5): e0154670

Top: Rachel Penczykowski, a postdoc on the project, counting aphid and wasps.

Bottom: Packing away our large cages half way through our experiment on the rapid evolution of pea aphid resistance via symbionts to the parasitic wasp *Aphidius ervi*.

CREDIT: ANTHONY IVES

The role of biodiversity for microbial adaptation to anthropogenic perturbations

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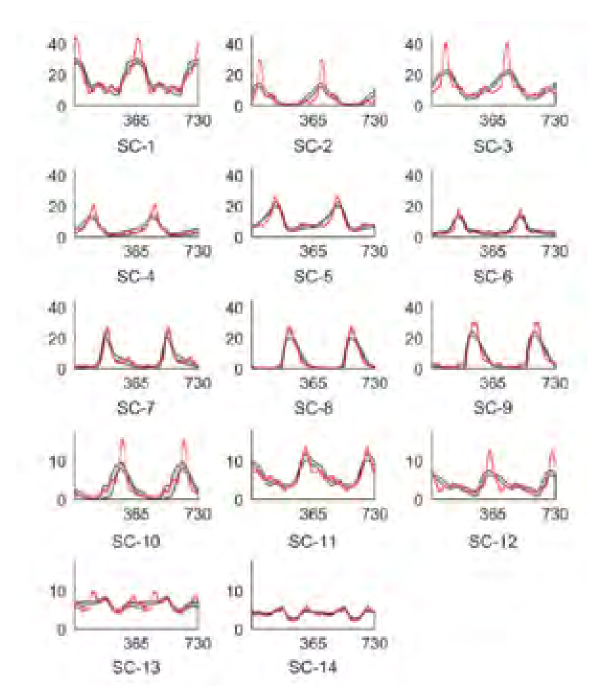
This project examines how low-abundance (rare) members of microbial communities enable community adaptation and resilience to disturbances and to the presence of new organic compounds such as petroleum hydrocarbons, pesticides, and antibiotics.

Update

We have developed differential equation models that quantify the dynamically changing abundance patterns and interactions of fourteen sub-communities, containing thousands of microbial species, in Lake Mendota, WI. Each sub-community contains species from numerous families, genera, and phyla in strikingly different abundances. The models also quantify the importance of temperature, ammonia/phosphorus and nitrate/nitrite for shaping the dynamics of the lake's metapopulation. While the environmental factors positively affect almost all sub-communities, most interactions between sub-communities are inhibitory. Our modeling may help us understand and explain what's wrong in a lake or another natural ecosystem, and predict consequences of changes in environmental conditions.



Time-dependent abundances of 14 bacterial sub-communities in Lake Mendota. Red lines: means of observed abundances collected between 2000 and 2011. Grey shading: ranges of abundances predicted by our ensemble of dynamical models. X-axis: days of a two-year period. Y-axis: abundances of the sub-communities (note different scales).

CREDIT: DAM P, ET AL. (2016)

Publications

Huang AD, et al. (2017) Metagenomics of two severe foodborne outbreaks provides diagnostic signatures and signs of coinfection not attainable by traditional methods. *Appl Environ Microbiol* 83(3): e02577-16

Orellana LH, Rodriguez-R LM, and Konstantinidis KT (2017) ROCker: accurate detection and quantification of target genes in short-read metagenomic datasets by modeling sliding-window bitscores. *Nucleic Acids Res* 45(3): e14

Dam P, et al. (2016) Dynamic models of the complex microbial metapopulation of Lake Mendota. *Nat Sys Biol App* doi:10.1038/npjsba.2016.7

Ertekin E, et al. (2016) Similar microbial consortia and genes are involved in the biodegradation of Benzalkonium Chlorides in different environments. *Environ Sci Tech* 50(8): 4304–13

Ertekin E, Konstantinidis KT, Tezel U (2017) A Rieske-type oxygenase of *Pseudomonas* sp. BIOMIG1 converts benzalkonium chlorides to benzyldimethyl amine. *Environ Sci Tech* doi: 10.1021/acs.est.6b03705

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Mojdeh F, Voit EO (2016) Nonparametric dynamic modeling. *Math Biosci* doi:10.1016/j.mbs.2016.08.004

Wang Y, et al. (2016) Quantifying the importance of the rare biosphere for microbial community response to organic pollutants in a freshwater ecosystem. *Appl Environ Microbiol* 83(8): e03321-16

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

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Frederick Sheldon
Louisiana State University & Agricultural and Mechanical College
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Robert G. Moyle
University of Kansas Center for Research Inc.
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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 examined physiological, life history, genetic and phylogeographic relationships of songbird species on Borneo to increase understanding of factors underlying tropical biodiversity. Long-held perspectives were overturned in a new explanation of tropical life histories diversification among passerines. Integration of life history and phylogeographic data yielded support for a new hypothesis of variation in dispersal proclivity and phylogeographic structure, providing new insight into potential influences on speciation. We have trained large numbers (>50) of undergraduate students and a high school student in lab and field work, as well as supported 9 graduate students, while also conducting outreach through numerous media articles.

^ The Indigo Flycatcher (*Eumyias indigo*) at its nest with two young in Malaysian Borneo, where work on these and co-occuring species of tropical songbirds attempts to understand phylogenetic, genetic and functional bases of their elevational distributions.

CREDIT: THOMAS E. MARTIN

Publications

Manthey JD, Geiger M, Moyle RG (2017) Relationships of morphological groups in the Northern Flicker superspecies complex (*Colaptes auratus* and *C. chrysoides*). *Sys Biodiv* 15(3): 183–191

Burner RC, et al. (2016) An ornithological survey of Gunung Mulu National Park, Sarawak, Malaysian Borneo. *Wilson J Ornith* 128: 242–254

Dejtaradol A, et al. (2016) Indochinese-Sundaic faunal transition and phylogeographical divides north of the Isthmus of Kra in Southeast Asian Bulbuls (Aves: Pycnonotidae). *Journal of Biogeography* 43: 471

Manthey JD, et al. (2016) Comparison of target-capture and restriction-site associated DNA sequencing for phylogenomics: a test in cardinalid tanagers (Aves, Genus: *Piranga*). *Systematic Biology* 65: 640–650

Manthey JD, Robbins MB, Moyle RG (2016) A genomic investigation of the putative contact zone between divergent Brown Creeper (*Certhia americana*) lineages: chromosomal patterns of genetic differentiation. *Genome* 59: 115

Moyle RG, et al. (2016) Tectonic collision and uplift of Wallacea triggered the global songbird radiation. *Nat Comm* 7: 12709

Shakya SB, Sheldon FH (2016) Supermatrix approach to infer the phylogeny of Pycnonotidae. *Ibis* doi:10.1111/ibi.12464

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van Els P, et al. (2016) Notes on the life history of *Harpactes whiteheadi* (Aves: Trogonidae), with a description of the juvenile plumage. *Raffles B Zool* 64: 76–78

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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University of North Carolina, Chapel Hill
(1240851)

Wayne Gardner
University of Texas, Austin
(1240798)

Steven Wilhelm
University of Tennessee, Knoxville
(1240870)

Ferdinand Hellweger
Northeastern University
(1240894)

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 cyanobacteria blooms.

Update

Nitrogen (N) over-enrichment of fresh waters promotes global expansion of toxic cyanobacterial blooms; this project examines the processes underlying this expansion. Research on eutrophic Lake Taihu, China, examining N inputs and cycling, biodiversity and modeling, has provided observations for developing nutrient management strategies. Taihu is a "looking glass" for similarly-impacted large lakes worldwide. Research shows that sediment phosphorus (P) accumulation supports long-term loading, while N escapes *via* denitrification, leading to perpetual N-deficit. Controlling both N and P inputs, at prescribed levels determined through bioassays, can help control blooms in Taihu and other lakes that have experienced decades of nutrient loading.

^ *Top:* A toxic cyanobacterial bloom near the shore of Lake Taihu, China during June, 2016.

Bottom: Chinese and US graduate students and Post-docs involved in working on experimental mesocosm, designed to examine the effects of nutrient enrichment on cyanobacterial bloom potentials at Lake Taihu, China in June, 2016.

