Dimensions of Biodiversity

NATIONAL SCIENCE FOUNDATION

2010 — 2013
PROJECTS

CO-FUNDED BY

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ACKNOWLEDGEMENTS

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. Finally, we are grateful to AAAS Science and Technology Policy Fellows Dr. Sara Chun, Dr. Sean M. Watts, and Dr. Karen Alroy, all of whom were most helpful in strategic planning for Dimensions of Biodiversity and the production of this abstract booklet.

INTERNATIONAL PARTNERS

China
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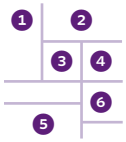


FRONT COVER IMAGES & CREDIT

1 A male *Adelpha capucinus*. Keith Willmott, University of Florida.

2 The island of Mecherchar in the southern Palau lagoon. Patrick L. Colin, Coral Reef Research Foundation.

3 A dissected gut from an individual *Drosophila melanogaster*. Angela Douglas, Cornell University.

4 *Oenothera harringtonii*. Krissa Skogen, Chicago Botanic Garden.

5 *Crotaphytus collaris*, Eastern Collared Lizard. Geoffrey A. Hammerson, NatureServe.

6 *Acineta tuberosa*. John C. Clamp, Department of Biology, North Carolina Central University.

Earth is losing species more rapidly than scientists can understand the roles they play and how they function. With this species loss, humanity is forfeiting opportunities to understand the history of life, to better predict the future of the living world, and to make beneficial discoveries in the domains of food, fiber, fuel, pharmaceuticals, and bio-inspired innovation.

Dimensions of Biodiversity

The National Science Foundation (NSF) is now in the fifth year of the 10-year Dimensions of Biodiversity program to characterize the least-well-known aspects of the diversity of life on Earth. NSF funded 13 new projects in FY 2013 bringing the total number of funded projects to 55.

Identifying species is just a first step in the journey of assessing the planet's biological diversity, but for many organisms even this step is far from complete. For example, insects are among the most diverse organisms and the total number of named, living insect species is estimated at 720,000. However, this represents as little as 7% of our 'best guesses' of insect diversity (4-10 million species)[1]. Furthermore, all species rely on a vast network of mostly invisible and largely unknown life forms (bacteria, fungi, etc.), that far outnumber the more obvious organisms on the planet in both abundance and diversity. Beyond taxonomy, the genetic diversity within even a single species can be vast. The tremendous variation among domestic dog breeds illustrates this, and the genetic diversity within crop plants continues to play a critical role in their resilience and durability. Finally, species and genetic diversity are best understood in a phylogenetic context and reflect how the functional dimension is shaped. This is true for ecological, physiological, behavioral, cellular and even molecular patterns and processes. Despite centuries of study, we still have much to learn about the origin and maintenance of diversity.

The innovative and interdisciplinary teams of the Dimensions of Biodiversity program "may accomplish in 10 years what, with a piecemeal approach, would have taken 50 years—a half century we can no longer afford to wait."

Dr. Joann P. Roskoski
NSF Deputy Assistant Director for Biological Sciences

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

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

"By establishing durable networks of interdisciplinary, globally-engaged scientists, the Dimensions of Biodiversity program will have a lasting positive effect on biodiversity science, with the potential to transform the way we conduct biological research in this area."

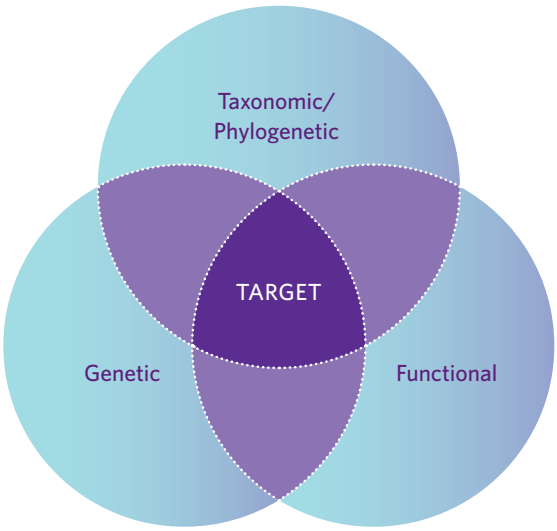
Dr. John C. Wingfield
NSF Assistant Director for Biological Sciences

Addressing the substantial knowledge gaps in our understanding of biodiversity requires new thinking and a coordinated effort among several sub-disciplines of biology. An important distinction the Dimensions initiative provides is the simultaneous investigation of the links and feedbacks between genetic, taxonomic/phylogenetic, and functional dimensions of biodiversity. 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 has previously partnered with NASA to fund projects that use remote sensing technologies to expand biodiversity investigations across broad spatial and temporal scales. International partnerships with the Chinese National Natural Science Foundation (NSFC) and the Brazilian funding agency [The São Paulo Research Foundation (FAPESP)] support the exchange of students and scientists, joint research projects, university partnerships and the digitization of biological collections.

Improving how we describe the scope and role of life on Earth will require novel, interdisciplinary and coordinated approaches. In rising to this challenge, Dimensions of Biodiversity is redefining the way we understand the evolutionary and ecological significance of biodiversity in today's changing environment, and in the geologic past.

Dimensions of Biodiversity involves five streams of activity. The approach for supporting these activities involves planning and partnering, developing baselines of our current understanding, and assessing progress periodically during the decade in order to align investments with newly-appreciated priorities.

By 2020, Dimensions of Biodiversity is expected to have transformed our understanding of the scope and role of life on Earth and how biodiversity science is conducted. The initial focus of Dimensions has been on the integration of genetic, taxonomic/phylogenetic, and functional aspects of biodiversity (below). The goal of this activity, which complements core programs at NSF, is to rapidly integrate the dimensions of biodiversity about which we know the least.



FY 2010	FY 2011	FY 2012	FY 2013	FY 2014
16 projects	12 projects	14 projects	13 projects	Partners
US Total ~$25.7M	US Total ~$28.0M	US Total ~$26.4M	US Total ~$25.1M	
BIO $18.9M	BIO $17.5M	BIO $21M	BIO $21.7M	
Other NSF $6.8M	Other NSF $10.5M	Other NSF $4.7M	Other NSF $1.0M	
		NASA $720K	NASA $2.5M	
NSFC ¥750K	NSFC ¥610K	NSFC ¥6M	NSFC ¥3M	NSFC Up to ¥6M
		FAPESP-São Paulo $20.8K	FAPESP-São Paulo $1.2M	FAPESP-São Paulo Up to $4M

[1] Finlay, Bland J., et al. "Self-similar patterns of nature: insect diversity at local to global scales." *Proceedings of the Royal Society B: Biological Sciences* 273.1596 (2006): 1935-1941.

A multidisciplinary framework for biodiversity prediction in the Brazilian Atlantic forest hotspot

(CO-FUNDED WITH NASA AND FAPESP)

US MEMBERS

Ana Carnaval
Michael Hickerson
Kyle Mcdonald
CUNY City College
(NSF 1343578)

Fabian Michelangeli
William Thomas
New York Botanical Garden
(NSF 1343612)

BRAZIL MEMBERS

Cristina Yumi Miyaki
Ricardo Pinto-da-Rocha
Francisco Cruz
Universidade de Sao Paulo

This project aims to develop a framework for predicting spatial patterns of biodiversity in the highly diverse environment of the Brazilian Atlantic Forest. This model will be constructed by integrating numerous types of data including remote sensing, meteorological, locality, phylogenetic, functional, biotic interaction and paleoenvironmental data.

The study of the geographic distribution of biological diversity, also known as biogeography, has strong links with the field of evolutionary biology. Building on the legacies of Charles Darwin and Alfred Wallace, evolutionary biogeographers combine observations of natural habitats with information about the history of local organisms to understand how evolution (descent with modification) interacts with environmental variation to determine how biological diversity is distributed in geographical space. Today, perhaps more than ever, science must integrate these disciplines to understand biodiversity in light of rapid global environmental change.

This research develops a broad interdisciplinary framework to explain and predict the distribution of animal and plant species in an endangered yet megadiverse tropical forest, the Brazilian Atlantic forest. In pre-Columbian times, the Atlantic forest extended for 3000 km, forming a fringe of forests sandwiched between the Atlantic Ocean and the drier uplands of the Brazilian shield. Today, the forest is reduced to less than 11% of its historical range, yet its fragments harbor one of the largest percentages of endemic species in the world. These are species that can be found nowhere else on Earth.

By studying the Atlantic forest climate and landscape and their changes over the last 120,000 years, our international team will understand how forest species have responded to repeated environmental shifts of the past. Data from Earth-orbiting satellites will be combined with meteorological data and information about former climates based on the fossil pollen record and on the geochemistry of deposits, such as stalagmites found in caves. These results will be integrated with information on the ranges of modern species, their genetic diversity, physiological tolerances and interactions with pathogens, and observed shifts in the composition of natural communities, to demonstrate how changes in climate and landscape have shaped patterns of biodiversity of the entire Atlantic forest biome. Targeted groups include flowering plants, frogs (and the diverse bacteria living on their skin), lizards, birds and their pathogens, as well as invertebrate species such as the spider relative, harvestmen.

This study will enable the reconstruction of historical factors influencing current biodiversity in three different dimensions (genetic, taxonomic and functional) and, given a range of climate change scenarios, permit the prediction of the future composition of biodiversity in the Atlantic forest. Forest areas of geological and climatic stability, physical connectivity, and higher genetic diversity will be identified, so that forests or species under extinction threat can be conserved. In response to current concern about the value of ecosystem services and climate change, this study provides a model of how to predict biodiversity change – in Brazil and beyond.

1 *Mitopernoides variabilis* is a species of harvestman from the Brazilian Atlantic forest.

2 Flowers of the tree *Caesalpinia echinata* (Pau-brasil, Brazilwood, Pernambuco), the national tree of Brazil, endangered, and endemic to the Atlantic forest.

3 Waterfall, Atlantic Rainforest of Brazil, Ribeira River Valley.

4 Stalagmite from Rei do Mato Cave, located in the center of Minas Gerais states, Southeastern Brazil.

5 This lizard, *Anolis punctatus*, occurs both in the Atlantic forests and Amazonia. By studying the distribution of genetic diversity within this anole, we will be able to better understand the former connections between these two South American forest systems.

6 This liana, *Dolichoura espiritusanctensis* (Melastomataceae) is a member of a group with elaborate anther appendages that is restricted to the Atlantic forest. Its closest relatives, however, are found more than 2,000 miles away in the Central Andes. Groups like this will be targeted by our work to understand the patterns of plant and animal distributions in Eastern Brazil.

7 View of the Bahia sub-montane forests, taken from the privately owned Serra Bonita reserve.

CREDIT: 1 R. PINTO-DA-ROCHA, UNIVERSIDADE DE SAO PAULO, 2 WAYT, THOMAS, NEW YORK BOTANICAL GARDEN , 3 CARLOS GROHMANN, UNIVERSITY OF SAO PAULO 4 NICOLAS MISAILIDIS STRIKIS, UNIVERSITY OF SAO PAULO, 5 7 MAURO TEIZEIRA JR, USP, 6 FABIAN A. MICHELANGELI, THE NEW YORK BOTANICAL GARDEN

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

(CO-FUNDED WITH NASA)

Jeannine Cavender-Bares
Sarah Hobbie
Rebecca Montgomery
University of Minnesota
Twin Cities
(NSF 1342872)

Michael Madritch
Appalachian State University
(NSF 1342827)

Philip Townsend
Richard Lindroth
University of Wisconsin
Madison
(NSF 1342778)

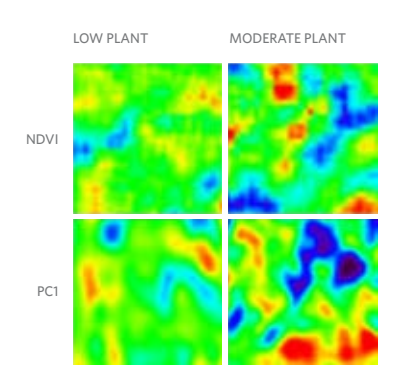
Arthur Zygielbaum
John Gamon
University of Nebraska
Lincoln
(NSF 1342823)

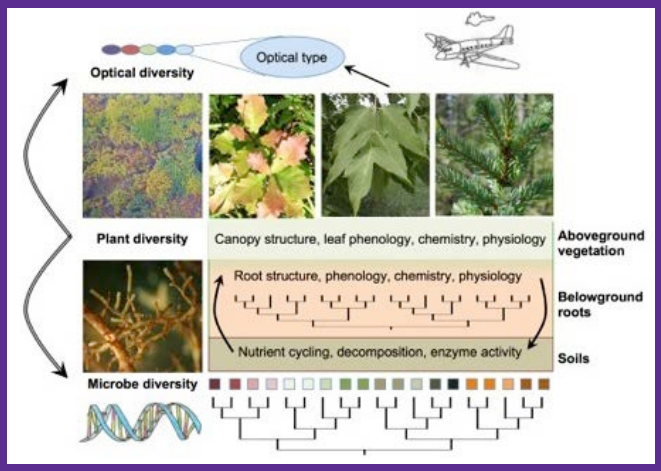
In this project, novel remote sensing methods for monitoring the Earth's biodiversity will be applied to experimental manipulations of plant diversity—allowing scientists to examine the linkages between plant biodiversity, soil microbe diversity and ecosystem function at multiple scales of spatial resolution.

