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.

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

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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

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<th>STREAMS OF ACTIVITY</th>
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<td>An integrated understanding of the key but unknown dimensions of biodiversity on earth</td>
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<td>Cyberinfrastructure</td>
<td>Informatics and infrastructure that support accessible, interoperable information capability for dimensions of biodiversity</td>
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<td>Collections</td>
<td>Digitization of collections and enhanced physical infrastructure to link to cyberinfrastructure and leverage the enormous investments of the past</td>
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<td>Workforce</td>
<td>A diverse, interdisciplinary, globally-engaged, scientific workforce capable of transforming and communicating our understanding of biodiversity on Earth</td>
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<tr>
<td>Synthesis</td>
<td>Scientific analyses and syntheses that generate and disseminate useful information for scientists, educators, decision makers and the public</td>
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<th>APPROACH</th>
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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.

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
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...

DATABASE & CYBERINFRASTRUCTURE

Through Dimensions, projects are connected with...
UNDERGRADUATE & GRADUATE EDUCATION

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

Microbiomes
Symbioses

Fungi
Genomics

Extinction Risk
Phytoplankton

Deep Shale
Nutrient Ratios

Herbaria
Copepods

Oxygen Minimum Zone

Nutrient Cycling
Dry Valleys

K-12 EDUCATION

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

The Pacific Northwest
Avian Malaria
Drought Tolerance

Color Pattern Divergence
Microbial Sciences
Trophic Interactions

Elevation Ranges
Plant Mating Systems
Soil Organic Matter

Wild Nightshades
Adaptive Radiation
Nitrogen Cycling

Mathematical Modeling
Video Game Design

Weather Station Data
Genetic Architecture
Diversification of sensory systems in novel habitat: Enhanced vision or compensation in other modalities?

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

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

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

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

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

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

Secondary metabolites as drivers of fungal endophyte community diversity

Desiccation and diversity in dryland mosses

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

Functional and genomic diversity in vitamin B1 metabolism and impacts on plankton networks and productivity
2016 abstracts
Diversification of sensory systems in novel habitat: Enhanced vision or compensation in other modalities?

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

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

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)

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 conceptual diagram showing diapausing flies and diapausing wasps on the left, and developing flies and wasps on the right. The timing of diapause 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
US-BIOTA-Sao Paulo: Scales of biodiversity — Integrated studies of snake venom evolution and function across multiple levels of diversity

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.

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

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*

A Melissa blue caterpillar feeding on alfalfa near Victor, ID while being tended by beneficial ants.
*CREDIT: LAUREN LUCAS, UTAH STATE UNIVERSITY*

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*

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

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

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 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.

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

High density of the giant barrel sponge *Xestospongia muta*, among other sponges, on 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
Genetic, functional, and phylogenetic diversity determines marine phytoplankton community responses to changing temperature and nutrients

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

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.

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.

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 amphibiocot stoneflies can be collected from one well.  

*CREDIT: JACK A. STANFORD AND AMANDA DELVECCHIA*

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*

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

*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*
Secondary metabolites as drivers of fungal endophyte community diversity

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
This research will investigate the links between the genes, physiology, life stages, populations, and communities of Syntrichia mosses that have facilitated 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 desiccation 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
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 diversity 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
Functional and genomic diversity in vitamin B₁ metabolism and impacts on plankton networks and productivity

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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 B₁ (thiamin) by planktonic cells at the base of the ocean food chain. Although it was once thought that all organisms either synthesize vitamin B₁, or obtain it from their environment, recent discoveries have revealed complex trafficking in B₁ components between cells, which can then be assembled to make complete vitamin B₁ 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 B₁ (thiamin pyrophosphate, TPP) use different enzymes at several steps. Some marine phytoplankton take up B₁ 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 B₁ 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 DESCOITRES, 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
Diversification dynamics of multitrophic interactions in tropical communities

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This project focuses on a species-rich tropical community of plants (Cucurbitaceae), tropical plant-feeding insects, and their predators (parasitic wasps). 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)
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.

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.

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

<table>
<thead>
<tr>
<th>Steven H. Haddock</th>
<th>Monterey Bay Aquarium Research Institute (1542679)</th>
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<tr>
<td>Joseph F. Ryan</td>
<td>University of Florida (1542597)</td>
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<tr>
<td>Erik V. Thuesen</td>
<td>Evergreen State College (1542673)</td>
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**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.