CREDIT: HANS PAERL

Publications

Tang X, et al. (2017) Spatiotemporal dynamics of bacterial diversity and community composition in large shallow eutrophic Lake Taihu: high overlap between free-living and particle-attached assemblages. *Limnol Oceanogr* doi:10.1002/lno.10502

Belisle BS, et al. (2016) Urea in Lake Erie: organic nutrient sources are potentially important drivers of phytoplankton biomass. *J Great Lakes Res* 42: 599–607

Bullerjahn GS, et al. (2016) Global solutions to regional problems: collecting global expertise to address the problem of harmful cyanobacterial blooms. A Lake Erie case study. *Harmful Algae* 54: 223–238

Hamilton DP, Salmaso N, Paerl HW (2016) Mitigating harmful cyanobacterial blooms: strategies for control of nitrogen and phosphorus loads. *Aquatic Ecol* 50(3): 351–366

Harke MJ, et al. (2016) A review of the global ecology, genomics, and biogeography of the commonly toxic cyanobacterium, *Microcystis*. *Harmful Algae* 54: 4–20

Havens K, et al. (2016) Extreme weather events and climate variability provide a lens to how shallow lakes may respond to climate change. *Water* 8(6): 229 doi:10.3390/w8060229

Hellweger F, et al. (2016) Dynamic, mechanistic, molecular-level modelling of cyanobacteria: *Anabaena* and nitrogen interaction. *Environ Microbiol* 18(8): 2721–273

McCarthy MJ, et al. (2016) Benthic nitrogen regeneration, fixation, and denitrification in a temperate, eutrophic lake: effects on the nitrogen budget and cyanobacteria blooms. *Limnol Oceanogr* 61: 1406–1423

Paerl HW (2016) Impacts of Climate Change on Cyanobacteria in Aquatic Environments. Pp.1-27. In: *Climate Change and Microbial Ecology: Current Research and Future Trends.* (J. Marxsen, ed.), Caister Academic Press, Norfolk, UK.

CONTINUE >

Close-up view of a cyanobacterial surface bloom at Lake Taihu, China, during June, 2016.

CREDIT: HANS PAERL

Paerl HW, et al. (2016) It takes two to tango: when and where dual nutrient (N & P) reductions are needed to protect lakes and downstream ecosystems. *Environ Sci Tech* doi:10.1021/acs.est.6b02575

Paerl HW, et al. (2016) Mitigating cyanobacterial harmful algal blooms in aquatic ecosystems impacted by climate change and anthropogenic nutrients. *Harmful Algae* 54: 213–222

Paerl HW, Otten TG, Joyner AR (2016) Moving towards adaptive management of cyanotoxin-impaired water bodies. *Microb Biotech* doi:10.1111/1751-7915.12383

Visser PM, et al. (2016) How rising CO2 and global warming may stimulate harmful cyanobacterial blooms. *Harmful Algae* 54: 128–144

Watson SB, et al. (2016) The re-eutrophication of Lake Erie: harmful algal blooms and hypoxia. *Harmful Algae* 56: 44–66

Proj. 13 / 14

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

(CO-FUNDED WITH NATIONAL SCIENCE FOUNDATION CHINA)

US TEAM	**Nathan Swenson** University of Maryland, College Park (1643052)	CHINA TEAM	**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 international team has acquired community transcriptome inventories for 129 temperate and subtropical species of trees. Much activity has been focused on de novo assembly and annotation, followed by the production of orthologous gene trees for all species in each plot. Two greenhouse studies were undertaken, including a drought experiment to investigate inter-specific similarity in gene expression and a phylogenetically structured competition experiment for *Acer* and *Prunus* species. PI Swenson held a training workshop CAS Institute of Botany in Beijing, China concerning the analysis of the 3 dimensions of biodiveristy and future directions in Dimensions research. He also proposed and edited an "omics in Ecology" edition of the Journal of Ecology, published in May, 2017.

Publications

Swenson NG, Jones FA (2017) Community transcriptomics, genomics and the problem of species co-occurrence. *J Ecol* 105(3): 563–568

Zambrano, et al. (2017) Neighbourhood defence gene similarity effects on tree performance: a community transcriptomic approach. *J Ecol* 105(3): 616–626

Samyda spinulosa sapling in the understory of the Luquillo Forest Dynamics Plot in Puerto Rico.

CREDIT: NATHAN SWENSON

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

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Zbigniew Kolber
University of California, Santa Cruz
(1241221)

Matthew Church
University of Hawaii, Honolulu
(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 several state-of-the-art methods for comprehensive community evaluation.

Update

The team analyzed the diversity and activity of the phytoplankton and microbial communities together with the physics and chemistry of seawater collected during the NEMO cruise in the North Pacific Ocean in 2014. Nitrogen, followed by phosphorus, limited bulk primary productivity and phytoplankton biomass at most of the experimental sites, except one station where both N and P were co-limiting. High resolution taxonomic analysis showed that individual phytoplankton groups, and populations within the groups, responded differently to nutrients; demonstrating a diversity of adaptions and physiology. Moreover, initial conditions, such as nutrient availability, affected rates of the phytoplankton and microbial responses. Finally, the team found that fluxes of new nitrogen associated with internal tides may fuel the summer diatom blooms that regularly appear in the northeastern subtropical Pacific.

Publications

Böttjer D, et al. (2016) Temporal variability in nitrogen fixation and particulate nitrogen export at Station ALOHA. *Limnol Oceanogr* doi: 10.1002/lno.103

Rii YM, et al. (2016) Temporal and vertical variability in picoplankton primary productivity in the North Pacific Subtropical Gyre. *Marine Ecology Progress Series* 562: 1

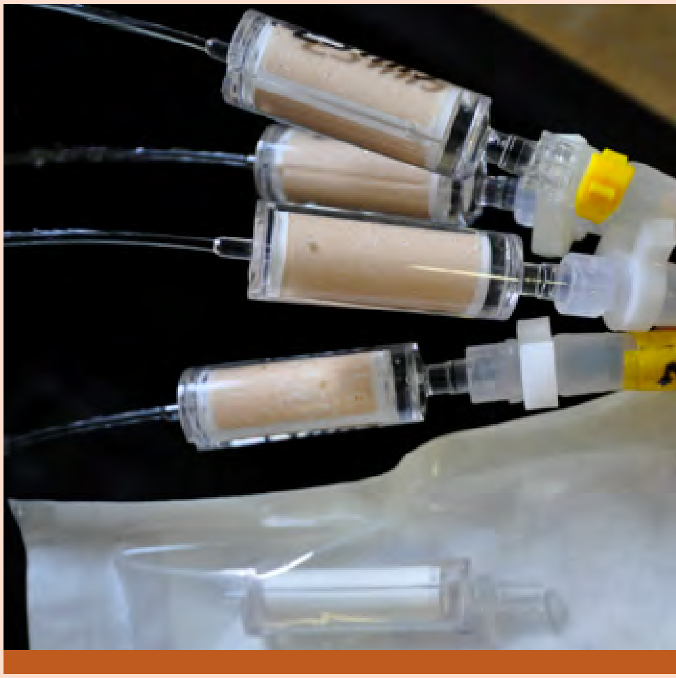
Shilova IN, et al. (2016) Genetic diversity affects the daily transcriptional oscillations of marine microbial populations. *PloS ONE* 11(1): e0146706

Top: A CTD (conductivity, temperature, and depth) rosette with 12L bottles is used to collect seawater from selected depths in the water column. It is equipped to measure salinity, temperature, and chlorophyll a concentrations.

CREDIT: IRINA SHILOVA, UC-SANTA CRUZ

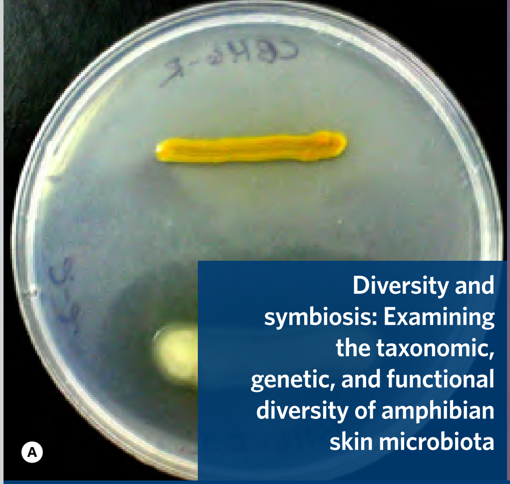
Bottom: On-deck incubators are used for conducting perturbation experiments at sea. Surface seawater flows through the incubators to maintain the temperature on natural environment.