Monitoring biodiversity and understanding its importance for ecosystem processes at regional and global scales are critical challenges, particularly in the face of rapid global change. Measurements of biodiversity are constrained, however, by limited physical and financial resources. Developing less expensive methods to assess biodiversity across multiple spatial and temporal scales will significantly advance biodiversity research. Aerial and space-borne remote sensing offers promise in this regard. Plants display themselves towards the sky in contrasting ways based on their evolutionary history, genetic and chemical composition, form, and phenology, and in the nature of their interactions with the environment. Differences among plants in these aspects can be detected by optical sampling, allowing remote sensing to assess diversity. Project scientists from four institutions, including the University of Minnesota, the University of Wisconsin, the University of Nebraska-Lincoln and Appalachian State University will apply novel methods to test the nature of linkages between plant biodiversity, soil microbe diversity and ecosystem function.

At the Cedar Creek Ecosystem Science Reserve, scientists will use three biodiversity manipulations that vary—genotypes within species, species with different functions and responses to resources, and species from different evolutionary lineages—to test whether these kinds of diversity, and their ecosystem consequences, can be detected and measured remotely at multiple spatial scales. These efforts will serve in the development of airborne and satellite platforms that can routinely and reliably monitor biodiversity. Because evolutionary relationships are best described by genetic sequences, next-generation sequencing technologies will be used to describe both plant and soil microbe diversity. Measuring diversity in multiple ways both above and below ground will allow project scientists to examine the evidence for the concept of surrogacy, such that one metric of biodiversity can be used to provide information about others. To assess how well remotely sensed biodiversity measures can predict ecosystem function, field measurements and controlled laboratory mesocosm studies will be combined to determine rates of decomposition, nitrogen cycling, and plant productivity under varying levels of diversity.

Ultimately, the project seeks to transform methods for detecting changes in biodiversity worldwide and will improve understanding of the linkages between biodiversity and the functional services provided by Earth's ecosystems. The project will provide numerous training opportunities in science, technology and math for young scientists. Results will be integrated into the Cedar Creek Schoolyard Ecology program and a NASA-funded science education center to train Native American reservation teachers. Citizen scientists will be engaged through the MN Phenology Network. Data and research outcomes will be made available through a website and archived in publicly accessible data repositories.





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1 Remotely sensed spectral images. Left: low diversity (3 species). Right: moderate diversity (6 species). Higher diversity plots show higher optical diversity.

2 Natural systems, such as this oak savanna system, have optical diversity patterns that can be detected both remotely and on the ground.

3 One of three biodiversity manipulation experiments at Cedar Creek.

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

5 Overview of project illustrating the concept of "surrogacy" in diversity. According to the surrogacy hypothesis, diversity at one level (e.g., plant diversity), which can be detected optically (optical diversity) translates to diversity belowground (microbial diversity), which can be detected using genomic approaches.

6 Automated tram for sampling optical diversity from manipulated vegetation plots at Cedar Creek. This proximal remote sensing method will be coupled with airborne and satellite sampling.

CREDIT: 1 EVAN DELANCEY, UNIVERSITY OF ALBERTA AND JOHN A. GAMON, UNIVERSITY OF ALBERTA & UNIVERSITY OF NEBRASKA (LINCOLN) 2 3 CEDAR CREEK ECOSYSTEM SCIENCE RESERVE, 4 MICHAEL MADRITCH, 5 JEANNINE CAVENDER-BARES (UMN) AND MICHAEL MADRITCH, CEDAR CREEK ECOSYSTEM SCIENCE RESERVE, 6 JOHN A. GAMON, UNIVERSITY OF ALBERTA & UNIVERSITY OF NEBRASKA (LINCOLN)

Experimental adaptive radiation: Genomics of diversification in bird lice

Dale Clayton
Sarah Bush
Michael Shapiro
University of Utah
(NSF 1342600)

Kevin Johnson
University of Illinois
Urbana-Champaign
(NSF 1342604)

The goal of this project is to expand our understanding of adaptive radiation by utilizing bird-specific ectoparasites as a model system. The researchers will conduct experimental studies and will link phylogenetic, phenotypic, and functional data in order to clarify how micro- and macro-evolutionary processes influence the generation of biodiversity.

Adaptive radiations occur when one species splits into multiple species that occupy distinct ecological niches. This evolutionary process is a common source of biodiversity, yet the genetic changes accompanying adaptive radiations are poorly understood. The goal of this project is to study the genetic architecture of adaptive radiation in parasites, which are one of the most diverse assemblages on earth. Parasites often adaptively radiate when they switch to various novel species of hosts. This project involves experimentally induced host switches in feather lice, which are host-specific, "permanent" parasites that spend all of their time on the host's body. Their unusual life cycle makes it possible to study lice under essentially natural conditions on captive birds in the lab. The project will explore evolutionary changes in parasite size and color, which are fundamental components of successful host use in feather lice. Different size and color breeds of pigeons (*Columba livia*) will be used as "stepping stones" to experimentally evolve lice capable of ultimately switching to host species on which they do not normally occur. Using a complete reference genome for the pigeon louse *Columbicola columbae*, genomic changes that accompany the experimental evolution of novel host use will be identified. These changes will be compared to genomic differences among different species of *Columbicola* lice that parasitize different species of pigeons under natural conditions. These genomic data will also be used to reconstruct the actual coevolutionary history of pigeons and their lice. Cophylogenomic approaches will be used to identify past host switches and the genomic changes that accompanied them. Genomic changes in experimental lice will be compared to the genomic changes accompanying past host switches from nature. The ultimate goal of this work is to integrate the micro- and macroevolutionary dimensions of evolution in order to improve understanding of the genetics of adaptive radiation as a generator of biodiversity.

Broader impacts of this project are closely related to the research objectives. They include data dissemination, training of new researchers, and K-12 outreach activities. Experimental evolution and comparative genomic data will be deposited in public, web-accessible databases. The PIs will train one postdoc, two graduate students, and several undergraduate students. The PIs are also strongly committed to inquiry-based science outreach for public school students. They will create two modules on natural selection that are cost effective and easy to implement. These modules will be distributed to 100 Utah K-12 teachers and their effectiveness assessed in collaboration with the University of Utah Center for Science and Math Education.

❶ ❷ ❸ ❹ Crypsis in feather lice of pigeons and doves: the light colored louse (insets: *Columbicola wolffhuegeli*) is a parasite of the pied imperial pigeon (*Ducula bicolor*), the dark louse (*C. columbae*) parasitizes the rock pigeon (*Columba livia*). Columbicola columbae is the source of the reference genome for this project.

❺ ❻ ❼ ❽ Crypsis in feather lice: the white louse (*Neopsittaconirums albus*) is a parasite of the sulfur-crested cockatoo (*Cacatua galerita*), the black louse (*N. borgiolii*) is a parasite of the yellow-tailed black cockatoo (*Calyptorhynchus funereus*).

❾ Variation in the sizes of breeds of the Rock pigeon (*Columba livia*).

❿ Variation in the color of rock pigeons. Different size and color pigeon breeds will be used as "stepping stone" hosts for experimentally evolving changes in the size and color of *Columbicola columbae lice*. These lice will eventually be transferred to different species of pigeons to simulate actual host switches in nature. Genomic changes associated with the experimental switches will be compared to genomic differences among the different species of lice that have switched to novel host species under natural conditions in the past.

CREDIT: ❶ ❺ FIR0002/FLAGSTAFFOTOS, ❷ RAZVAN SOCOL, ❸ ❹ ❼ ❽ S. E. BUSH AND D. H. CLAYTON, ❻ DAVID COOK, ❾ ❿ S. E. BUSH

The biogeography and evolution of drought tolerance in grasses

(CO-FUNDED WITH NASA)

Joseph Craine
Jess Nippert
Mark Ungerer
Kansas State University
(NSF 1342787)

Lynn Clark
Iowa State University
(NSF 1342787)

Melvin Duvall
Northern Illinois University
(NSF 1342782)

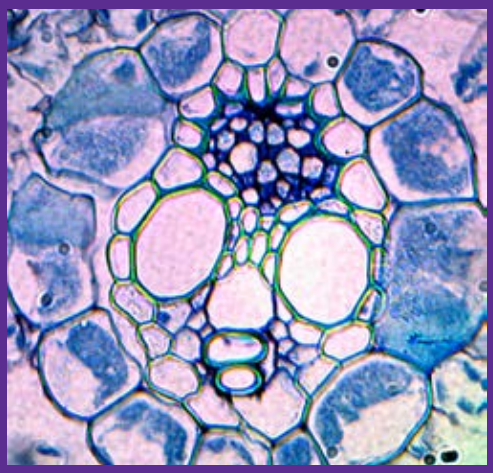
Christopher Still
Oregon State University
(NSF 1342703)

The goal of this project is to understand the genetics, functional traits, and evolution of drought tolerance in grasses. A deeper understanding of the relationship between grass genetics and the capability of these grasses to tolerate drought conditions has the potential to inform agricultural productivity in changing environments.

Drought has structured grasslands for millions of years and continues to affect their functioning today, as well as the provision of ecosystem services such as livestock production and carbon sequestration. Drought can strike with little warning and it can take decades for the grassland to recover from its effects. Despite the certainty that droughts will continue to affect grasslands in the future and the strong potential that they will become more frequent and/or more severe, we know too little about how different grasses have evolved to cope with drought. There is limited understanding about the genetic basis tolerance in grasses, how many times drought-tolerance has evolved in grasses, how it is distributed geographically, and its potential role in determining future grassland productivity.

At the core of the research, the investigators will determine physiological drought tolerance and associated anatomical and physiological traits for 400 species of grass distributed across eight major evolutionary groups and broad geographic and environmental ranges. To better understand the genetics of grasses, new techniques will be employed to quantify gene expression in droughted grasses with transcriptomes as well as root and leaf anatomy, morphology, and physiology. The overall goal will be to assess the degree to which plants can withstand the physical stresses of dry soils while still continuining to photosynthesize. With new sequence data complementing current efforts, the phylogenetic relationships among the 400 species and their environmental niche spaces will be determined, which will shed light on how frequently drought tolerance evolved and where in the world it is most concentrated. The research will also parameterize models of global productivity in the face of drought, coupling data on drought tolerance with gas exchange and environmental data, which will be critical in modeling responses of vegetation to future climate change.

Understanding the different dimensions of drought tolerance and photosynthesis will contribute broadly to our understanding of grasslands. Understanding the genetic and anatomical basis of drought tolerance has the potential to affect crop selection. Understanding the global distribution of drought tolerance and how grasses function under drought can be worked into improving our predictions of future grassland function in a drier, warmer world. More narrowly, beyond working to recruit underrepresented individuals at the graduate and post-doctoral level, this research will contribute to multiple public datasets and educational materials such as a temporary exhibit on the phylogeny of grasses and grass roots at the new Flint Hills Discovery Center in Manhattan, KS.



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1 *Paspalum vaginatum*, a grass native to the Americas and one of the more than 11,000 species of grass in the world. To assess its drought tolerance, an individual is grown under well-watered conditions, watering is ceased, and the water potential at which transpiration ceases is determined.

2 Grassland of Konza Prairie, KS. More than 80 species of grass are present at Konza. They span the global range of physiological drought tolerance at a single site and this diversity provides high resilience to drought.

3 Vascular bundle from a *Panicum queenslandicum* leaf. Xylem within these bundles undergoes strong selection for physiological drought tolerance.

4 Sally Tucker, former graduate student at Kansas State University, assessing the water potential of a droughted grass. To determine how well grasses can withstand the physical stresses of drought, a section of leaf is placed in an instrument known as a pressure bomb and increasing pressure is applied to a portion of the leaf until water is forced out of the cut portion on top. This pressure is equivalent to the stress imposed by drought on the plant before it was harvested.

5 Various grasses from around the world planted at Kew Gardens, UK.

CREDIT: 1 2 3 4 5 JOE CRAINE, KANSAS STATE UNIVERSITY

Biodiversity of the gut microbiome of herbivorous woodrats

Denise Dearing
Colin Dale
Robert Weiss
University of Utah
(NSF 1342615)

This project seeks to understand how the evolution and environment of the gut microbiome in herbivorous mammals has helped to create a biodiversity hotspot of microbial organisms and in turn, how this diversity can influence the physiology of the host mammal. More broadly, this research may impact our understanding of chronic bowel diseases, the metabolism of toxic compounds, and how gut flora controls the host's digestion of variable diets.