**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.

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*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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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**


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*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.

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

CREDITS: LENA C. HILEMAN (TOP) AND CAROLYN WESSINGER (BOTTOM)
Biodiversity gradients in obligate symbiotic organisms: A case study in lichens in a global diversity hotspot

**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.

**Publications**


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*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*

*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

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 \( ^{15}\text{N} - ^{13}\text{CH}_4 \) 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

**US TEAM**

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**CHINA TEAM**

Jianquan Liu  
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**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**


*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

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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.

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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(1542240)

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

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 accessible 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.

Publications


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

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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Niklaus Grünwald  
USDA-ARS  
James Lutz  
Utah State University  
Margaret R. Metz  
Lewis & Clark College  
David K. Oline  
Southern Oregon University  

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 participated 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

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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


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

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

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

CREDIT: ALEKA SADIER, UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN
US-BIOTA-São Paulo: Chemically mediated multi-trophic interaction diversity across tropical gradients
(CO-FUNDED WITH FAPESP)

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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.

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.

Publications


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

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


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 15N₂ labeling of pine foliage.

**Publications**


The making of biodiversity across the yeast subphylum

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University of Wisconsin, Madison  
Cletus Kurtzman  
USDA

Antonis Rokas  
Vanderbilt University

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

**Update**

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**


**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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University of Texas, Austin

Katia Silvera  
University of California, Riverside

Victor Albert  
State University of New York, Buffalo (1442190)

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 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.

Publications


Oncidium sotoanum (left) and Oncidium sphacelatum (right). Both are epiphytic C₃ species.  
CREDIT: KATIA SILVERA

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

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Kenneth Locey
Indiana University
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Stuart Jones
University of Notre Dame
(1442230)

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

Update

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

Publications


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


Bacteria cultured from an agricultural soil sample.

CREDIT: JAY T. LENNON
Identifying how the ecological and evolutionary interactions between host and symbiont shape holobiont biodiversity

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George Washington University  
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Drexel University  
(1442144)

John Wertz  
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(1442156)

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


*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*

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

(CO-FUNDED WITH FAPESP)

US TEAM

<table>
<thead>
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<tbody>
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BRAZIL TEAM

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<th>Institution</th>
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<td>Dernando Andreote</td>
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<td>Plinio Camargo</td>
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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.

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.

Publications

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.

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

View from Pickens Nose, Coweeta Hydrologic Lab, Coweeta, North Carolina.
CREDIT: MARK WHITTEN, FLORIDA MUSEUM OF NATURAL HISTORY

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

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.

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.

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


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

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Denise M. Dearing
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US-BIOTA-São Paulo: Improving biodiversity prediction in the Atlantic rainforest

(CO-FUNDED WITH FAPESP)

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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.

Publications


Our team searches for rare endemic plants at the top of the Parque Nacional da Serra dos Órgãos, in Eastern Brazil.

CREDIT: FABIAN A. MICHELANGELI

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.

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


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


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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.

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.

Publications


Experimental adaptive radiation—genomics of diversification in bird lice

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(1342600)

Kevin P. Johnson
University of Illinois,
Urbana-Champaign
(1342604)

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

Update

A reference genome for the pigeon louse Columbicola columbae has been sequenced, and 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 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

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

CREDIT: SCOTT M. VILLA, UNIVERSITY OF UTAH

Publications


Biodiversity of the gut microbiome of herbivorous rodents

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

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.

Publications


Top: An image of the White-throated Woodrat, Neotoma albignula. 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
Functional diversity of chemosymbiosis in lucinid bivalves from coastal biomes

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Laurie C. Anderson  
South Dakota School of Mines and Technology  
(1342721)

Barbara J. Campbell  
Clemson University  
(1342763)

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 anthropogenically-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


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.

Publications


Mohapatra BR, et al. (2016) Comparative proteomics of temperate and polar Phaeocystis species. Nova Hedvégia 103: 3-4


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

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.

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.

Publications


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


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

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

CREDIT: MICHAEL D. JOHNSTON, OHIO STATE UNIVERSITY

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

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


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.

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.

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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.

Publications


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. primivers is one of 16 taxa where we have measured intraspecific floral trait variation in relation to biotic interactions.