CREDIT: GERT VAN DIJKEN, STANFORD UNIVERSITY



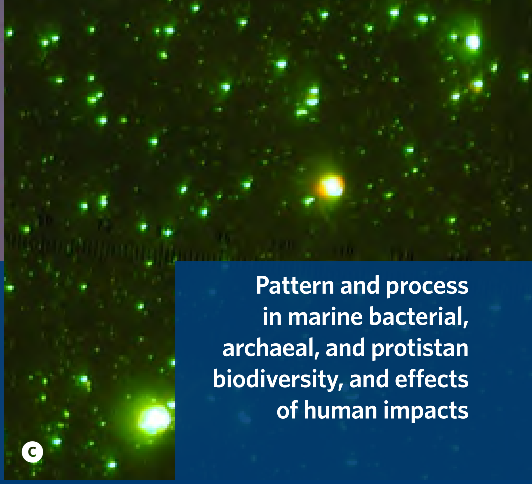
A bloom of nitrogen-fixing cyanobacterium *Trichodesmium* was observed during the cruise. The Sterivex cartridges are used to filter the seawater and collect microbial biomass on the filters. The filters are then frozen and brought back to the lab for extraction of nucleic acids.

CREDIT: GERT VAN DIJKEN, STANFORD UNIVERSITY



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

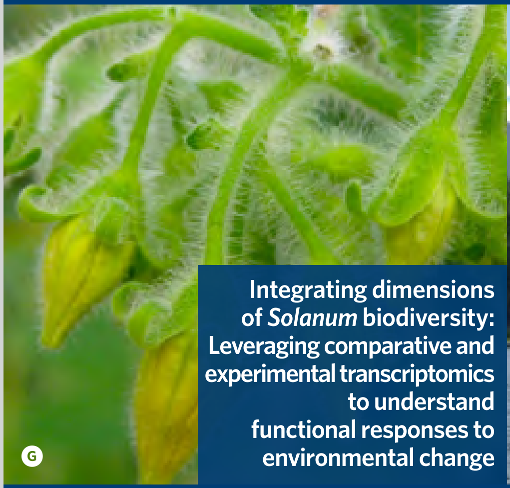


Pattern and process in marine bacterial, archaeal, and protistan biodiversity, and effects of human impacts

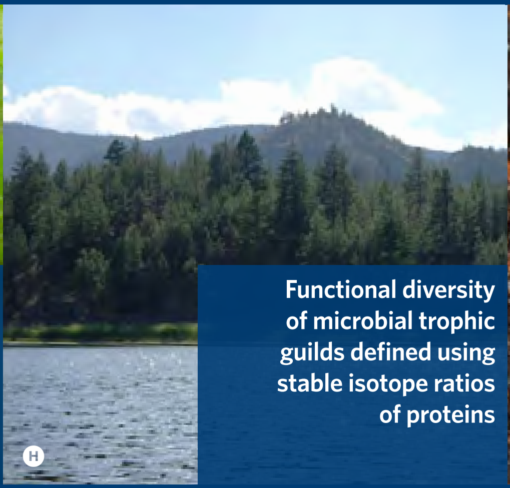
Testing the potential of pathogenic fungi to control the diversity, distribution, and abundance of tree species in a Neotropical forest community

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

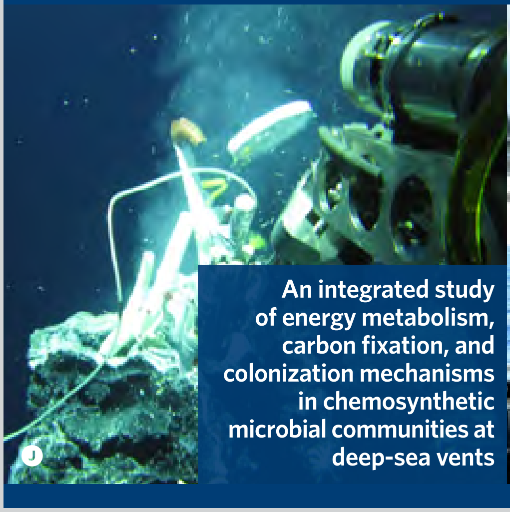


Integrating dimensions of *Solanum* biodiversity: Leveraging comparative and experimental transcriptomics to understand functional responses to environmental change



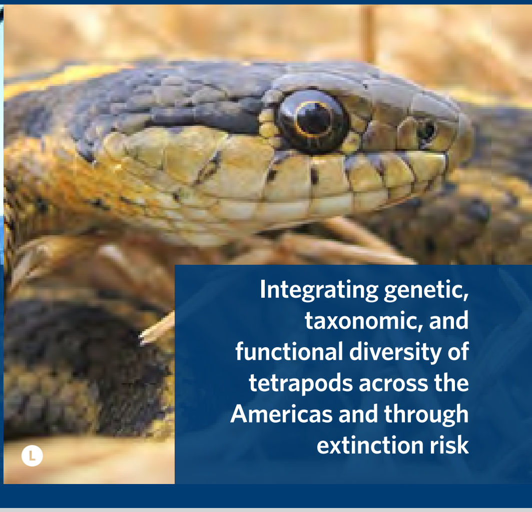
Functional diversity of microbial trophic guilds defined using stable isotope ratios of proteins

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

- Ⓐ Jenifer Walke
- Ⓑ John Clamp
- Ⓒ Jed Fuhrman
- Ⓓ Gregory S. Gilbert
- Ⓔ Thomas Kursar
- Ⓕ Bart De Stasio
- Ⓖ David Haak
- Ⓗ Jennifer Glass
- Ⓘ Aaron Ellison
- Ⓙ Stefan Sievert
- Ⓚ Sarah Fawcett
- Ⓛ Geoffrey Hammerson

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

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Reid Harris
James Madison University
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Kevin Minbiole
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(1136662)

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.

The bacterial species *Pseudomonas* spp. (lower streak) is found on amphibian skins and is shown inhibiting *Batrachochytrium dendrobatidis* (light colored lawn on the agar plate). The bacterial species at the top of the plate is a control that does not inhibit fungi.

CREDIT: JENIFER WALKE, VIRGINIA TECH

Publications

Rebollar EA, et al. (2017) Prevalence and pathogen load estimates for the fungus *Batrachochytrium dendrobatidis* are impacted by ITS DNA copy number variation. *Diseases of Aquatic Organisms* 123(3): 213–226

Hughey MC, et al. (2016) Impact of short-term exposure to coal combustion waste on the skin microbiome of spring peepers, *Pseudacris crucifer*. *Appl Environ Microb* 82(12): 3493–3502

Kueneman JC, et al. (2016) Probiotics restore bacteria lost during amphibian captivity that protect from fungal infection. *Proc R Soc* B 283: 1839

Loudon AH, et al. (2016) Vertebrate Hosts as Islands: Dynamics of selection, immigration, loss, persistence, and potential function of bacteria on salamander skin. *Front Microb* 7: 333

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

Walke JB, Belden LK (2016) Harnessing the microbiome to prevent fungal infections: lessons from amphibians. *PloS Pathogens* 12(9): e1005796

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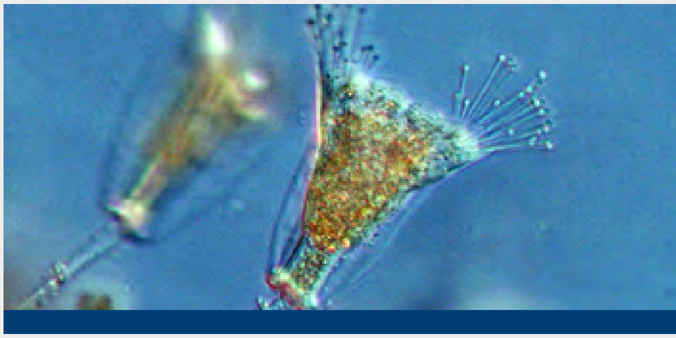
Rollins-Smith LA, et al. (2015) Immunomodulatory metabolites released by the frog-killing fungus *Batrachochytrium dendrobatidis*. *Infection and immunity* 83(12): 4565–70