Recent studies have revealed that mammals are not individuals but rather are "superorganisms" that host diverse and interactive communities of microbes. Some of the most critical interactions facilitating mammalian life occur between mammals and the complex communities of microbes that reside within their guts. Plant-eating mammals harbor the most diverse microbial communities. Many of these microbes are important in the degradation of fiber; however, gut microbes may also play an essential role in detoxifying the natural toxins common in plants. The proposed project will investigate how host evolutionary history and dietary toxins shape the diversity of the gut microbiome of herbivorous mammals by focusing on a group of rodents (woodrats) that specialize on toxic plants. The objectives of this project are to 1) identify and compare the microbial communities across chambers of the woodrat gut to understand their function; 2) investigate the influences of evolutionary history and dietary toxins in sculpting microbial diversity function and 3) determine how diversity interacts with the liver of the host to facilitate detoxification. This project will provide some of the first insights into the microbial diversity of wild herbivores and the role that plant toxins play in shaping diversity.

This work will advance our understanding of microbial diversity and may reveal new microbes useful for human probiotics. The discovery of novel microbes and genes associated with detoxification is anticipated; such biological material is of great interest to agricultural scientists wishing to improve husbandry practices in livestock. A one-week summer workshop will be offered annually to middle school students to teach concepts of microbial diversity through the development of interactive computer simulations and games. In addition, high school, undergraduate, and graduate students and post doctoral fellows will be trained in molecular approaches to study biodiversity.

1

1 Stephen's woodrat *(Neotoma stephensi)*. The work will characterize the gut microbial community of Stephen's woodrat. This community is likely to have many species of microbes new to science given that its diet consists of many compounds found in turpentine, at doses that are lethal to humans.

CREDIT: 1 M. DENISE DEARING, BIOLOGY DEPARTMENT, UNIVERISTY OF UTAH

Functional diversity of chemosymbiosis in lucinid bivalves from coastal biomes

Annette Engel
University of Tennessee Knoxville
(NSF 1342785)

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

Barbara Campbell
Clemson University
(NSF 1342763)

This project will uncover the genetic, taxonomic, and functional diversity of modern lucinid bivalve chemosymbioses from uncharacterized coastal marine biomes and will test for ways to characterize lucinid-bacteria biodiversity in the geologic past.

Chemosymbiosis, the association of bacteria that fix carbon and supply it to their hosts in the absence of sunlight, remains largely unexplored in shallow marine, coastal environments. Lucinids are the most taxonomically diverse clade of bivalve clams that exploit chemosymbionts to gain energy and avoid toxins. Lucinid endosymbionts have previously been considered to be sulfur-oxidizing bacteria from the class Gammaproteobacteria. However, recent molecular studies of *Phacoides pectinatus* endosymbionts reveal novel genetic and metagenomic diversity associated with other biogeochemical cycles. As such, this effort reveals just how little we know of chemosymbiotic associations in shallow marine, coastal environments.

Lucinid-bacteria chemosymbiotic associations are an ideal system to unify the dimensions in biodiversity. Because lucinids have an extensive fossil record, geologic time is a "4th dimension" of biodiversity that can reveal more about the evolutionary history of lucinid chemosymbiosis. Our research will determine (1) how lucinid taxonomy, habitat, and biogeography influence endosymbiont genetic diversity, (2) how the microbial diversity and ecology of the lucinid habitat affect symbiont diversity, distribution, and biogeochemical cycling, (3) how lucinid host morphology may serve as a proxy for the presence of endosymbionts and/or degree or type of symbiotic dependence in fossil taxa, and (4) how disturbances (e.g., anthropogenic activities) within the coastal biome affect the nature and type of lucinid chemosymbiotic association.

Shallow marine biomes from Florida, California, and The Bahamas will be sampled, and Lucininae, Leucosphaerinae and Codakiinae subfamilies will be targeted. The presence of chemosymbionts and/or degree or type of symbiotic dependence in fossil taxa will provide more accurate data to reconstruct trophic relationships in paleocommunities and extant habitats. The effects of anthropogenic activities on the functional diversity of chemosymbiotic associations will be evaluated from innovative geochemical, metagenomic and transcriptomic approaches and compared to pristine and low-impact systems. Anthropogenic impacts will be quantitatively assessed using geochemistry and disturbance indices developed for benthic marine sediments.

This research will fill gaps in our understanding about lucinid biodiversity loss that may occur in habitats sensitive to natural and anthropogenic disturbances and will be important for coastal resource management decisions.

At each of the PI institutions, graduate and undergraduate students will be trained in interdisciplinary geochemistry, microbiology, and paleobiology disciplines, including a field studies course to occur in The Bahamas, as well as museum collection standards, laboratory research, and computational bioinformatics. Students from underrepresented STEM groups will be involved on the project, and involvement with university outreach and mentoring programs will target symbiosis and biodiversity topics through formal and informal classroom, public speaking opportunities, and museum activities.

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1 Lucinids will be studied from shallow marine habitats, including seagrass meadows and mangrove swamps, that vary in natural and anthropogenic disturbances.

2 The Thick Lucine, *Phacoides pectinatus*, collected from sediments near Fort Pierce, Florida. Ongoing metagenomic and biochemical research focused on *P. pectinatus* is revealing a much more diverse assemblage of chemosymbionts than previously recognized, including bacteria associated with nitrogen and methane in addition to sulfur and cycling.

3 Collecting *Phacoides pectinatus* from sandy sediments near Fort Pierce, Florida.

4 Dissected *Phacoides pectinatus* showing purple gills, white foot, and other internal parts.

CREDIT: 1 LAURIE C. ANDERSON, SOUTH DAKOTA SCHOOL OF MINES AND TECHNOLOGY
2 3 4 ANNETTE SUMMERS ENGEL, UNIVERSITY OF TENNESSEE-KNOXVILLE

Phylogenetic, functional, and genetic diversity and ecosystem functions in a fragmented landscape

(CO-FUNDED BY NSF-CHINA)

US MEMBERS

Lin Jiang
Georgia Institute of Technology
(NSF 1342754)

Jianguo Wu
Arizona State University
(NSF 1342757)

CHINA MEMBERS

Ming-jian Yu
Zhihong Xu
Zhejiang Agriculture and Forestry University

Jianbo Lu
Hangzhou Normal University

Xiao-Yong Chen
East China Normal University

In this project researchers will study the genetics, interrelationships, and linkages to ecosystem function of woody plants and arthropods at different stages of succession in the Thousand-Islands Lake of China. By studying a system in succession, the project seeks to expand understanding of the relationship between biodiversity and ecosystem functioning.

Many of Earth's ecosystems are currently experiencing tremendous biodiversity loss. While biodiversity has multiple dimensions, existing studies have focused mainly on one dimension of biodiversity—species diversity—in an undisturbed world. As a result, there is comparatively little knowledge on the ecological causes and consequences of other biodiversity dimensions, particularly in highly fragmented environments. Furthermore, a large number of studies during the last two decades have examined the relationship between biodiversity and ecosystem functioning in an effort to understand potential functional consequences of biodiversity loss, but the question of how ecological succession influences biodiversity and ecosystem functioning relationships remains largely unexplored.

This project aims to investigate phylogenetic, functional, and genetic diversity of plant and insect assemblages on the islands of the Thousand-Island Lake of China – the lake with the most islands in the world (about 1,100 islands). This man-made lake, created in 1959 as the result of dam construction, transformed thousands of former hilltops to islands, fragmenting previously continuous terrestrial habitats into discontinuous ones. Smaller islands in the lake are flooded more frequently than larger ones, creating a succession series. The researchers will combine field surveys of plant and insect communities, experimental manipulations of biodiversity, and laboratory-based functional and genetic analyses of plant and insect samples to examine biodiversity and ecosystem function patterns on the Thousand-Island Lake islands.

The proposed research will advance scientific knowledge in three main areas. First, it will explore how phylogenetic, functional, and genetic diversity, relate to each other and change with island characteristics. Second, it will answer the largely unexplored question of how islands with different biodiversity-related characteristics differ in ecosystem functions. Third, it will compare biodiversity and ecosystem functioning patterns in experimentally established and natural communities in the same environmental setting and identify the causal effects of multiple dimensions of biodiversity on ecosystem functioning. These activities together will allow the researchers to gain a better understanding of linkages among the multiple dimensions of biodiversity, ecosystem functioning, and habitat fragmentation, by taking advantage of the Thousand-Island Lake islands as highly replicated natural insular ecosystems.

This project will serve as a long-term platform for collaborations between US and Chinese scientists and students who work on biodiversity, ecosystem functions, and habitat fragmentation. The project will provide high-quality research opportunities for young scientists and students, and emphasize the involvement of underrepresented minorities. Genuine efforts will be made to communicate research findings to the public, resource managers and decision makers in the study region. The researchers will also work with local managers and tourist groups on the Thousand-Island Lake islands to promote public education of biodiversity in the face of habitat fragmentation.

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1 The Thousand Island Lake, located in Zhejiang Province, China, harbors thousands of islands of various sizes and shapes. Biodiversity of plant and insect assemblages will be studied on these islands.

2 A dead individual of *Pinus massoniana*, killed by flooding. *Pinus massoniana* is a common early successional tree species on the Thousand-Island-Lake islands.

3 The understory of the evergreen broadleaved forest on the Thousand-Island-Lake islands.

CREDIT: 1 2 3 LIN JIANG, SCHOOL OF BIOLOGY, GEORGIA INSTITUTE OF TECHNOLOGY

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

Mary Ann Moran
William Whitman
University of Georgia
(NSF 1342694)

James Birch
Christopher Scholin
Monterey Bay Aquarium Research Institute
(NSF 1342734)

Ronald Kiene
University of South Alabama
(NSF 1342699)

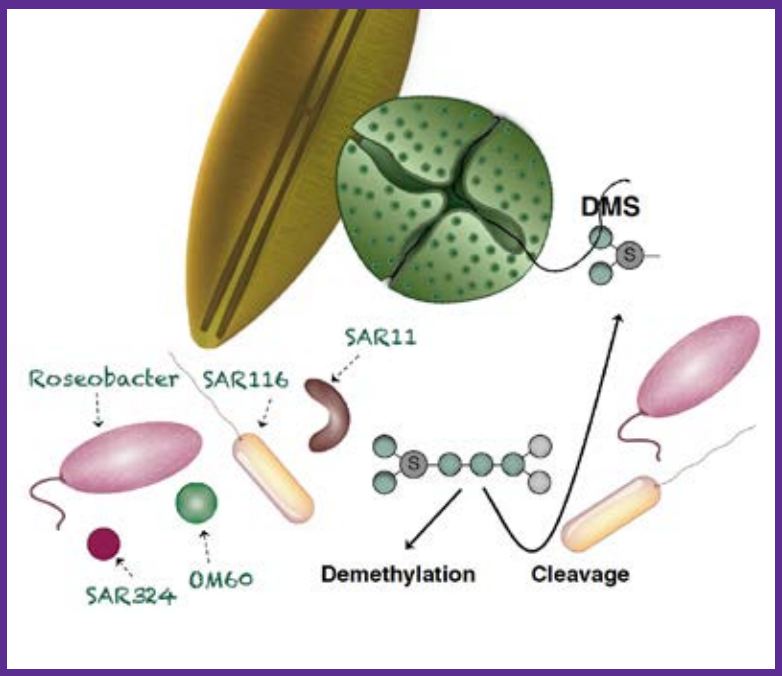
This project seeks to understand how the regulation of dimethylsulfoniopropionate (DMSP) metabolism in marine bacteria affects the fate of organic sulfur in the ocean and the emission of climate-relevant sulfur gas to the atmosphere. The goal of this research is to understand how the diversity of microbial life impacts the geochemical environment of the oceans and atmosphere.

Marine bacteria are major recyclers of the organic sulfur compound DMSP. This compound is synthesized by marine phytoplankton in surface waters of the ocean and used by them as an osmolyte (an organic compound that helps maintain fluid balance), an antioxidant, and a predator deterrent. A large fraction of DMSP is eventually released by phytoplankton into seawater, where it is subsequently assimilated and degraded by marine bacteria.

Interest in bacterial degradation of this somewhat obscure sulfur compound arises from the two competing pathways bacteria use, since each has a very different environmental outcome. In the cleavage pathway, DMSP is converted to the volatile sulfur gas dimethylsulfide (DMS), which is a major source of sulfur to the atmosphere and impacts atmospheric chemistry both directly and through its degradation products. It is of particular interest because it plays a role in cloud formation and the reflection of climate-warming solar radiation back into space. By contrast, the demethylation pathway does not produce DMS and instead serves as a major route of sulfur and carbon acquisition by the microbes in ocean surface waters.

While it is well recognized that bacteria control this critical juncture in the marine sulfur cycle, it is not yet understood how the competing pathways are regulated by the diverse bacteria that populate the ocean. Recent advances in bacterial physiology, bacterial genetics, and ocean instrumentation are now providing the tools necessary to make substantial strides in our knowledge of this control point. Our research will determine how representatives of each major taxon of DMSP degraders regulate their pathways, addressing implications of bacterial functional, genetic, and taxonomic diversity for global sulfur cycling. We will conduct studies on bacteria in pure culture, in marine microcosms, and in their natural environment (using an autonomous instrument, known as an ESP, that carries out gene assays in the ocean). Concurrent with gene abundance and expression assays, we will measure the rates and end products of DMSP degradation.