CREDIT: TANIA JOGESH, CHICAGO BOTANIC GARDEN

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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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


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*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.

Publications


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

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

CREDIT: JOE CRAINE, KANSAS STATE UNIVERSITY
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


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)


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

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US-China: An integrated understanding of how polyploidy generates biodiversity
(CO-FUNDED WITH NSFC)

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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.

Update
The team extended their elucidation of polyploidization history in Fragaria to the decaploid (2n=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


 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.

Publications


6 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

(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.

Publications


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


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
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.

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.

Publications


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

Angela E. Douglas

Gregory Loeb

Cornell University (1241099)

John Jaenike

University of Rochester (1241099)

**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**


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.

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


Top: Spores of the ascomycete fungus *Dictyosporum* 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


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


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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(1241031)

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.

Publication


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: 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

Konstantinos Konstantinidis
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Georgia Institute of Technology (1241046)

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.

Publications


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

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.

Publications


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


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

CREDIT: THOMAS E. MARTIN
Anthropogenic nutrient input drives genetic, functional and taxonomic biodiversity in hypereutrophic Lake Taihu, China

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

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

Publications


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

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.

**US TEAM**
Nathan Swenson
University of Maryland, College Park
(1643052)

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

**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 biodiversity 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**

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

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 adaptations 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

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

Lisa Belden
Roderick Jensen
Leanna House
Virginia Polytechnic Institute and State University (1136640)

Reid Harris
James Madison University (1136602)

Kevin Minbiole
Villanova University (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. (2016) Skin bacterial diversity of Panamanian frogs is associated with host susceptibility and presence of *Batrachochytrium dendrobatidis*. *ISME J* 10: 1682


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

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.

**US TEAM**

<table>
<thead>
<tr>
<th>Name</th>
<th>Institution</th>
<th>Code</th>
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<td>Chris Lobban</td>
<td>University of Guam</td>
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**CHINA TEAM**

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<th>Name</th>
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<td>Weibo Song</td>
<td>Ocean University of China Qingdao</td>
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**OTHER COUNTRIES**

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<th>Name</th>
<th>Institution</th>
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<td>Micah Dunthorn</td>
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<td>Laura Utz</td>
<td>Pontificia Universidade Católica do Rio Grande do Sul Brazil</td>
</tr>
<tr>
<td>Alan Warren</td>
<td>Natural History Museum London, United Kingdom</td>
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</table>

**Publications**


**Images**

- Acineta tuberosa. *CREDIT: JOHN CLAMP*
- Diophysys sp, a hypotrich. *CREDIT: JOHN CLAMP*
Pattern and process in marine bacterial, archael, and protistan biodiversity, and effects of human impacts

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

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.

Publications


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


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

Stephen Hubbell
Smithsonian Institution

Travis C. Glenn
University of Georgia

Gregory S. Gilbert
University of California, Santa Cruz

Brant C. Faircloth
University of California, Los Angeles

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


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


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**


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

<table>
<thead>
<tr>
<th>Name</th>
<th>Affiliation</th>
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<tbody>
<tr>
<td>Elena G. Litchman</td>
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<td>Christopher A. Klausmeier</td>
<td>East Tennessee State University</td>
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<td>Edward C. Theriot</td>
<td>University of California, Santa Barbara</td>
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<tr>
<td>Stephanie E. Hampton</td>
<td>Wellesley College</td>
</tr>
<tr>
<td>Lev Yampolsky</td>
<td>Michigan State University</td>
</tr>
</tbody>
</table>

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**


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

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


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*

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

Nathan Sanders
University of Tennessee, Knoxville
(1136703)

Aaron Ellison
Harvard University
(1136646)

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

Robert Dunn
North Carolina State University
(1136717)

Publications


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


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.

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 m² atmospheric warming chamber in situ at the Harvard Forest.

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

Stefan Sievert
Jeffrey Seewald
Craig Taylor
Woods Hole Oceanographic Institution (1136727)

Costantino Vetriani
Rutgers University
New Brunswick (1136451)

Ramunas Stepanauskas
Bigelow Laboratory for Ocean Sciences (1136488)

Dionysios I. Foustoukos
Carnegie Institution of Washington (1136608)

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


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

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

Bess Ward
Daniel Sigman
Princeton University (1136345)

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.