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

(CO-FUNDED WITH NSFC)

US TEAM	**John Clamp** North Carolina Central University (1136580)	**Laura Katz** Smith College (1136580)	**Chris Lobban** University of Guam (1136580)
CHINA TEAM	**Xiaofeng Lin** South China Normal University Guangzhou	**Weibo Song** Ocean University of China Qingdao	
OTHER COUNTRIES	**Micah Dunthorn** University of Kaiserslautern, Germany	**Laura Utz** Pontificia Universidade Católica do Rio Grande do Sul Brazil	**Alan Warren** Natural History Museum London, United Kingdom

This project establishes an international research coordination network (IRCN) for the biodiversity of ciliates, including researchers from the US, Brazil, China, Germany, and the United Kingdom. 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 CLAMP

Publications

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Mayén-Estrada R, Clamp JC (2016) An annotated checklist of species in the family Lagenophryidae (Ciliophora, Oligohymenophorea, Peritrichia), with a brief review of their taxonomy, morphology, and biogeography. *Zootaxa* 4132(4): 45–492

Warren A, et al. (2016) Report on the 2015 workshop of the International Research Coordination Network for Biodiversity of Ciliates (IRCN-BC) held at Ocean University of China (OUC), Qingdao, China, 19–21 October 2015. *Acta Protozool* 55(2): 119

Diophrys sp, a hypotrich.

CREDIT: JOHN CLAMP

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

Jed Fuhrman
David Caron
Fengzhu Sun
John Heidelberg
William Nelson
University of
Southern California
(1136818)

This project compares 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.

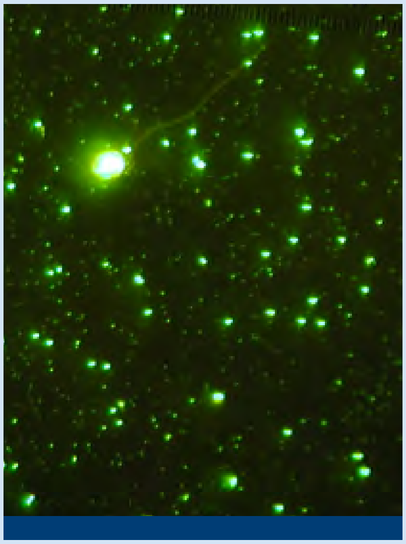
HTTP://BITBUCKET.ORG/CHARADE/ELSA
HTTP://WWW-RCF.USC.EDU/-FSUN/PROGRAMS/NGS-MC/NGS-MC.HTML

Publications

Bialonski S, et al. (2016) Phytoplankton dynamics in the Southern California Bight indicate a complex mixture of transport and biology. *J Plankton Res* fbv122

Cram JA, Parada AE, Fuhrman JA (2016). Dilution reveals how viral lysis and grazing shape microbial communities. *Limnol Oceanogr* 61: 889–905

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



An epifluorescence microscopy image of viruses (tiniest dots), bacteria (medium sized dots) and protists (larger ones) from the USC Microbial Observatory.

CREDIT: JED FUHRMAN

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

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

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Weiss S, et al. (2016) Correlation detection strategies in microbial datasets vary widely in sensitivity and precision. *ISME J* 10: 1669

YY Lu, et al. (2016) COCACOLA: binning metagenomic contigs using sequence COmposition, read CoverAge, CO-alignment, and paired-end read LinkAge. *Bioinformatics* btw290

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

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. *Environ 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

Walters W, et al. (2015) Improved V4, V4-5, and ITS marker gene primers for microbial community survey. *mSystems* doi: 10.1128/mSystems.00009-15

Xia LC, 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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Smithsonian Institution
Travis C. Glenn
University of Georgia
(1136626)

Gregory S. Gilbert
University of California, Santa Cruz
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Brant C. Faircloth
University of California, Los Angeles
(1136626)

The abundance and diversity of tropical trees and fungal pathogens of trees are functionally interconnected with forest dynamics. This project tested 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.

Publications

Glenn TC, et al. (2017) Adapterama I: Universal stubs and primers for thousands of dual-indexed Illumina libraries (iTru & iNext). *Mol Ecol Resour* doi: 10.1101/049114

Young HS, et al. (2017) Introduced Species, Disease Ecology, and Biodiversity-Disease Relationships. *TREE* 32(1): 41

Gilbert GS, Parker IM (2016) The evolutionary ecology of plant disease: a phylogenetic perspective. *Ann Rev Phytopath* 54: 549

Gilbert GS, et al. (2016) Use of sonic tomography to detect and quantify wood decay in living trees. *Appl Plant Sci* 4(12): 1600060

^ A crew of project interns collecting data on internal decay of mature living trees.
CREDIT: GREGORY S. GILBERT

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

Thomas Kursar
Phyllis Coley
University of Utah
(1135733)

This project studies interactions among 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.

Publications

Bixenmann RJ, et al. (2016) High herbivore pressure favors constitutive over induced defense. *Ecol Evol* doi:10.1002/ece3.2208

Wiggins NL, 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(2): 478–492

Top & Bottom: An inflorescence of *Inga punctata* at Los Amigos, Peru.

CREDIT: THOMAS KURSAR

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

CREDIT: THOMAS KURSAR

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

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Michigan State University
(1136710)

Edward C. Theriot
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(1136667)

Stephanie E. Hampton
University of California, Santa Barbara
(1136637)

Lev Yampolsky
East Tennessee State University
(1136706)

Marianne Moore
Wellesley College
(1136657)

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.

Publications

Kremer CT, Thomas MK, Litchman E (2017) Temperature- and size-scaling of phytoplankton population growth rates: reconciling the Eppley curve and the metabolic theory of ecology. *Limnol Oceanogr* doi:10.1002/lno.10523

Osmond MM, Otto SP, Klausmeier CA (2017) When predators help prey adapt and persist in a changing environment. *Am Nat* 190(1) doi: 10.1086/691778

O'Donnell DR, P Wilburn, E Silow, Yampolsky LY, Litchman E (2017) Nitrogen and phosphorus co-limitation of phytoplankton in Lake Baikal, Siberia: insights from the lake survey and nutrient enrichment experiments. *Limnol Oceanogr* doi:10.1002/lno.10505

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

Sitnikova T, et al. (2016) Stable isotope signatures and distribution of deepwater sponges in Lake Baikal. *Hydrobiol* 773: 11

Timofeyev MA, et al. (2016) Safe-guarding the world's largest lake. *Nature* 538: 41

Timoshkin OA, et al. (2016). Rapid ecological change in the coastal zone of Lake Baikal (East Siberia): Is the site of the world's greatest freshwater biodiversity in danger? *J Great Lakes Res* 42: 487

Top: 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

Bottom: Under-ice sampling on Lake Baikal, Siberia. Periodically winds and underwater currents cause large ice slabs to form and rise up.

CREDIT: PAUL WILBURN, W.K. KELLOGG BIOLOGICAL STATION, MICHIGAN STATE UNIVERSITY

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

Leonie Moyle
Matthew Hahn
David Haak
Indiana University
(1136707)

The project 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. *Lycopersicum*. It highlights the role of drought and herbivore defense in driving remarkable diversity.

Some populations of *S. habrochaites* have flowers thickly covered in sticky plant hairs (trichomes).

CREDIT: DAVID HAAK

Publications

Guerrero RF, et al. (2016) Genome-wide patterns of regulatory divergence revealed by introgression lines. *Evolution* 70(3): 696

Hahn MW, Nakhleh L (2016). Irrational exuberance for resolved species trees. *Evolution* 70(1): 7–17

Mendes FK, Hahn W (2016) Gene tree discordance causes apparent substitution rate variation. *Sys Biol* 65(4): 711–721

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

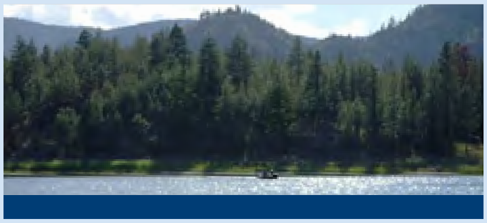
Ann Pearson
Peter Girguis
Harvard University
(1136484)

Jennifer Macalady
Pennsylvania State University
(1136218)

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.