This research will address fundamental questions of how the diversity of microbial life influences the geochemical environment of the oceans and atmosphere. It will provide extensive interdisciplinary training opportunities for young scientists at the graduate, undergraduate, and high school levels. Working with local high school students and teachers, we will develop microbe-centered lessons and laboratory exercises to convey basic biological concepts while enhancing understanding of the diversity of marine microbes and their roles in global elemental cycles. We will also participate in education and outreach efforts at two public aquaria, the Dauphin Island Sea Laboratory Estuarium and the Monterey Bay Aquarium.



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1 Staff at the Monterey Bay Aquarium Research Institute deploying an Environmental Sample Processor in Monterey Bay.

2 The genes harbored by DMSP-degrading bacterioplankton determine their functional role in the global sulfur cycle. Members of the SAR11, OM60, and SAR324 lineages carry genes only for demethylation, and while they consume DMSP they do not contribute directly to DMS formation. The Roseobacter and SAR116 lineages carry genes for both demethylation and cleavage, and therefore more immediately influence the fate of DMSP and the emission of DMS to the atmosphere.

3 University of Georgia Ph.D. students Bryndan Durham and Vanessa Varaljay process experimental samples for nucleic acid extraction at the Dauphin Island Sea Lab.

4 University of South Alabama Ph.D. student Ali Rellinger and REU student Melissa Collini prepare samples for chlorophyll a analysis at the Dauphin Island Sea Laboratory.

5 Left to right: Vanessa Varaljay, Ron Kiene, Noah Lawler, and Bryndan Durham.

CREDIT: 1 ©2006 MBARI, 2 CAMILLE ENGLISH, UNIVERSITY OF GEORGIA
3 4 5 RON KIENE, UNIVERSITY OF SOUTH ALABAMA

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

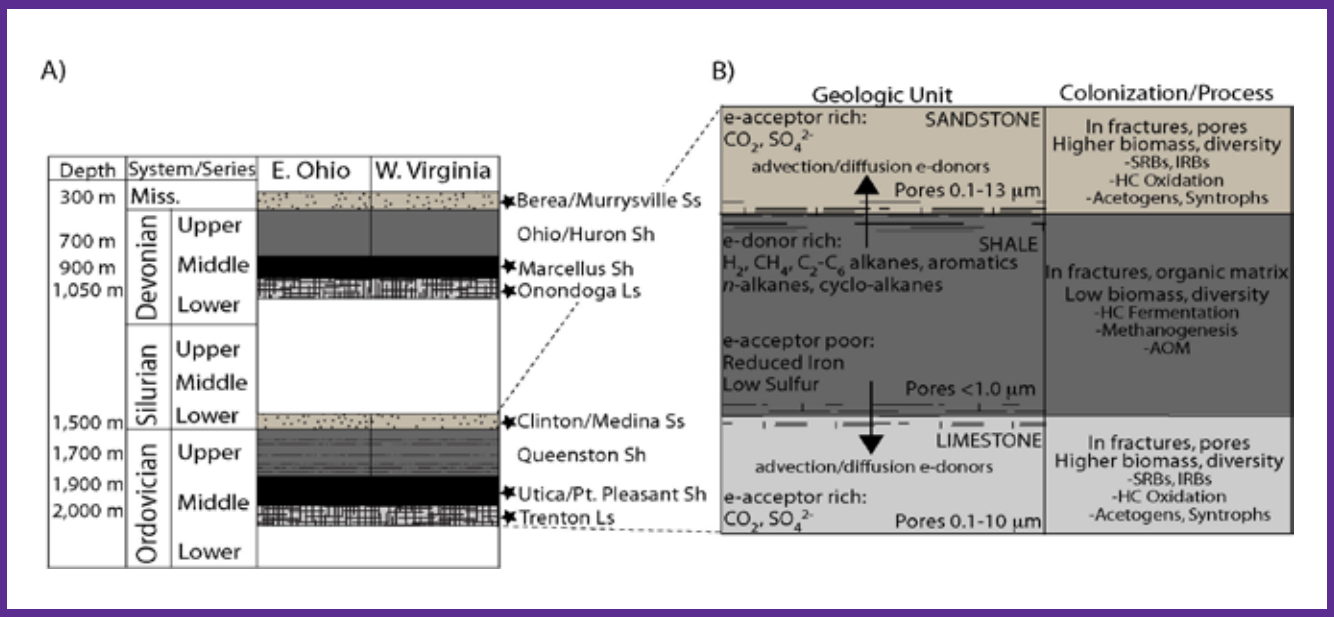
Paula Mouser
David Cole
Michael Wilkins
Kelly Wrighton
Ohio State University
(NSF 1342701)

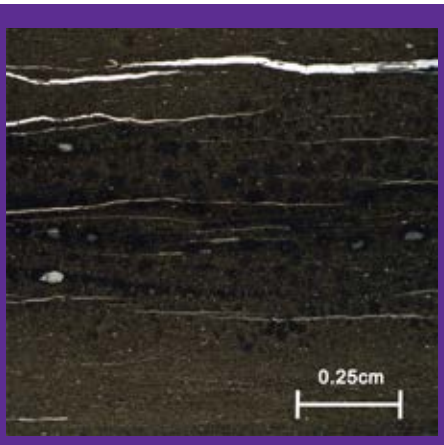
Shikha Sharma
West Virginia University
(NSF 1342732)

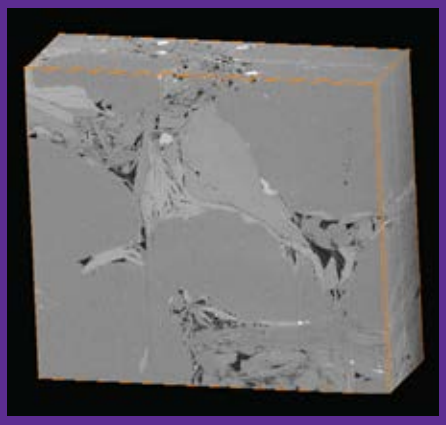
This project has three goals: to broadly characterize the diversity of microbes living at deep shale interfaces, to identify the microbial origin within geologic history, and to assess how this microbial community is adapting to changing environments. With the growing energy industry of hydraulic fracturing, these deep shale environments may be particularly at risk for biodiversity change.

This research will probe microbial life and function in a rarely examined habitat: kilometer-deep black shale, which is a critical component of the United States energy portfolio. It also represents an ecosystem under immediate risk for biodiversity change as a result of new horizontal drilling and hydraulic fracturing technologies. The deep shale biosphere stores an abundance of methane and other oil hydrocarbons that provide carbon and energy resources for microorganisms both within the shale and along its bounding formations. The environmental conditions encountered within these rocks include the absence of light for photosynthesis, sub-micron (μm) pore-spaces, elevated temperatures of 50-70°Celcius, pressures 500-600 times atmospheric levels, and brine fluid chemistry.

Each of these environmental factors may strongly influence the origin, adaptation and function of the microbial population. As one of the largest unconventional reserves in the United States, the Marcellus and Utica-Point Pleasant shale within the Appalachian basin of West Virginia and Ohio will serve as a case study to broadly characterize the microbial biodiversity and function in black shale and its bounding sandstone and limestone rock interfaces. Research objectives include inferring the origin of microbial life with respect to geologic history of these formations, exploring how microorganisms have adapted to the current deep biosphere environment, and investigating the metabolic strategies used to sequester nutrient resources given the environmental conditions encountered in this ecosystem. To realize these objectives, the project will integrate pore-scale spectroscopic techniques, elemental and compound-specific isotope chemistry methods, and community genomics tools to investigate uncultured and cultivable biodiversity and function in rock and fluid samples. Genomics and isotopic information will inform high pressure and high temperature cultivation approaches to enrich for representative microbial members that may be involved hydrocarbon oxidation, hydrocarbon fermentation, and hydrogen respiration activities. This project will serve as the first survey of community genomics and transcriptomics of indigenous microbial of indigenous microbial populations in shale and its interfaces, and provide the first baseline study of kilometer deep biodiversity in black shale within a region slated for significant energy development in the coming decades. This research will greatly expand our knowledge of microbial life and function in shale prior to environmental disturbance and will provide further insight into microbial carbon cycling in the deep terrestrial biosphere.







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1 A) Geologic cross-section between southeast Ohio and southwest West Virginia. Stars represent key shale (Sh) and its sandstone (Ss) and limestone (Ls) formations. B) Expected carbon and energy flow between shale and its sandstone and limestone interfaces. The Marcellus and Utica shale are the primary source rocks for migrating electron donors into adjacent units, supporting sulfate reducing bacteria (SRB), sulfur-reducing bacteria (Sulf), acetogens (AcGen), fermenters (Ferm), anaerobic methane oxidizing bacteria (AOM), methanogens (Gen), and syntrophs (Syn).

2 Natural fractures within small section of Marcellus shale core from the Appalachian Basin.

3 Thin section showing peloidal textures along horizontal thin fractures in black shale.

4 3-D reconstruction of shale using focused ion beam (FIB) and Scanning Electron Microscopy (SEM) backscattered electron (BSE) imaging. Dark regions represent organic matter or void space (pores) while bright regions represent primarily pyrite. Intermediate-gray regions with layered morphologies are phyllosilicates. Large intermediate-gray grains are carbonates and/or silicates (calcite, dolomite, quartz, feldspar). Pixel resolution is 10 nanometers. Individual FIB slices are 10 nm, representing 400 slices.

CREDIT: 1 PAULA MOUSER, THE OHIO STATE UNIVERSITY, 2 DAVID COLE, SCHOOL OF EARTH SCIENCES, THE OHIO STATE UNIVERSITY
3 4 SHIKHA SHARMA, DEPARTMENT OF GEOLOGY AND GEOGRAPHY, WEST VIRGINIA UNIVERSITY

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

Sean Mullen
Boston University
(NSF 1342712)

Ryan Hill
University of the Pacific
(NSF 1342706)

Marcus Kronforst
University of Chicago
(NSF 1342790)

Keith Willmott
University of Florida
(NSF 1342705)

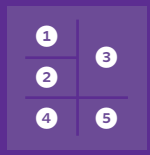
Adriana Briscoe
University of California Irvine
(NSF 1342759)

This project will connect different scales of biological organization from the proximate mechanisms—such as genetic, molecular and cellular mechanisms—to the ultimate causes of higher-order species diversity. Utilizing the radiation of neotropical *Adelpha* butterflies as a model system, this team will integrate information on phylogenetic relationships and specific genes underlying adaptive traits, as well as the ecology and natural history of the butterflies, to test hypotheses about what is driving the development of biodiversity.

The latitudinal gradient in species diversity is one of the most striking biogeographic patterns in nature, with species richness peaking in equatorial regions for nearly all groups. Despite considerable effort to understand the origin and maintenance of latitudinal gradients in species diversity, a multitude of potentially interacting, non-mutually exclusive hypotheses exist, and no single overriding explanation has emerged. However, multiple hypotheses link the latitudinal diversity gradient to a presumed gradient in the strength of biotic interactions between temperate and tropical environments. While biotic interactions are believed to play a major role in the origin and maintenance of diversity and may drive increased rates of adaptation and speciation in tropical regions, this hypothesis remains virtually untested. This project will bridge this gap by performing a comprehensive analysis of the evolutionary mechanisms underlying adaptive phenotypic variation in color, vision, and smell across a rapidly diversifying lineage of butterflies. Commonly referred to as 'sisters', the butterfly genus *Adelpha* ranges from northwestern USA to Uruguay. Containing >90 described species and at least 124 additional subspecies, it is one of the largest neotropical butterfly groups, with species richness peaking at the base of the eastern Andes, where local community diversity can be as high as ~35 species. In addition to the latitudinal and elevational gradients in species richness, extraordinary diversity also exists among *Adelpha* species in morphology, behavior, and host-plant use.

The research will leverage the diversity of *Adelpha* to thoroughly test, for the first time, the hypothesis that stronger biotic interactions in tropical environments are associated with the ubiquitous pattern of latitudinal species diversity gradients by both directly measuring the strength of these interactions using field experiments, and by indirectly inferring their strength by examining the mode and tempo of adaptive molecular evolution across tropical and temperate communities for genes responsible for color, vision, taste, and smell. By integrating diverse datasets and analytical methods, this research will provide important new insights into some of the most important outstanding questions in ecology and evolutionary biology.

Completion of this project will advance our understanding of the ecological and evolutionary processes that shape temporal and spatial patterns of biodiversity, and shed light on important facets of endangered species management, particularly in a time of rapid global climate change. This project links together biodiversity researchers from across the US and Latin America, and will lead to sustained international collaboration, to broadened access to STEM fields for both women and minorities through targeted recruitment, and finally, to an enhanced public understanding of the science and of the current and developing threats to global biodiversity.



1 The common cloud forest butterfly, *Adelpha alala*, feeding at damp sand on the ground in northeastern Ecuador. This 'puddling' behavior is believed to provide the insect with essential salts.

2 Canopy towers provide an opportunity to see otherwise rare, tree-top dwelling creatures such as this *Adelpha iphicleola*, butterfly, resting on the side of the tower at Yarina Lodge in the east Ecuadorian Amazon.