Publication

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

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**

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

Seth Bordenstein
Vanderbilt University
(1046149)

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


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

Thomas Bruns
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University of California, Berkeley
(1046115)

Kabir G. Peay
Stanford University
(1249341)

Rytas Vilgalys
Duke University
(1046052)

Many of the fungi involved in ectomycorrhizal symbiosis produce conspicuous fruiting bodies, commonly known as mushrooms. CREDIT: KABIR G. PEAY

Publications


Peay KG, Bruns TD (2014) Spore dispersal of fungi at the landscape scale is driven by stochastic and deterministic processes and generates variability in plant-fungal interactions. New Phytol 204: 180–191


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

**Bradley Cardinale**  
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**Charles F. Delwiche**  
University of Maryland,  
College Park  
(1046075)

**Todd H. Oakley**  
University of California,  
Santa Barbara  
(1046307)

**Publications**

- Cardinale BJ, et al. (2013) Primary producer diversity simultaneously increase the productivity and stability of ecosystems, but the effects are independent. *Ecology* 94: 1697–1707
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
Min Cao
Xiangcheng Mi
Institute of Botany, CAS

Publications


Gonzalez-Akre E, et al. (2016) Patterns of tree mortality in a temperate deciduous forest derived from a large forest dynamics plot. Ecosphere 7: e01595


Lebrija-Trejos E, et al. (2016) Species with greater seed mass are more tolerant of conspecific neighbours: a key driver of early survival and future abundances in a tropical forest Ecol Lett 19: 1071


Top: Research plot at Yasuni, Ecuador.
CREDIT: STUART DAVIES
Bottom: Canopy of the plot at Lambir, Malaysia.
CREDIT: CHRISTIAN ZIEGLER

Memiaghe HR, et al. (2016) Ecological importance of small-diameter trees to the structure, diversity and biomass of a tropical evergreen forest at Rabi, Gabon. *PloS ONE* e0154988


Yuan Z, et al. (2016) Multiple metrics of diversity have different effects on temperate forest functioning over succession. Oecologia 182: 1175–1185


Hu YH, et al. (2014) Size-class effect contributes to tree species assembly through influencing dispersal in tropical forests. *PloS ONE* e108450

Huang, J., et al. (2014) Different relationships between temporal phylogenetic turnover and phylogenetic similarity in two forests were detected by a new null model. *PloS ONE* 9: e95703


Mi X, et al. (2014) Point process models, the dimensions of biodiversity and the importance of small-scale biotic interactions. *J Plant Ecol* 7: 126–133


Wang Q, et al. (2014) Species associations in a species-rich subtropical forest were not well-explained by stochastic geometry of biodiversity. *PloS ONE* 9: e97300


Research plot at Changbaishan, China.

CREDIT: STUART DAVIES

Chen YA (2013) Multiscale variation partitioning procedure for assessing the influence of dispersal limitation on species rarity and distribution aggregation in the 50-ha tree plots of Barro Colorado Island, Panama. *Chen J Ecosys Ecograph* 3: 1000134


Swenson NG (2012) The functional ecology and diversity of tropical tree assemblages through space and time: from local to regional and from traits to transcriptomes. *ISRN Forestry* doi: 10.5402/2012/743617


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

Richard Lankau
University of Wisconsin, Madison
(1552412)

**Publications**


Lankau RA, Keymer DP (2016) Ectomycorrhizal fungal richness and community consistency decline toward the host species’ range edge. *Molec Ecol* 25: 3224


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

Carol Lee
University of Wisconsin, Madison
(1046372)

Joana Carneiro da Silva
University of Maryland, Baltimore
(1046371)

**Publications**


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

François Lutzoni  
Duke University  
(1046065)

Ignazio Carbone  
North Carolina State University  
(1046167)

Georgiana May  
University of Minnesota, Twin Cities  
(1045608)

Anne Arnold  
University of Arizona  
(1045766)

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Publications


David AS, et al. (2016) Beachgrass invasion in coastal dunes is mediated by soil microbes and lack of disturbance dependence. *Ecosphere* 7(11) e01527


Bruns E, et al. (2014) The jack-of-all-trades is master of none: a pathogen’s ability to infect a greater number of host genotypes comes at a cost of delayed reproduction. *Evolution* 68: 2453-2466