Mahoney Lake, Penticton, BC Canada.

CREDIT: JENNIFER GLASS, ASU



Publication

Tang T, et al. (2016) Geochemically distinct carbon isotope distributions in *Allochromatium vinosum* DSM 180T grown photoautotrophically and photoheterotrophically. *Geobio* 15(2): 324–339

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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Aaron Ellison
Harvard University
(1136646)

Robert Dunn
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(1136717)

Sara Cahan
Bryan Ballif
Nicholas Gotelli
University of Vermont and State Agricultural College
(1136644)

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.

Publications

Gibb H, et al. (2017) A global database of ant species abundances. *Ecology* 98(3): 883–884

Hendershot JN, et al. (2017) Consistently inconsistent drivers of microbial abundance and diversity at macroecological scales. *Ecology* doi: 10.1002/ecy.1829

Parr CL, et al. (2017) GlobalAnts: a new database on the geography of ant traits (Hymenoptera: Formicidae). *Insect Div Conserv* 10(1): 5–10

Penick CA, et al. (2017) Beyond thermal limits: comprehensive metrics of performance identify key axes of thermal adaptation in ants. *Functional Ecol* 31: 1091–1100

Roura-Pascual N, Sanders NJ, Hui C (2016) The distribution and diversity of insular ants: do exotic species play by different rules? *Global Ecol Biogeo* 25(6): 642–654

Stuble KL, et al. (2017) Dominance hierarchies are a dominant paradigm in ant ecology, but should they be? And what is a dominance hierarchy anyways? *Myrmecological News* 24: 71–81

Diamond SE, et al. (2016) Climate warming destabilizes forest ant communities. *Sci Adv* DOI: 10.1126/sciadv.1600842

Top: One of the species in the *Aphaenogaster rudis* complex, the taxonomy and systematics of which is being disentangled with this Dimensions of Biodiversity project.

Bottom: A 22 m^3 atmospheric warming chamber *in situ* at the Harvard Forest.

CREDIT: AARON ELLISON

Proj. 10 / 12

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

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Rutgers University New Brunswick
(1136451)

Ramunas Stepanauskas
Bigelow Laboratory for Ocean Sciences
(1136488)

Dionysios I. Foustoukos
Carnegie Institution of Washington
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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.

Publications

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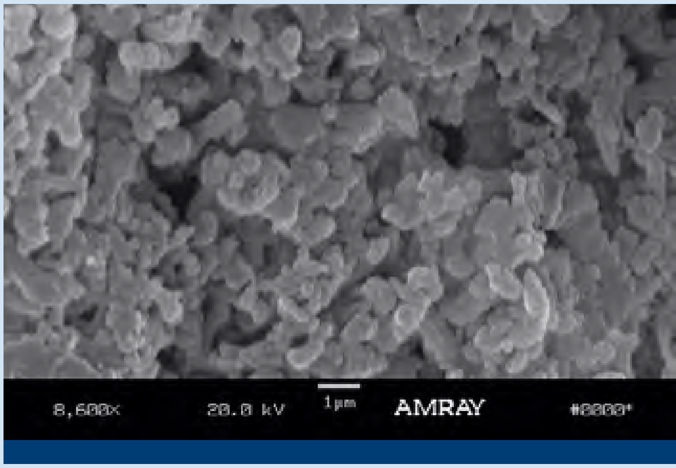
Dyksma S, et al. (2016) Ubiquitous *Gammaproteobacteria* dominate dark carbon fixation in coastal sediments. *ISME J* 10: 1939

Giovannelli D, et al. (2016) Insight into the evolution of microbial metabolism from the deep-branching bacterium, *Thermovibrio ammonificans.* *eLife* 10.7554/eLife.18990

McNichol J, et al. (2016) Assessing microbial processes in deep-sea hydrothermal systems by incubation at *in situ* temperature and pressure. *Deep-Sea Research Part 1* 155: 221–232

McNichol J (2016) Productivity, Metabolism and Physiology of Free-Living Chemoautotrophic *Epsilonproteobacteria*. PhD Thesis. Massachusetts Institute of Technology/Woods Hole Oceanographic Institution Joint Program in Oceanography/Applied Ocean Science and Engineering.



^ Scanning electron micrograph of chemosynthetic biofilm collected from a deep-sea hydrothermal vent.
CREDIT: CONSTANTINO VETRIANI

Proj. 11 / 12

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

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Andrew Allen
J. Craig Venter Institute, Inc.
(1136477)

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.

HTTP://WWW.BCO-DMO.ORG/PROJECT/544343

Publication

Ward BB, et al. (2016) Phytoplankton assemblage during the North Atlantic spring bloom assessed from functional gene analysis. *J Plankton Res* 38(5): 1135–1150

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

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Bruce Young
NatureServe
Gabriel C. Costa
Federal University of Rio Grande do Norte
(1136586)

Volker Radeloff
University of Wisconsin, Madison
(1136592)

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

Stephen B. Hedges
Pennsylvania State University
(1455761)

This project has 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.

Publications

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Zhu L, Radeloff VC, Ives AR (2017) Characterizing global patterns of frozen ground with and without snow cover using microwave and MODIS satellite data products. *Remote Sensing of Environment* 191: 168–178

Zurano JP, et al. (2017) Morphological and ecological divergence in South American canids. *J Biogeo* 44(4): 821–833

Brooks TM, et al. (2016) Analysing biodiversity and conservation knowledge products to support regional environmental assessments. *Sci Data* 10.1038/sdata.2016.7

Costa GC, et al. (2016) Microhabitat use and coexistence in two closely related species of *Herpsilochmus* (Aves: Thamnophilidae). *Cogent Environ Sci* 2(1): 1264126

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Marin J, Hedges SB (2016) Time best explains global variation in species richness of amphibians, birds and mammals. *J Biogeo* 43: 1069–1079

Maxwell SL, et al. (2016) The ravages of guns, nets and bulldozers. *Nature* 531: 143

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Nóbrega RP, et al. (2016) Intraspecific variation of the snake *Thamnodynastes pallidus* (Linnaeus, 1758) (Serpentes, Dipsadidae, Tachymenini) based on morphology, and the analysis of its geographic distribution. *Herp J* 26: 167

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Ralph G, et al. (2016) Assessing the cost of global biodiversity and conservation knowledge. *PloS ONE* 11(8): e0160640

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Brooks TM, et al. (2015) Harnessing biodiversity and conservation knowledge products to track the Aichi Targets and sustainable development goals. *Biodiversity* 16: 157–174

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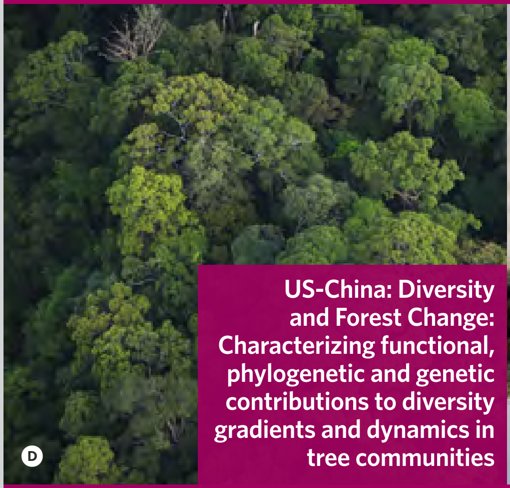
Gambelia wislizenii long-nosed leopard lizard, Colorado, USA.