3 A male *Adelpha capucinus* dries its wings after emerging from its pupa at the Napo Wildlife Center in the east Ecuadorian Amazon. The host plants of about half of all *Adelpha* species are known and they belong to a remarkably wide range of plant families, suggesting that colonization of new plant resources by *Adelpha* caterpillars may have helped the group to diversify.

4 5 Pupa and pre-pupa larva of a species in the "*Adelpha serpa* group" photographed in Honduras. The larva was found feeding on a plant in the family Melastomataceae.

CREDIT: 1 2 3 KEITH WILLMOTT, UNIVERSITY OF FLORIDA
4 5 RYAN HILL, UNIVERSITY OF THE PACIFIC

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

Krissa Skogen
Jeremie Fant
Norman Wickett
Chicago Botanic Garden
(NSF 1342873)

Rachel Levin
Amherst College
(NSF 1342805)

Robert Raguso
Cornell University
(NSF 1342792)

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.

Relationships among flowering plants and insects represent one of the great engines of terrestrial diversity. Floral scent and other plant volatiles are important drivers of these relationships (e.g., pollination, herbivory, plant defense), but remain poorly integrated into our understanding of floral evolution and pollination ecology. Few studies have tested the spectrum of plant fitness outcomes when volatiles attract both pollinators and floral/seed predators. Thus, the hidden diversity of floral/seed predators and their potential as selective agents constitutes a considerable gap in understanding floral evolution. These "forgotten predators" have co-diversified with flowering plants and are likely influential in the evolution of most plant-pollinator interactions.

This project focuses on how chemically-mediated interactions between flowering plants, pollinators, and floral/seed predators affect diversification at the population, species, and higher taxonomic levels. Onagraceae (evening primrose family) is one of the most species-rich families of night-blooming plants in North America. Many Onagraceae, particularly species in tribe Onagreae, produce floral scent that likely dictates the primary biotic drivers impacting plant fitness, including legitimate pollinators (hawkmoths, bees) and floral and seed predators (*Mompha* moths). The same floral characteristics (color, shape, scent) that attract pollinators are also suspected to attract floral antagonists to host plants. *Mompha* is one such moth genus that specializes on Onagraceae. A thorough survey of these micromoths associated with Onagreae in western North America will result in a more accurate assessment of diversity in this group. Three dimensions of biodiversity will be integrated through studies of (1) floral trait variation, (2) its genetic basis, and (3) their roles in driving patterns of diversity in Onagreae and *Mompha*. The identification of "hot" and "cold" spots of selection will provide a test of the role of scent in the creation and maintenance of biodiversity across landscapes and time.

Understanding the dynamics among plants, mutualists, and floral/seed predators is essential for documenting and conserving biodiversity and may impact conservation in a changing world. The PIs will engage over 200 students (high school to graduate school, interns, and postdocs) in the field and laboratory. A social network and online webinars will link participants, strengthening the connections between students, citizens, and scientists. The PIs and their partnering institutions have well-established programs for recruiting unrepresented groups and training students. Private and public landowners and volunteers will participate in and/or be informed of conservation-focused components of this study. Public lectures and an integrated project website/blog will report results and on-going progress.

1 *Manduca quinquemaculata* hawkmoth drinking nectar from *Oenothera harringtonii* at dusk.

2 *Lasioglossum sp.* bee robbing pollen from *O. harringtonii* at dawn.

3 4 5 *Mompha stellella* microlepidopteran adult, larva inside fruit (seed predator), and cocoon inside *O. harringtonii* fruit.

6 Comanche National Grasslands, Colorado, an example of the arid shortgrass habitat where the focal plants (Onagraceae), pollinators and antagonists co-occur.

7 8 *O. harringtonii*—scented, white, night-opening flowers; and *O. capillifolia*—unscented, yellow, day-opening flowers.

9 *Hyles lineata* larvae eating an *O. hartwegii* subsp. *filifolia* flower bud.

CREDIT: 1 5 6 7 8 9 KRISSA SKOGEN, CHICAGO BOTANIC GARDEN
2 SADIE LUNA TODD, CHICAGO BOTANIC GARDEN, 3 4 TERRY HARRISON, UNIVERSITY OF ILLINOIS

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

Sharon Strauss
University of California Davis
(NSF 1342841)

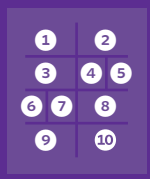
Maren Friesen
Michigan State University
(NSF 1342793)

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

Understanding how species coexist, and the role of genetic diversity within and across species in that coexistence, remains a fundamental challenge in biodiversity research. This project focuses on the highly diverse communities of *Trifolium* clover plants and their bacterial nitrogen-fixing symbionts, rhizobia. Symbiotic nitrogen fixation has global importance on par with photosynthesis, and this project will assess its functionality in light of genetic variation in symbionts and clover species, and its role in outcomes of interactions among *Trifolium* species. This project will test the importance of N-fixation and soil communities in determining long-term coexistence of *Trifolium* clover species, and will build on—and contribute four additional years to—an existing six-year survey of coexistence in clover communities at the field site in Bodega Bay California.

Using observational approaches, manipulative field, greenhouse, and growth chamber experiments, genomic techniques and phylogenetic analyses, this project will test the importance of rhizobial symbionts and soil feedbacks in coexistence and N-fixation. *Trifolium* species will be grown in the presence and absence of other species, and with varying strains of rhizobia collected from soils and plant nodules, where rhizobia are housed. Gene expression in *Trifolium* and functional traits when species are planted in their 'home' and 'away' niches will serve as descriptors of the ecological niche. This project will also determine how these niche dimensions evolve using phylogenetic trees that capture the evolutionary history of *Trifolium* species and rhizobial strains. This project will yield an integrated insight into the molecular, functional, and ecological mechanisms of diversity maintenance and will greatly increase our understanding of biological nitrogen fixation through our manipulations and genomic descriptions of these interactions. Nitrogen fixation is a critical function of legumes and rhizobia in natural and agricultural ecosystems.

This project will train two post-docs, and two graduate students and will provide research experiences to undergraduate students through the 'Plant Genomics @ MSU' program, and ESA's SEEDS (Strategies for Ecology Education, Diversity and Sustainability: Diverse People for a Diverse Science) and through an exchange program with Howard University at UC Davis . The project will train high school students in 'High School Honors Science Program' at MSU and Young Scholars Program at UC Davis.



1 Quadrat to measure community composition.

2 Student evaluating quadrat at Bodega Marine Reserve.

3 Growing *Trifolium* species alone and in competition with other species in different soil communities.

4 5 *Trifolium fucatum* with nodules housing nitrogen fixing rhizobia bacteria.

6 7 Plant community with *Trifolium* at Bodega Marine Reserve.

8 Four of the 10 native species of *Trifolium* found at Bodega Bay Marine Reserve.

9 *Trifolium* at Bodega Bay, California.

10 *Trifolium fucatum*.

CREDIT: 1 2 7 9 MAREN FRIESEN, 3 4 5 6 10 BRIAN ANACKER , 8 JACKIE SONES

Costs and benefits of chronic viral infections in natural ecosystems

Mark Young
Montana State University
(NSF 1342876)

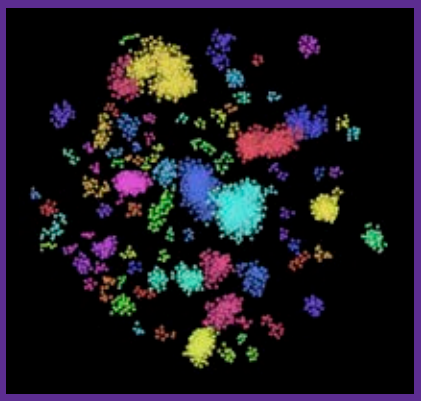
Joshua Weitz
Georgia Institute of Technology
(NSF 1342876)

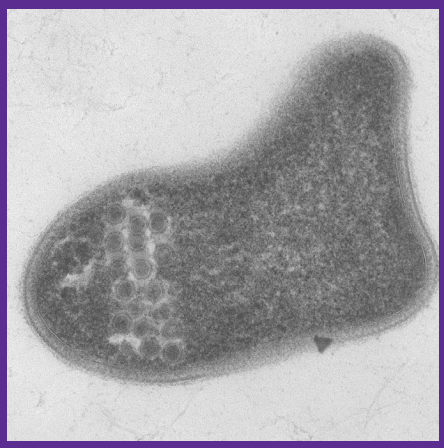
Rachel Whitaker
University of Illinois at Urbana-Champaign
(NSF 1342876)

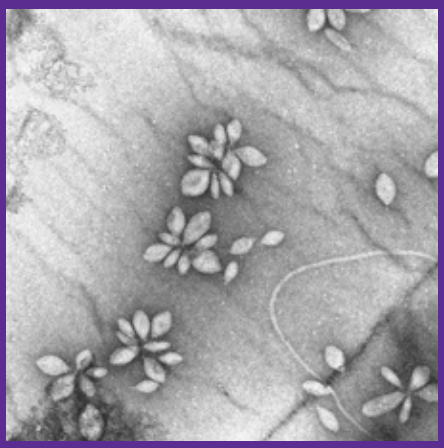
This project will investigate the genetic and functional basis of chronic viral infections in a hot spring model system in Yellowstone National Park. The study of viruses and host organisms in different environmental contexts has the potential to broaden our understanding of biodiversity and in particular to clarify the ways in which viruses influence the composition of microbial communities.

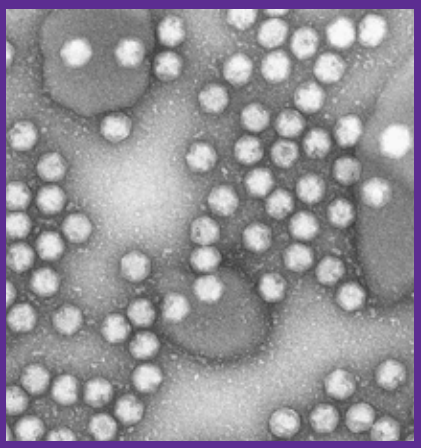
The traditional view is that viruses act solely as pathogens in which the host tries to eliminate viral infection. Hence, viruses are thought to control community composition by negatively impacting the fitness of infected hosts. This research investigates an alternative hypothesis that chronic viral infections contribute positively to host fitness, increasing the success of the virus-host pair. This hypothesis holds that in highly competitive microbial communities, chronic virus infection protects hosts from infection by more pathogenic viruses. Under this model, the competitive advantage provided by viruses plays a direct role in maintaining microbial biodiversity. This work lies at the intersection of three levels of biodiversity: (i) the taxonomic & phylogenetic level, by examining the evolution and coexistence of distinct viral and host taxa, (ii) the genetic level, by identifying specific microevolutionary changes emerging during host-virus coevolution, and (iii) the functional level, by characterizing how variation in host and viral life-history traits affect community structure and stability. This study will use a tractable Yellowstone hot spring model system that provides a unique opportunity to (i) link temporal changes in virus abundance and diversity to host genetic and taxonomic diversity, (ii) identify chronic viruses, and quantify the fitness consequences of chronic viral infections using a laboratory-based system, (iii) assess the effects of removing viruses in laboratory and in situ experiments, and (iv) develop a theoretical and computational model of eco-evolutionary, host-viral interactions that includes the costs and benefits of chronic infections. We anticipate that this research will provide new insights into how viruses influence not only microbial biodiversity, but also biodiversity of plants and animals.

This research will have broad scientific importance. Microbes play a significant role in life on earth, including as the foundation for Earth's food webs, influencing carbon and nitrogen chemical cycles, and in human health. Viruses infect all forms of life, including microbes. However, there is a poor understanding of how viruses control the composition and function of ecosystems. This work will help to deepen understanding of how viruses affect the composition of life in microbial communities. This research will engage K-12 teachers, students, and the public on the science of biodiversity using Yellowstone National Park as a highly attractive and visible venue for public interest in science. It will create and deliver learning opportunities to a global spectrum of communities via field courses for K-12 science teachers, virtual classrooms from Yellowstone to K-12 schools, online courses and workshops, and nationally aired films focused on microbial research in Yellowstone. It is fully anticipated that the results of this research will have far reaching implications for ecosystems beyond that of Yellowstone by impacting the understanding of the role viruses on influencing the biodiversity of life on Earth.









1 2 Typical high temperature Yellowstone hot springs sampled for this project.

3 A boiling Yellowstone mud hot spring, also sampled for this project.

4 Bioinformatic-based network analysis of the total RNA virus community present in a Yellowstone hot spring community.

5 6 7 Electron micrographs of a virus infected cell (left) and purified virus (middle and right) from a Yellowstone hot spring.

CREDIT: 1 2 3 4 5 6 7 MARK YOUNG, MONTANTA STATE UNIVERSITY

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

US MEMBERS

Tia-Lynn Ashman
University of Pittsburgh
(NSF 1241006)

Aaron I. Liston
Oregon State University

Richard Cronn
U.S. Forest Service
(NSF 1241217)

CHINA MEMBERS

Ming Dong
Jiliang Pang
Hangzhou Normal University

Jumin Li
Shisheng Ke
Taizhou University

Minghua Song
Chinese Academy of Sciences

Species that are polyploid contain more than two pairs of chromosomes. This project examines the role that polyploidy has played in the evolution of a group of strawberry species growing in the U.S. and in China.