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Boreal lichens harbor a diverse array of secondary fungi (Endolichenic fungi).  
CREDIT: A. ELIZABETH ARNOLD, UNIVERSITY OF ARIZONA
Biological Controls on the Ocean C:N:P ratios

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University of California, Irvine  
(1046297)

Benjamin Van Mooy  
Woods Hole Oceanographic Institution  
(1032877)

Simon Levin  
Princeton University  
(1046001)

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Michael Lomas  
Bigelow Laboratory for Ocean Sciences  
(1303287)

Benjamin Van Mooy  
Woods Hole Oceanographic Institution  
(1303287)

Publications


Martin P, et al. (2014) Marine microbial response to low phosphorus results in accumulation and enhanced cycling of polyphosphate in the Sargasso Sea. PNAS 111: 8089


Cruise picture taken close to the wreck of the RMS Titanic on September 2, 2013. CREDIT: CELINE MOUGINOT, UNIVERSITY OF CALIFORNIA, IRVINE
Genomics, functional roles, and diversity of the symbiotic gut microbiota of honey bees and bumble bees

Nancy Moran  
University of Texas, Austin  
(1415604)

Jay Evans  
USDA Agricultural Research Service Beltsville Area  
(1046153)

Publications


Schwarz RS, Moran NA, Evans JD (2016) Early gut colonizers shape parasite susceptibility and microbiota composition in honey bee workers. PNAS 113(33): 9345–9350


Tian B, Moran NA (2016) Genome sequence of Hafnia alvei bta3_1, a bacterium with antimicrobial properties isolated from honey bee gut. Genome Announce 4(2): e00439–16


Cariveau DP, et al. (2014) Variation in gut microbial communities and its association with pathogen infection in wild bumble bees (Bombus) ISME J 8: 2369–2379


Kwong W, et al. (2014) Genomics and host specialization of honey bee and bumble bee gut symbionts. PNAS 111: 11509

Li JL, et al. (2014) Systemic spread and propagation of a plant-pathogenic virus in European honeybees, Apis mellifera. mBio 5: e00898–13


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**Image A:** Honey bee queen being tended by her workers on the comb.
*Credit: Waldan Kwong, Yale University*

**Image B:** *Bombus impatiens* individual foraging on flowers.
*Credit: Nancy Moran*
Dimensions of Biodiversity Distributed Graduate Seminar

Julia Parrish
University of Washington (1050680)

Publications


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

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

Steven Thomas  
University of Nebraska, Lincoln (1045991)  

Alexander Flecker  
Joseph Bernardo  
Kelly Zamudio  
Cornell University (1045960)  

Publications


Students on their way to sample aquatic insects in streams in the Colorado Front Range for the ECOTRAC project.  
CREDIT: KELLY ZAMUDIO
Shedding light on viral dark matter—genetic, taxonomic, and functional diversity of coral reef viromes

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

Publications


Aziz RK, et al. (2012) SEED servers: high-performance access to the SEED genomes, annotations, and metabolic models. Plos ONE 7: e48053


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

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

**Andrew Latimer**  
University of California, Davis (1045985)

**Justin O. Borevitz**  
Australian National University (1242294)

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**Publications**


Significance of nitrification in shaping planktonic biodiversity in the ocean

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

James Moffett
University of Southern California
(1046098)

Publications


Amin SA, et al. (2013) Copper requirements of the ammonia-oxidizing archaean Nitrosopumilus maritimus SCM1 and implications for nitrification in the marine environment. Limnol Oceanogr 58: 2037


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
The role of viruses in structuring biodiversity in methanotrophic marine ecosystems

David Valentine
University of California, Santa Barbara
(1046144)

Publications


Handa S, et al. (2016) Conservation of the C-type lectin fold for accommodating massive sequence variation in archaeal diversity-generating retroelements. BMC Structural Biol 16


Valentine DL, et al. (2014) Fallout plume of submerged oil from Deepwater Horizon. PNAS 111: 15906-15911

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

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

Publications


Alstad AO, et al. (2016) The pace of plant community change is accelerating in remnant prairies. *Sci Comm* 2 e1500975


Spalink D, et al. (2016) Biogeography of the cosmopolitan sedges (Cyperaceae) and the area-richness correlation in plants. *J Biogeogr* 43(10): 1893–1904