CREDIT: GEOFFREY A. HAMMERSON

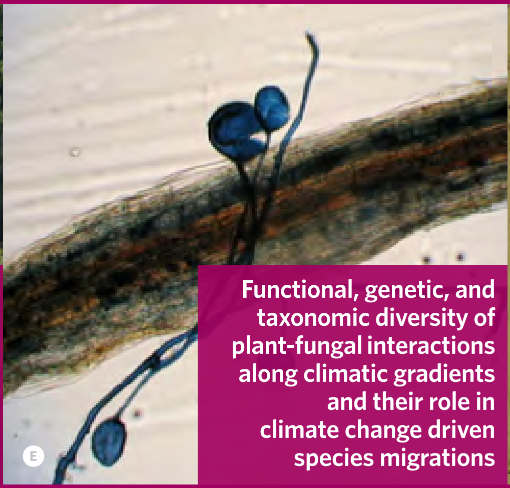
The microbial basis of animal speciation

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

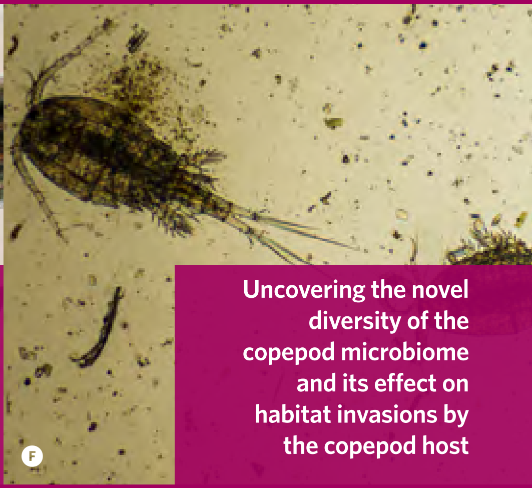
Can evolutionary history predict how changes in biodiversity impact the productivity of ecosystems?



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

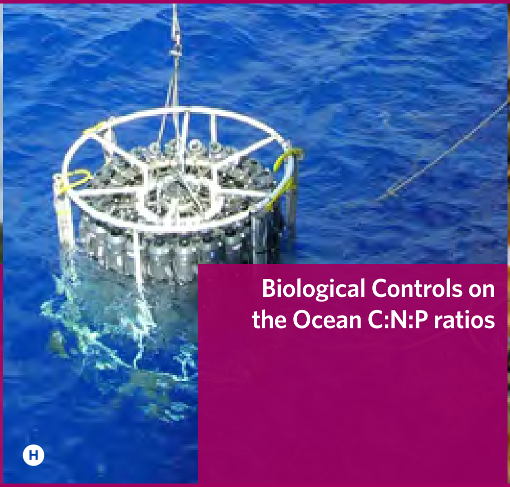


Functional, genetic, and taxonomic diversity of plant-fungal interactions along climatic gradients and their role in climate change driven species migrations

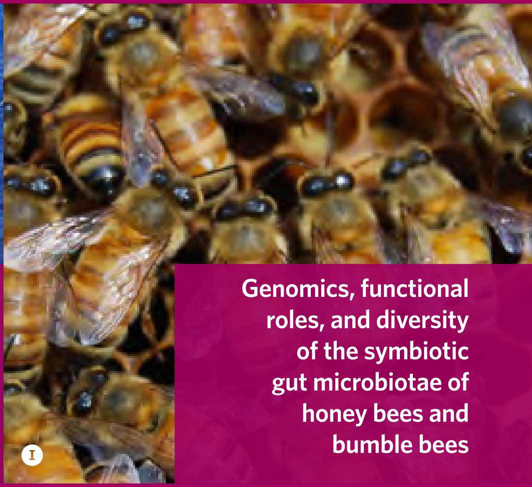


Uncovering the novel diversity of the copepod microbiome and its effect on habitat invasions by the copepod host

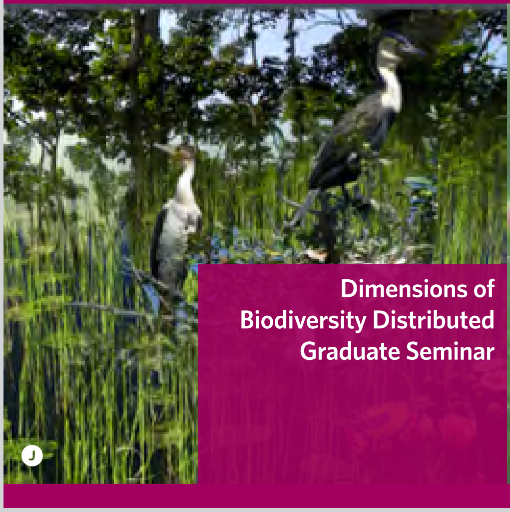
An interdisciplinary study of hyperdiverse endophytic fungi and their function in boreal forests



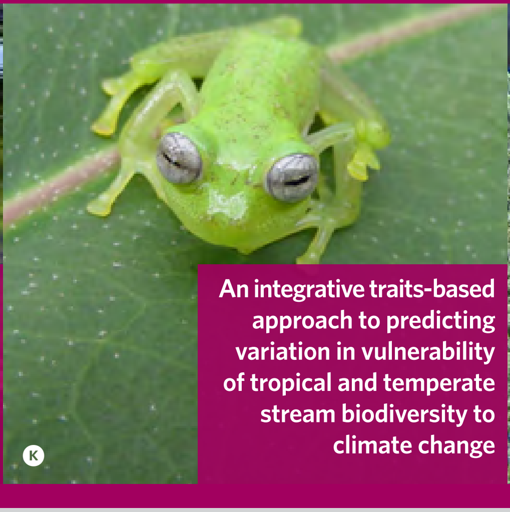
Biological Controls on the Ocean C:N:P ratios



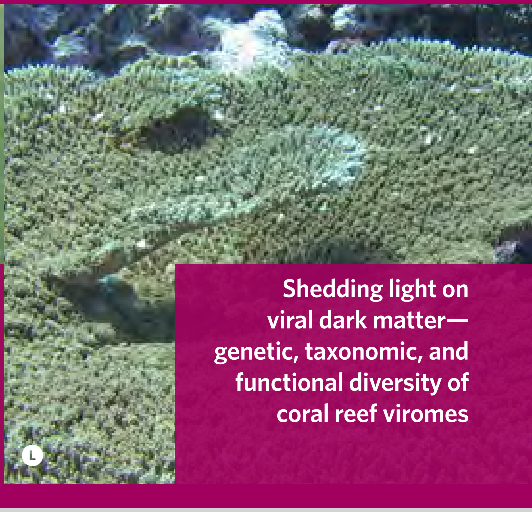
Genomics, functional roles, and diversity of the symbiotic gut microbiotae of honey bees and bumble bees



Dimensions of Biodiversity Distributed Graduate Seminar



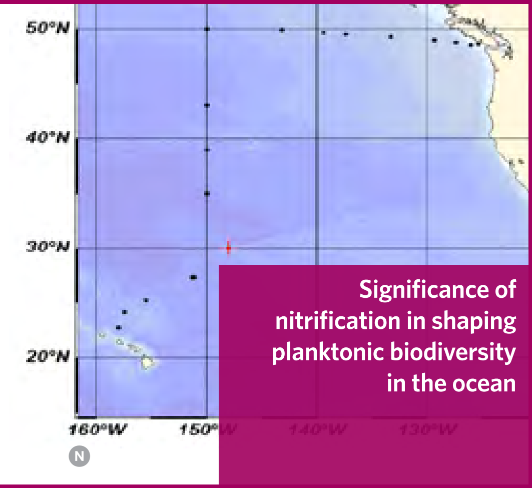
An integrative traits-based approach to predicting variation in vulnerability of tropical and temperate stream biodiversity to climate change



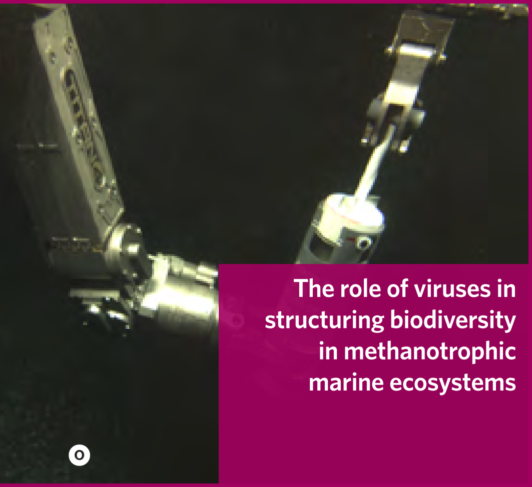
Shedding light on viral dark matter—genetic, taxonomic, and functional diversity of coral reef viromes