WEBSITE: WILDSTRAWBERRY.ORG

Update

The major activity in 2013 was the coordination of the collection of *Fragaria* populations in North America, Europe, China and Japan. The collections were made by project participants and collaborations with more than 50 different collectors. An average of 50-60 seeds per plant and 18-21 plants per population were collected from more than 250 sites, resulting in more than 200,000 seeds. This global collection will serve as the foundation for our research into the role of polyploidy in generating biodiversity, as well as a community resource for ecological and evolutionary studies in strawberry.

Publication

Ashman, T-L., A. Kwok, and B. C. Husband. "Revisiting the dioecy-polyploidy association: Alternate pathways and research opportunities." *Cytogenetic and Genome Research* 140.2-4 (2013): 241-255.

Eagle Glacier and River, Juneau Alaska, a high latitude site of *Fragaria chiloensis*.

CREDIT: ARLO MIDGETT

Research on Airborne Ice Nucleating Species (RAINS)

Brent C. Christner
Louisiana State University
(NSF 1241161)

David C. Sands
Montana State University
Cindy Morris
INRA-PACA, France
(NSF 1241054)

Boris A. Vinatzer
David Schmale
Virginia Tech
(NSF 1241068)

Carolyn F. Weber
Idaho State University
(NSF 1241069)

This project examines the diversity and activity of airborne microbes that catalyze the formation of ice crystals in the atmosphere. These ice nucleating organisms may influence cloud development, cloud chemistry, and ultimately weather.

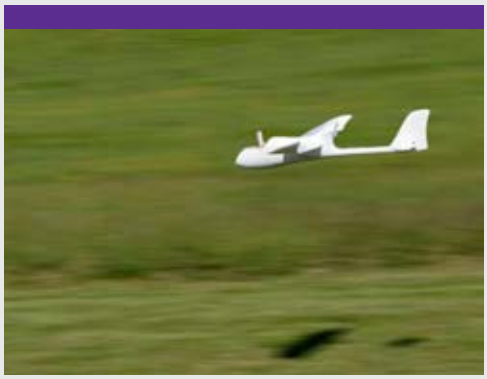
WEBSITE: BIOICE.WORDPRESS.COM

Update

Infrastructure for rain sampling has been designed and installed, and preliminary sampling was initiated in March 2013. Two novel remote rain-sampling techniques were additionally designed and developed: an unmanned aerial vehicle (UAV) platform, as well as a balloon sampler. Genetic analysis of rain bacteria has begun and more than 50,000 colonies cultured from rain samples have been tested for ice nucleation activity. The research is generating an increased knowledge and awareness of the associations of microorganisms with rain, and researchers believe that it could transform the way our society perceives the relationships between microorganisms and weather.

Publication

Morris, Cindy E., et al. "Bioprecipitation: a feedback cycle linking Earth history, ecosystem dynamics and land use through biological ice nucleators in the atmosphere." *Global Change Biology* (2013).



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A water-resistant unmanned aerial vehicle (UAV) developed through the Schmale lab to collect samples in the lower atmosphere before, during, and after rain.

CREDIT: DAVID SCHMALE, VIRGINIA TECH

<

Left Top: Collection of fresh snow samples at Storm Peak Laboratory, Steamboat Springs, Colorado. Left Bottom: Sampling snowpack in late winter in the southern French Alps to isolate the ice nucleation active bacterium and plant pathogen *Pseudomonas syringae*.

CREDIT: BRENT CHRISTNER, LOUISIANA STATE UNIVERSITY (LEFT TOP), CINDY E. MORRIS, INRA, FRANCE (LEFT BOTTOM)

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

US MEMBERS

Joel L. Cracraft
American Museum of Natural History
(NSF 1241066)

Christopher W. Dick
University of Michigan
(NSF 1240869)

Robert P. Guralnick
University of Colorado
(NSF 1241029)

Kenneth E. Campbell
LA County Museum of Natural History
(NSF 1241042)

Andrew V. Z. Brower
Middle Tennessee State University
(NSF 1241056)

John M. Bates
Field Museum of Natural History
(NSF 1241075)

Barbara M. Thiers
Scott Mori
New York Botanical Garden
(NSF 1241127)

BRAZIL MEMBERS

Lucia Garcez Lohmann
Diogo Meyer
Francisco Cruz
Universidade de Sao Paulo

Andre Freitas
Universidade Estadual de Campinas

This project seeks to understand the evolutionary and ecological history of Amazonia, one of the most diverse ecosystems on Earth. A goal of the project is to build a comprehensive database of plants and vertebrates, which, together with remote sensing, geology, and Earth-systems modeling, will be used to understand how the Amazonian biota assembled across space and time.

WEBSITE: AMAZONIABIODIVERSITY.ORG

Update

Great efforts have been invested towards planning and coordination between international research teams. A meeting of collaborators in Brazil in March 2013 resulted in fruitful discussions among colleagues and provided multiple directions for collaborative research. Major database and georeferencing activities have also been initiated for plants and birds, and the team is building a library of hundreds of DNA extracts of our target taxa from across Amazonia to undertake genetic analyses.

Publications

Rodrigues Nogueira, Afonso César, Rosemery Silveira, and José Tasso Felix Guimarães. "Neogene-Quaternary sedimentary and paleovegetation history of the eastern Solimões Basin, central Amazon region." *Journal of South American Earth Sciences* 46 (2013):89-99.

Lutz, Holly L., et al. "Biogeography and spatio-temporal diversification of *Selenidera* and *Andigena* Toucans (Aves: Ramphastidae)." *Molecular Phylogenetics and Evolution* 69.3 (2013): 873-883.

Lohmann, Lucia G., et al. "Pattern and timing of biogeographical history in the Neotropical tribe Bignonieae (Bignoniaceae)." *Botanical Journal of the Linnean Society* 171.1 (2013): 154-170.

Zuntini, Alexandre R., et al. "Primers for Phylogeny Reconstruction in Bignonieae (Bignoniaceae) Using Herbarium Samples." *Applications in Plant Sciences* 1.9 (2013): 1300018.

The wetlands of Amazonia is home to the largest rodent in the world, the Capybara (*Hydrochoerus hydrochaeris*), which can weigh as much as 150 pounds (60kg).

CREDIT: JOEL CRACRAFT, AMERICAN MUSEUM OF NATURAL HISTORY

Proj. 4 / 14

Do parallel patterns arise from parallel processes?

Michael N Dawson
Michael Beman
University of California Merced
(NSF 1241255)

Julian P. Sachs
University of Washington
(NSF 1241247)

This project examines the current and historical diversity in marine lakes that formed as melting ice sheets raised sea level. Many of these lakes were isolated from each other, providing opportunities for species in the lakes to evolve independently under similar environmental conditions.

WEBSITE: MARINELAKES.UCMERCED.EDU

Update

The first year's fieldwork for the collections of marine invertebrates, fishes, algae and mangroves was conducted in Palau, and the trip was highly successful. More than 1,900 tissue samples across 15 lakes and 21 species of macrobiota were sampled for genetic information. Over 400 microbial DNA samples were also collected and will be sequenced in depth, while microbial functional diversity is already being analyzed. The team also surveyed species diversity of fishes and of foraminifera from these lakes and several ocean locations, including resurveying a transect in Jellyfish Lake that previously was sampled in 1994. To find out how communities have changed through time, coring operations were initiated in Fall 2013. Analysis has begun on a subset of cores using visual imagery, x-radiography, and x-ray fluorescence. Initial data are already yielded intriguing results.

Mastigias papua medusa morphology in the ocean (top left) and five marine lakes.

CREDIT: MICHAEL N DAWSON, UC MERCED AND PATRICK COLIN, CORAL REEF RESEARCH FOUNDATION

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

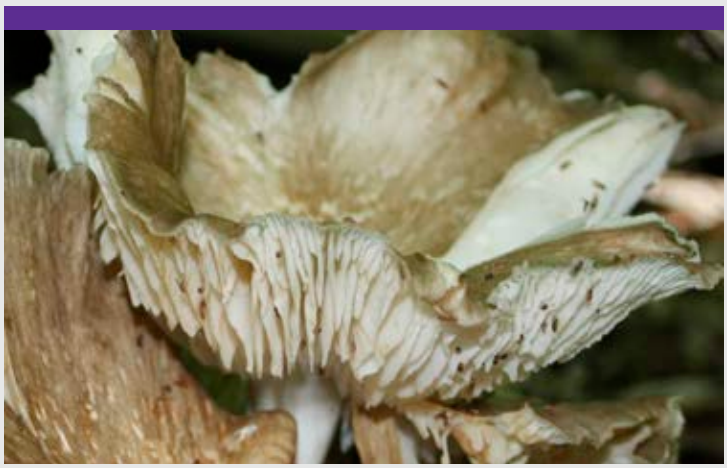
Angela E. Douglas
Gregory Loeb
Cornell University
(NSF 1241099)

John Jaenike
University of Rochester
(NSF 1241099)

This project examines the microbial communities in the gut of fruit flies to understand how the fruit fly hosts and bacteria influence each other, and how this type of interaction may contribute to the process of evolution of hosts and the diverse assemblages of microbes that live within them.

Update

Major research activities thus far have focused on the taxonomic and functional diversity of gut microbiota. This has been accomplished by determining the bacterial composition of drosophilid flies with 16S rRNA gene amplicon sequencing and bacterial function by metatranscriptomic analysis. Various *Drosophila* species have been assembled and or cultured for analysis, and laboratory workflow methods have been optimized. Additional fluorescent *in situ* hybridization (FISH) microscopy techniques have been developed to visualize bacteria within the guts of wild drosophilids. For educational purposes, the research team has also been collaborating on an exhibition outreach activity entitled the "Art of Animal-Microbes."



Several *Drosophila* feeding and mating on a wild mushroom in Corbett's Glen Nature Park, Brighton, New York.

CREDIT: VINCENT G. MARTINSON, UNIVERSITY OF ROCHESTER

Top and Bottom: *Drosophila falleni* female on a wild mushroom cap in Corbett's Glen Nature Park, Brighton, New York.

CREDIT: VINCENT G. MARTINSON, UNIVERSITY OF ROCHESTER

Proj. 6 / 14

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

Astrid Ferrer
James Dalling
Katy Heath
University of Illinois
Urbana Champaign
(NSF 1241212)

Diverse groups of freshwater and marine fungi remain to be described from tropical waters. This project will look at the role that these aquatic fungi play in the decomposition of wood along salinity gradients in coastal rivers in Panama. A goal of the project will be to determine how gene expression patterns among these diverse fungi influence the rate and trajectory of wood decay in water.

WEBSITE: PUBLISH.ILLINOIS.EDU/AQUATICFUNGI

Update

During the first year of this project, infrastructure for the major field experiments were submerged at sites with four different salinity levels in three replicate watersheds on the Island of Coiba, on the Pacific coast of Panama. Additional inland replicates were also set up on Barro Colorado Island, Panama. In the Fall of 2013, two graduate students from the University of Illinois began working on the project. These students and other junior project members have already undergone extensive training in fungal culturing techniques, genetic extraction tools, and aquatic fungal identification and classification methods.

Top: Mouth of the Boca Grande River, Coiba Island, Panama. Aquatic fungi are being studied at this site and two other undisturbed rivers. Right: Axenic cultures of two aquatic fungal species. In general, aquatic ascomycetes grow very slowly in culture. This study screens culture-grown fungi for activity against tropical diseases.

CREDIT: KEVAN MANTELL (TOP), ASTRID FERRER (RIGHT)

Proj. 7 / 14

A community level approach to understanding speciation in Hawaiian lineages

Rosemary G. Gillespie
John Harte
Rasmus Nielsen
Patrick O'Grady
University of California
Berkeley
(NSF 1241253)

Daniel S. Gruner
University of Maryland
(NSF 1240774)

Kerry L. Shaw
Cornell University
(NSF 1241060)

Donald K. Price
University of Hawaii
(NSF 1241228)

This project examines arthropod communities on two Hawaiian islands to understand patterns and rates of evolution. The two islands differ in age, providing an opportunity to study evolution in multiple lineages in different ecological contexts.

Proj. 8 / 14

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

Bruce A. Hungate
J. Gregory Caporaso
Paul Dijkstra
Jane Marks
Egbert Schwartz
Northern Arizona University
(NSF 1241094)

Lance Price
Translational Genomics
(NSF 1241115)

This project examines the roles that taxonomic and genetic diversity of microbes play in the processing of new and old carbon in soils.

Update

An important part of this project has been to strengthen the relationship and scientific exchange between researchers at Northern Arizona University and the Translational Genomics Research Institute (TGen). Together, they have been developing molecular and bioinformatics tools that can be user-friendly to field biologists and ecologists. The web-based bioinformatics tools, in particular, may have a widespread impact for scientists worldwide. Major laboratory activities have been focused on extracting DNA from soil samples. Eighty samples from three different ecosystems are being evaluated for their bacterial and fungal loads and these samples are being further analyzed using pyrosequencing techniques.

Proj. 9 / 14

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

Anthony R. Ives
Volker Radeloff
University of Wisconsin
(NSF 1240804)

Kerry M. Oliver
University of Georgia
(NSF 1240892)

Jason Harmon
North Dakota State University
(NSF 1241031)

The project examines how genetic, taxonomic, ecological, and landscape diversity influence the control of agricultural pests by their natural enemies.

Update

The Ives research team has completed their first field season, including preliminary surveys of pea aphids in North Dakota and Georgia as well as long term monitoring of aphids and natural enemy abundances in alfalfa, soybean, and corn fields in Wisconsin. The team has been optimizing their genetic protocols and has made great progress in calculations of climate extremes for weather data from the last three decades. Additionally, in an effort to engage the general public in science and the scientific method, the research team has been preparing a pilot citizen science project designed to collect aphids throughout the United States.

Publication

Harmon, Jason P., and Brandon T. Barton. "On their best behavior: how animal behavior can help determine the combined effects of species interactions and climate change." *Annals of the New York Academy of Sciences* 1297.1 (2013): 139-147.

Proj. 10 / 14

The role of biodiversity for microbial adaptation to anthropogenic perturbations

Kostas Konstantinidis
Jim Spain
Eberhard Voit
Georgia Tech
(NSF 1241046)

This project examines how microbial species and communities respond to disturbance and to the presence of new organic compounds such as petroleum hydrocarbons, pesticides, and antibiotics.

WEBSITE: ENVE-OMICS.CE.GATECH.EDU

Update

Konstantinidis et al. have made great strides in recruiting and training talented personnel. The preliminary data is not only advancing the understanding of rare and abundant microbial plankton in Lake Lanier, but the research team has also provided a practical "how-to" guide for the analysis of metagenomics and metatranscriptomics datasets. The bioinformatics tools that have been developed in conjunction with this research, are complementary with existing tools and approaches, freely available for online analysis through the lab website, and fulfill current needs in the field of metagenomics.

Publication

Oh, Seungdae, et al. "Microbial community adaptation to quaternary ammonium biocides as revealed by metagenomics." *Environmental Microbiology* 15.10 (2013): 2850-2864.

Luo, Chengwei, Luis M. Rodriguez-R, and Konstantinos T. Konstantinidis. "A User's Guide to Quantitative and Comparative Analysis of Metagenomic Datasets." *Methods in Enzymology* 531 (2013): 525-547.

Above Image: Photo of Lake Eufaula, AL.

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

Proj. 11 / 14

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

Thomas E. Martin
Robert Fleischer
Ellen Martinsen
University of Montana
(NSF 1241041)

Frederick H. Sheldon
Louisiana State University
(NSF 1241059)

Robert G. Moyle
University of Kansas
(NSF 1241181)

This project examines multiple factors that may contribute to the maintenance of elevational gradients in biodiversity, using a diverse tropical bird fauna in Borneo.

Update

Major efforts have been invested towards monitoring, sample collection and genetic analysis of tropical bird species in Borneo. Over 1000 birds have been captured and banded, with blood samples obtained from over 900 individuals. Numerous microsatellite and single nucleotide polymorphism (SNP) genetic markers have been identified and over 20 microsatellite primer sets are being optimized. Phylogenies of these species are in the process of being constructed.

Publications

Martin, Thomas E., Riccardo Ton, and Alina Niklison. "Intrinsic vs. extrinsic influences on life history expression: metabolism and parentally induced temperature influences on embryo development rate." *Ecology Letters* 16.6 (2013):738-745.

Ghalambor, Cameron K., Susana I. Peluc, and Thomas E. Martin. "Plasticity of parental care under the risk of predation: how much should parents reduce care?." *Biology Letters* 9.4 (2013).

Arriero, Elena, Ania Majewska, and Thomas E. Martin. "Ontogeny of constitutive immunity: maternal vs. endogenous influences." *Functional Ecology* 27.2 (2013): 472-478.

Proj. 12 / 14

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

Hans W. Paerl
University of North Carolina
(NSF 1240851)

Wayne S. Gardner
University of Texas at Austin
(NSF 1240798)

Steven W. Wilhelm
University of Tennessee
(NSF 1240870)

Ferdinand L. Hellweger
Northeastern University
(NSF 1240894)

This project examines the species and genetic diversity of microbes in a lake that experiences massive blooms of toxic cyanobacteria, and links that diversity to the processing of nitrogen that is the cause of the toxic blooms.

WEBSITE: UNC.EDU/IMS/PAERLLAB/RESEARCH/CYANOHABS

Update

In the summer of 2013 the research team traveled to Lake Taihu, where fieldwork, laboratory experiments and data modeling were initiated. The research team is currently involved in integrating algal growth rates, nitrogen fixation activity, algal community structures, genetic and diversity data into a biogeochemical ecosystem model of N cycling dynamics in Taihu. Media attention was brought to the Paerl et al. research team when NPR Science Friday did an interview with Dr. Paerl on harmful algal blooms. Additionally, a website has been developed to inform the public on the topic of cyanobacterial harmful algal blooms.

Publications

Paerl, Hans W., and Timothy G. Otten. "Harmful cyanobacterial blooms: causes, consequences, and controls." *Microbial Ecology* (2013): 1-16.

Scott, J. Thad, et al. "Comment: An alternative interpretation of the relationship between TN: TP and microcystins in Canadian lakes." *Canadian Journal of Fisheries and Aquatic Sciences* 70.8 (2013): 1265-1268.

Paerl, Hans W., and Timothy G. Otten. "Blooms Bite the Hand That Feeds Them." *Science* 342.6157 (2013): 433-434.

Otten, T. G., et al. "Spatiotemporal patterns and ecophysiology of toxigenic Microcystis blooms in Lake Taihu, China: implications for water quality management." *Environmental science & technology* 46.6 (2012): 3480-3488.

Xu, Hai, et al. "Growth response of Microcystis spp. To iron enrichment in different regions of Lake Taihu, China." *Hydrobiologia* 700.1 (2013): 187-202.

Paerl, H.W. "Combating the global proliferation of harmful cyanobacterial blooms by integrating conceptual and technological advances in an accessible water management toolbox." *Environmental Microbiology Reports* 5 (2013): 12-14.

Proj. 13 / 14

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

US MEMBERS

Nathan Swenson
Michigan State University
(NSF 1241136)

CHINA MEMBERS

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

This project integrates genetic data with phylogenetic and functional trait approaches to the study of tree biodiversity, with the goal of developing a predictive framework that can be used to understand processes that generate and maintain forest diversity.

Miconia racemosa seedling in the understory of the Luquillo Forest Dynamics Plot.

CREDIT: NATHAN SWENSON, MICHIGAN STATE UNIVERSITY

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

Jonathan P. Zehr
Zbigniew Kolber
University of California Santa Cruz
(NSF 1241221)

Kevin R. Arrigo
Stanford University
(NSF 1241093)

Matthew J. Church
University of Hawaii
(NSF 1241263)

This project uses genomics, molecular biology, and stable isotope tracers to investigate how changes in the form and availability of nitrogen affect taxonomic, genetic, and functional diversity of marine phytoplankton.

Update

The UCSC, Stanford, and UH research team has begun investigating the role of nitrogen in shaping plankton biodiversity and physiology in the low nutrient (oligotrophic) waters of the central North Pacific Ocean. Through a series of targeted "at sea" experiments, they have examined how different forms of nitrogenous substrates alter microbial community structure, metabolism and growth and the resulting impact on rates of plankton biomass production and photosynthetic energy generation. In addition, they are working with the San Francisco Exploratorium in developing an exhibition that demonstrates the importance of marine microbes to global biogeochemical cycling and highlights the various tools (flow cytometry and metagenomics) commonly used by microbial oceanographers.

A view from the bridge aboard the R/V Kilo Moana, the UNOLS research vessel operated by the University of Hawaii, at Station ALOHA, the field site for the Hawaii Ocean Time-series (HOT) program.

CREDIT: PAUL LETHABY, UNIVERSITY OF HAWAII

Proj. 1 / 12

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

Lisa K. Belden
Leanna L. House
Roderick Jensen
Virginia Polytechnic Institute and State University
(NSF 1136640)

Reid N. Harris
James Madison University
(NSF 1136602)

Kevin P. C. Minbiole
Villanova University
(NSF 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.

Update

Major collection efforts were conducted in Panama in 2012, where three amphibian species at four distinct sites and a total of 138 amphibian hosts were sampled. Data processing is ongoing to investigate the bacterial community structure and metabolite function from the field surveys. In the summer of 2013, laboratory trials were conducted to evaluate pre- and post- chytrid exposure on microbial communities. This will be followed by additional analyses of bacterial community structure, transcriptome and metabolites, which should be completed by the spring of 2014. Major news media, such as the Washington Post and the Today Show have highlighted some of this team's work.

The red-eyed treefrog, *Agalychnis callidryas*, is found in Panamanian rain forests. The skin bacteria from this species and four additional species are being studied to determine how diverse communities of microbes provide protection from a lethal skin fungus *(Batrachochytrium dendrobatidis)*.

CREDIT: BRIAN GRATWICKE, SMITHSONIAN CONSERVATION BIOLOGY INSTITUTE

Proj. 2 / 12

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

Thomas Brooks
Gabriel C. Costa
Bruce Young
NatureServe
(NSF 1136586)

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

Stephen B. Hedges
Pennsylvania State University University Park
(NSF 1136590)

Volker C. Radeloff
University of Wisconsin Madison
(NSF 1136592)

Brooks and colleagues are using a database of the 13,000 land vertebrates of the Americas to consider how changes in one dimension of biodiversity influences changes in others. Understanding how species composition influences the diversity of functional traits, for example, will improve the efficiency and effectiveness of conservation actions.

Update

The Brooks et al. research team has focused their efforts on data compilation in preparation for the subsequent analytical phases in coming years. This has included the compilation of timetree data for mammals and squamates, as well as data on squamate extinction risk and distribution. Further efforts have been extended towards methods testing for measuring and mapping beta-diversity as well as the development of metadata standards.

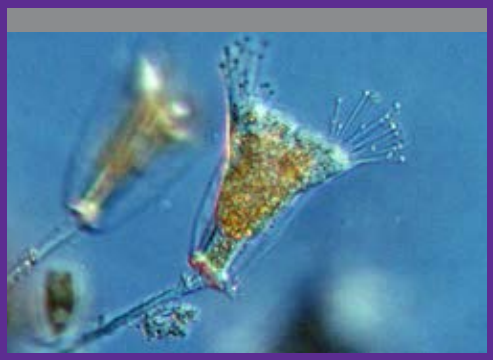
Publication

Young, B. "Red Listing Central American Squamates." *Herpetological Review* 43 (2012): 368.

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

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

This project, jointly supported by the National Natural Science Foundation of China, establishes an International Research Coordination Network for Biodiversity of Ciliates. The network includes researchers from the U.S., China, the U.K., and Brazil and broadens exploration of these important protists.



WEBSITE: IRCN-BC.MYSPECIES.INFO

Update

An international symposium on ciliates research was organized and took place in September 2012 with more than 40 participants from nine countries. As a part of this workshop, the team identified "20 Grand Challenges of Biodiversity of Ciliates" to provide a means to organize and encourage ciliate diversity research. Beyond this, the grand challenges will serve as a model for developing a similar set of challenges for other groups of protists. These challenges have already generated momentum and enthusiasm toward the practice of an integrative approach to biological research.

Top: *Acineta tuberosa*. Bottom Left: The group of students and faculty at the Laboratory of Protozoology, Ocean University of China, Qingdao. Bottom Right: *Diophrys sp*, a hypotrich; these ciliates form one of the largest groups in the phylum and are significant components of food webs in marine, freshwater, ephemeral and terrestrial habitats.

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

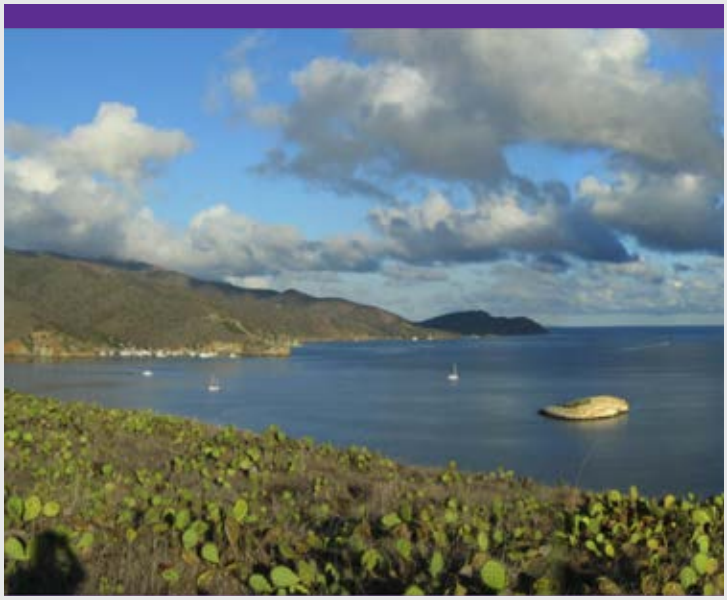
Pattern and process in marine bacterial, archaeal, and protistan biodiversity, and effects of human impacts

Jed A. Fuhrman
David A. Caron
John F. Heidelberg
William C. Nelson
Fengzhu Sun
University of Southern California
(NSF 1136818)

Fuhrman and colleagues compare heavily disturbed harbor regions and relatively pristine ocean habitat in the Los Angeles basin to better understand links between marine microbial diversity and ecosystem function.