2010 updates

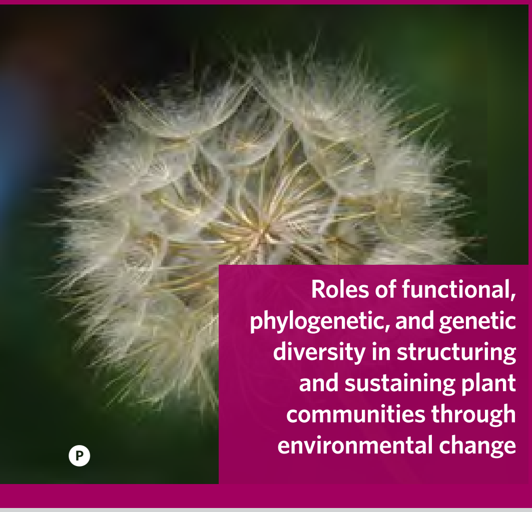
Parallel evolutionary radiations in *Protea* and *Pelargonium* in the Greater Cape Floristic Region



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

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

The microbial basis of animal speciation

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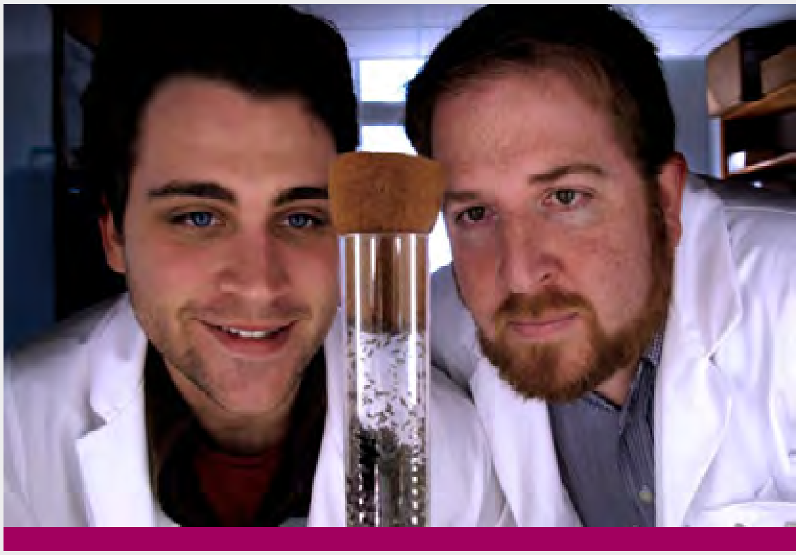
The head of *Nasonia* wasp that was captured in detail by a scanning electron microscope. The image is false colored purple.

CREDIT: ROBERT BRUCKER AND SETH BORDENSTEIN



Seth Bordenstein (right) and Robert Brucker, examining a bottle filled with *Nasonia* wasps.

CREDIT: ROBERT BRUCKER AND SETH BORDENSTEIN

Publications

Dobson SL, Bordenstein SR, Rose RI (2016) *Wolbachia* mosquito control: Regulated. *Science* 352(6285): 526–527

Kohl KD, et al. (2016) Physiological and microbial adjustments to diet quality permit facultative herbivory in an omnivorous lizard. *J Exp Biol* 219: 1903–1912

Shropshire JD, Bordenstein SR (2016) Speciation by symbiosis: The microbiome and behavior. *mBio* 7(2): e01785-15

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Newton ILG, et al. (2015) Comparative genomics of two closely related *Wolbachia* with different reproductive effects on hosts. *Genome Biol Evol* 8(5): 1526–1542

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Brucker RM, Bordenstein SR (2013) The hologenomic basis of speciation: Gut bacteria cause hybrid lethality in the genus *Nasonia*. *Science* 341: 667–669

Funkhouser LJ, Bordenstein SR (2013) Mom knows best: the universality of maternal microbial transmission. *PLoS Biol* 11: e1001631

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Brucker RM, et al. (2012): Insect innate immunity database (IIID): an annotation tool for identifying immune genes in insect genomes. *PloS ONE* 7: e45125

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

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Duke University
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^ Many of the fungi involved in ectomycorrhizal symbiosis produce conspicuous fruiting bodies, commonly known as mushrooms.

CREDIT: KABIR G. PEAY

Publications

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

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Santa Barbara
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Undergraduate research assistant maintains chemostats.

CREDIT: BRADLEY CARDINALE

Publications

Narwani, et al. (2017) Ecological interactions and coexistence are predicted by gene expression similarity in freshwater green algae. *J Ecol* 105(3): 580–591

Cardinale BJ, et al. (2015). Further re-analyses looking for effects of phylogenetic diversity on community biomass and stability. *Functional Ecology* 29(12): 1607–1610

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

(CO-FUNDED BY NSFC)

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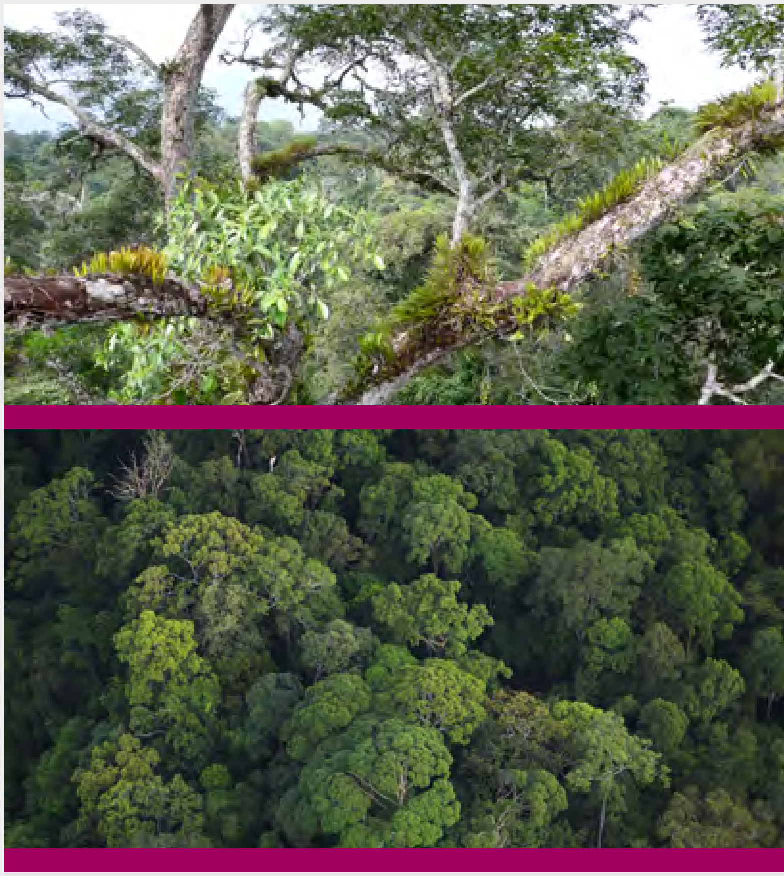
Keping Ma
Xiangcheng Mi
Institute of Botany, CAS

Wanhui Ye
South China Botanical Garden, CAS

Min Cao
Jie Li
Xishuangbanna Tropical Botanical Garden, CAS



^ *Top:* Research plot at Yasuni, Ecuador.
CREDIT: STUART DAVIES

Bottom: Canopy of the plot at Lambir, Malaysia.
CREDIT: CHRISTIAN ZIEGLER

Publications

Chang-Yang C-H, et al. (2016) ENSO and frost co-determine decade-long temporal variation in flower and seed production in a subtropical rain forest. *J Ecol* 104: 44–54

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Understory in the plot at Wabikon Lake Forest, USA.

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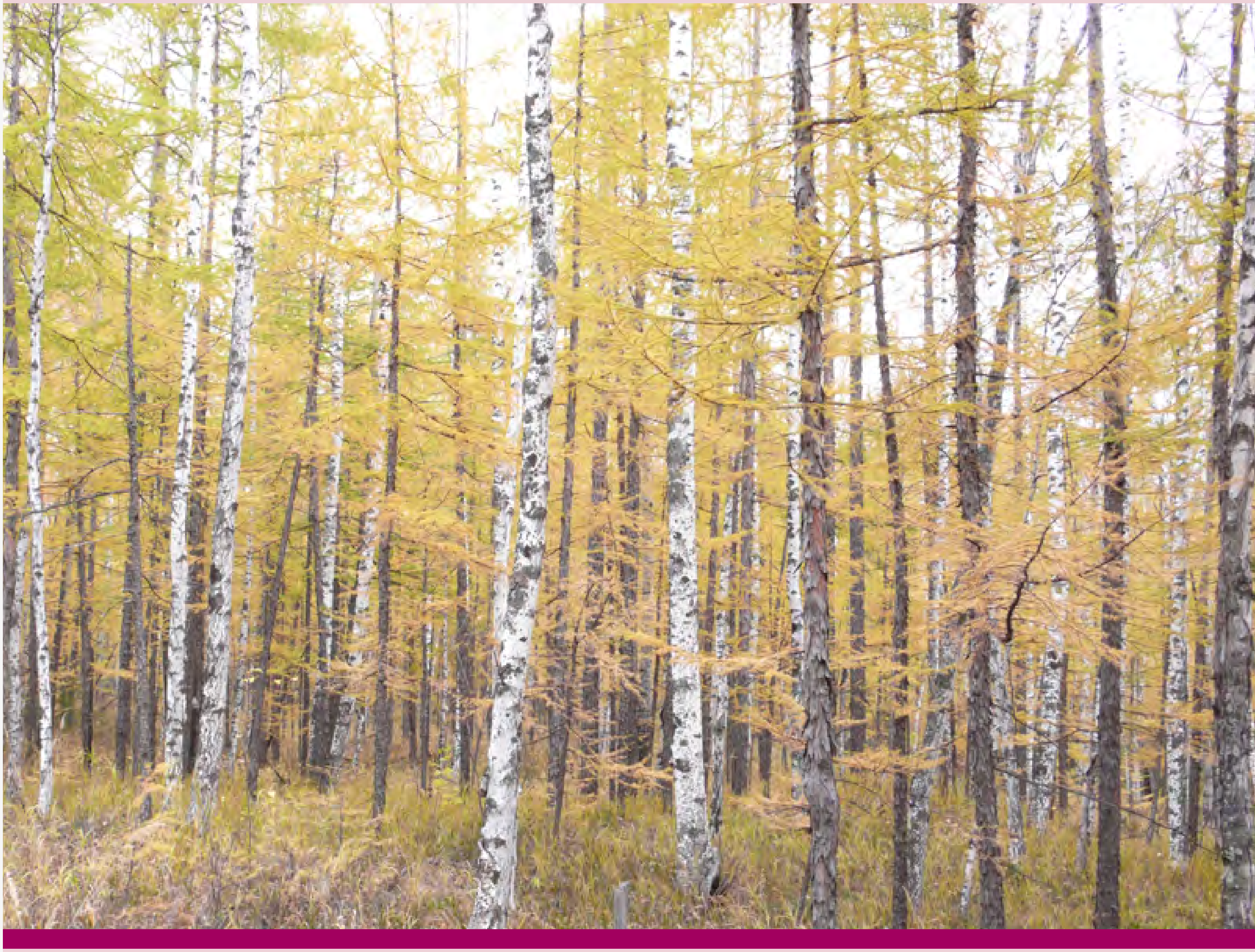

Research plot at Changbaishan, China.

CREDIT: STUART DAVIES

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^ Temperate Forest at CTFS plot in Changbaishan, China.

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Proj. 5 / 16

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

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

CREDIT: RICHARD LANKAU

Publications

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

CREDIT: ISTOCK

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

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University of Minnesota,
Twin Cities
(1045608)

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

CREDIT: A. ELIZABETH ARNOLD, UNIVERSITY OF ARIZONA

Publications

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Biological Controls on the Ocean C:N:P ratios

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

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Cruise picture taken close to the wreck of the RMS Titanic on September 2, 2013.

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

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Honeybee workers and queen on the hive (*Apis mellifera*).
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Honey bee queen being tended by her workers on the comb.

CREDIT: WALDAN KWONG, YALE UNIVERSITY

Bombus impatiens individual foraging on flowers.

CREDIT: NANCY MORAN

Dimensions of Biodiversity Distributed Graduate Seminar

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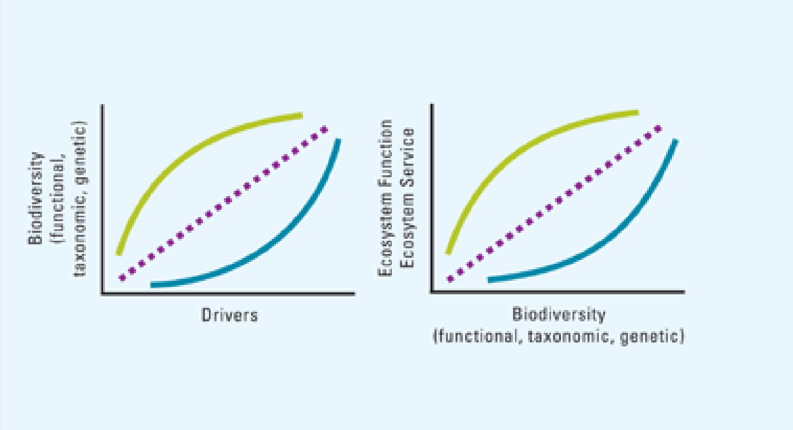

DBDGS teams addressed one of two broad framing questions:
1) What forces create/maintain biodiversity pattern, and
2) What patterns of system function, service, or even associated human well-being does biodiversity drive?

CREDIT: CATHY SCHWARTZ

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

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

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

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

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Acropora corals.
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Publications

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

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^ *Pelargonium sericifolium.*
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^ *Pelargonium peltatum*.

CREDIT: CARL D. SCHLICHTING

Significance of nitrification in shaping planktonic biodiversity in the ocean

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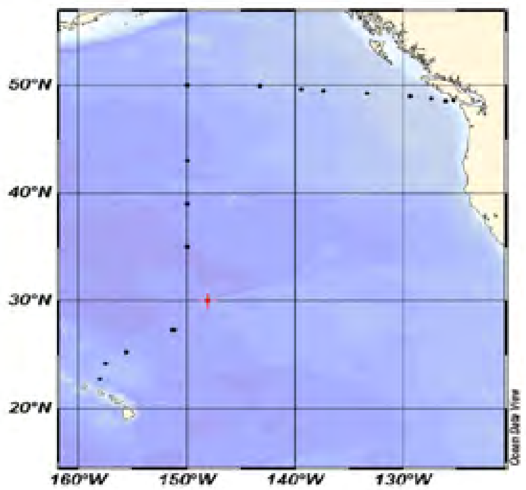

^ Research stations sampled for analyses of biological and chemical controls of nitrogen form and availability. Research conducted in August 2013 on the Kilo Moana.

CREDIT: ANITRA INGALLS AND DAVID STAHL

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The role of viruses in structuring biodiversity in methanotrophic marine ecosystems

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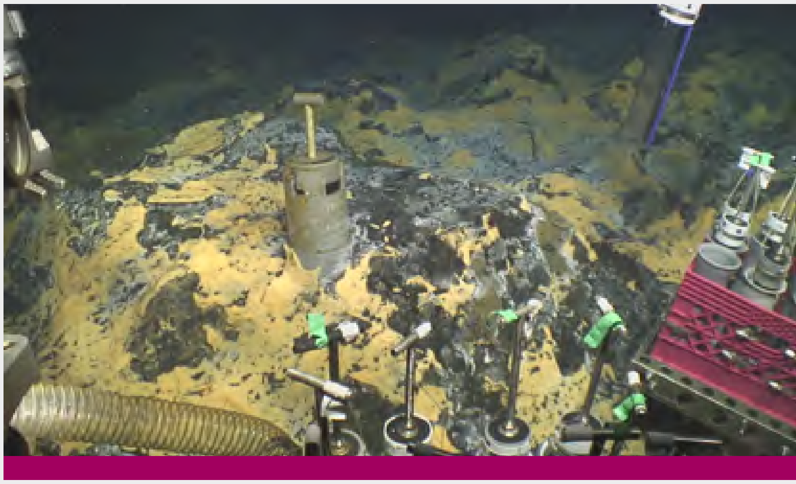

An incubator as first seen on the return to a second study site in 2013, showing substantial growth of microbial mats on the outer surfaces.

CREDIT: DAVID VALENTINE

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

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

CREDIT: GREGORY SONNIER, UNIVERSITY OF WISCONSIN, MADISON

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Dimensions of Biodiversity

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