Update

Routine sampling efforts, cell counts by microscopy and flow cytometry, as well as genetic data analysis have yielded a substantial amount of data. Thus far data analysis has indicated that spatial heterogeneity around the research station was on the same order of magnitude as day-to-day variability. This small-scale spatial and temporal variability, however, does not appear to mask shifts in the microbial community composition on longer time scales (months, seasons, years). Numerous publications have already resulted from this research.



Looking out to sea towards the USC Microbial Observatory from Catalina Island, near the USC Wrigley Marine Science Center.

CREDIT: JED FUHRMAN, UNIVERSITY OF SOUTHERN CALIFORNIA

Publications

Schnetzer, Astrid, et al. "Depth matters: microbial eukaryote diversity and community structure in the eastern North Pacific revealed through environmental gene libraries." *Deep Sea Research Part I: Oceanographic Research Papers* 58.1 (2011): 16-26.

Caron, David A., et al. "Marine protistan diversity." *Annual Review of Marine Science* 4 (2012): 467-493.

Caron, David A., and David A. Hutchins. "The effects of changing climate on microzooplankton grazing and community structure: drivers, predictions and knowledge gaps." *Journal of Plankton Research* 35.2 (2013): 235-252.

Kim, Diane Y., et al. "A combined sequence-based and fragment-based characterization of microbial eukaryote assemblages provides taxonomic context for the Terminal Restriction Fragment Length Polymorphism (T-RFLP) method." *Journal of Microbiological Methods* 91.3 (2012): 527-536.

Chang, Qin, et al. "Computational methods for the analysis of tag sequences in metagenomics studies." *Frontiers in Bio-science (Scholar Edition)* 4 (2012): 1333-1343.

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Proj. 5 / 12

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

Stephen P Hubbell
Brant C Faircloth
University of California
Los Angeles
Gregory S Gilbert
University of Southern
California
Travis C Glenn
University of Georgia
(NSF 1136626)

The basis of this research is to understand how the abundance and diversity of tropical trees, the diversity of fungal pathogens of trees, and forest dynamics are functionally interconnected. There is strong evidence that fungal pathogens play a major role in controlling the composition, abundance and population dynamics of trees in tropical forests. Because most tropical tree species are rare (occur at low density), understanding rarity is key to explaining the biodiversity of tropical forests.

Update

Major activities thus far have included doing tomographic scans of common and rare tree species in the Barro Colorado Island plot in Panama to determine which have hollow trunks. The research team has also been establishing a living collection of saplings of 100 tree species to test the pathogenicity and host range of heart-rot fungi. Lastly, efforts have been invested towards developing molecular protocols for identifying the fungal species in environmental samples. The team has scanned approximately 30% of the trees so far, but preliminary results have already been intriguing.

Publications

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Proj. 6 / 12

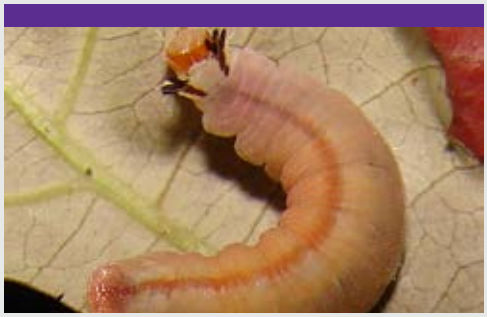
Coexistence, herbivore host choice, and plant-herbivore evolution in the recently radiated and speciose Neotropical tree genus, *Inga*

Thomas Kursar
Phyllis D. Coley
University of Utah
(NSF 1135733)

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

Update

Numerous international field collections have taken place, including field sites in Ecuador, Peru, Panama, Brazil, and French Guiana. A state-of-the-art UPLC-MS (ultra-performance liquid chromatography with mass detection) instrument has proven successful with the first metabolomics analysis of *Inga* secondary metabolites. In addition, preliminary efforts in barcoding have proven to be extremely important in species of sawfly and Lepidoptera that are not distinguishable.



A caterpillar, *Nymphidium sp.*, in the family Riodinidae consuming *Inga cylindrica* (Nouragues, French Guiana).

CREDIT: TOM KURSAR, UNIVERSITY OF UTAH

Proj. 7 / 12

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

Leonie C. Moyle
David C. Haak
Matthew W. Hahn
Indiana University
(NSF 1136707)

This research highlights the role of drought and herbivore defense in driving the remarkable diversity of wild tomato species. Given the economic importance of tomatoes and their relatives (e.g. peppers, potatoes), studies of this sort will help prepare societies for the future challenges facing global food security.

Update

Major research efforts have focused on preparing and beta-testing genetic data analysis and visualization software tools. The research team has also made great strides in characterizing drought and defense traits in the genus *Solanum*. Overall the data has supported assertions that these traits are decoupled from phylogenetic constraints and rather that they show evidence of a response to ecological factors.

Tobacco hornworm *Manduca sexta* on densely hairy leaves and buds of wild species of *S. habrochaites*.

CREDIT: D. HAAK

Proj. 8 / 12

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

Elena G. Litchman
Christopher A. Klausmeier
Michigan State University
(NSF 1136710)

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

Marianne Moore
Wellesley College
(NSF 1136657)

Edward C. Theriot
University of Texas Austin
(NSF 1136667)

Lev Yampolsky
East Tennessee State University
(NSF 1136706)

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.

WEBSITE: BAIKALDIMENSIONS.WORDPRESS.COM

Update

Both winter and summer sampling trips have been very productive and collections have taken place at numerous locations on Lake Baikal, including shallow and offshore areas as well as under-ice transects. Thermal experiments with *Epischura baikalensis*, the copepod that dominates the lake's pelagic zooplankton biomass, have already yielded exciting results.

Publications

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Litchman, Elena, et al. "Phytoplankton niches, traits and eco-evolutionary responses to global environmental change." *Mar Ecol Prog Ser* 470 (2012): 235-248.

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

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

Proj. 9 / 12

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

Ann Pearson
Peter Girguis
Harvard University
(NSF 1136484)

Jennifer Macalady
Pennsylvania State University
(NSF 1136218)

This project uses isotopic ratios of carbon, nitrogen, hydrogen, and sulfur produced during microbial metabolism to link guilds of microbes to their roles in biogeochemical and ecosystem processes. This novel approach will contribute to our understanding of what maintains functional and genetic diversity in microbes and, by extension, the roles those microbes play in ecosystems.

Update

Metagenomic, lipid, and isotope data indicate a diverse group of organisms mediating multiple functions in an anoxic, sulfidic lake. This includes both oxidation and reduction of sulfur; nitrogen fixation; and photoautotrophy, chemoautotrophy, and heterotrophy; all likely driven by fluctuating supplies of both carbon and sulfur.

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

Nathan J. Sanders
University of Tennessee Knoxville
(NSF 1136703)

Robert P. Dunn
North Carolina State University
(NSF 1136717)

Aaron M. Ellison
Harvard University
(NSF 1136646)

Nicholas J. Gotelli
Bryan A. Ballif
Sara I. Cahan
University of Vermont and State Agricultural College
(NSF 1136644)

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

Update

Major activities from the Sanders research team have already resulted in several publications. Research findings indicate that climatic warming may alter patterns of foraging behavior in predictable ways, however, these shifts vary among species and across sites. Preliminary genetics work has resulted in more than 70,000 transcripts with a total length of greater than 60 million base pairs. Methods are currently being adapted for species distribution modeling to use single nucleotide polymorphisms (SNP) and other genetic data markers to characterize evolutionary response to climate change.

The Climate Cascade Team.
CREDIT: A.M. ELLISON

Publications

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Proj. 11 / 12

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

Stefan M. Sievert
Jeffrey S. Seewald
Craig D. Taylor
Woods Hole Oceanographic Institution
(NSF 1136727)

Dionysios I. Foustoukos
Carnegie Institution of Washington
(NSF 1136608)

Ramunas Stepanauskas
Bigelow Laboratory for Ocean Sciences
(NSF 1136488)

Costantino Vetriani
Rutgers University New Brunswick
(NSF 1136451)

This project establishes an interdisciplinary, international research program to better understand the underlying microbiology and biogeochemistry in deep-sea hydrothermal vent ecosystems.

WEBSITE: DIVEDISCOVER.WHOI.EDU/EXPEDITION15

Update

The team just successfully completed the first research cruise to the deep-sea hydrothermal vents at 9ºN on the East Pacific Rise, which was featured on the educational Dive & Discover website. A science writer also reported for Scholastic's Science World Magazine. Prior to the cruise, the team had optimized their experimental setup to be fully integrated with isobaric gas tight samplers that collect and transfer natural microbial communities under high-pressure conditions. This allowed them to carry out novel experiments to assess the activity of chemosynthetic microorganisms under simulated sea floor conditions. Furthermore, this team discovered that several of the sequenced single cell amplified genomes obtained previously contained phage DNA, suggesting that their novel research methods may enable studies of horizontal gene transfer and *in situ* phage-host interactions in hydrothermal systems.

Publications

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Rinke, Christian, et al. "Insights into the phylogeny and coding potential of microbial dark matter." *Nature* 499 (2013): 431.3.

Proj. 12 / 12

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

Bess B. Ward
Daniel M. Sigman
Princeton University
(NSF 1136345)

Andrew E. Allen
J. Craig Venter Institute, Inc.
(NSF 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.

Update

The Ward research team has already led two cruises to the Sagrasso Sea in the North Atlantic Ocean, where they have conducted extensive sample and data collections. Based on the nitrate concentration data yielded from these cruises, the research team confirmed that they were successful in targeting two different sets of environmental conditions. An Accuri portable flow cytometer is in preparation for future subarctic North Atlantic cruises. The team continues to optimize the bioinformatics pipelines for phylogenetic analysis.

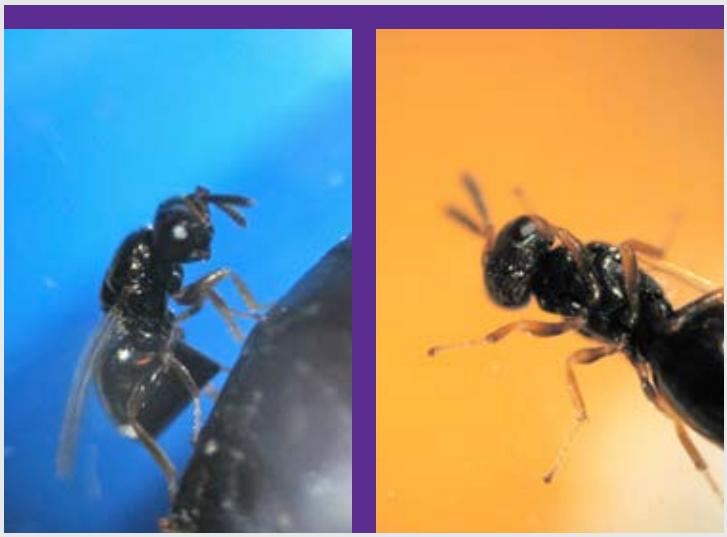
The microbial basis of animal speciation

Seth Bordenstein
Vanderbilt University
(NSF 1046149)

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

Update

The research conducted by Bordenstein et al. has upgraded the definition of Life / Biodiversity to be understood as a hologenome: a conglomerate of genomes from the nucleus, organelles, and microbiota that together change in response to Darwinian natural selection. This research team has coined the term "Phylosymbiosis" for the pattern seen in *Nasonia* and they believe that this pattern will be found in other animal and plant species. With these studies, the *Nasonia* wasp continues to emerge as a model system for genomic and now microbiomic studies. Microbiome research is relevant to health and disease, and this evolutionary-focused work now takes one step further to ask: Who are we as animal/microbe chimeras? And how did evolution shape these interactions?



A *Nasonia* parasitoid wasp, the model organism of the Bordenstein et al. Dimensions project. These wasps are smaller than a fruit fly and only parasitize house flies or blow flies.

CREDIT: ROBERT BRUCKER AND SETH BORDENSTEIN, DEPARTMENT OF BIOLOGICAL SCIENCES, VANDERBILT UNIVERSITY

Publications

Brucker, Robert M., and Seth R. Bordenstein. "The roles of host evolutionary relationships (genus: Nasonia) and development in structuring microbial communities." *Evolution* 66.2 (2012): 349-362.

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Proj. 2 / 16

Function at multiple spatial and genetic scales in a keystone plant-microbe symbiosis

Thomas Bruns
John W. Taylor
University of California Berkeley
(NSF 1046115)

Kabir G. Peay
University of Minnesota Twin Cities
(NSF 1045658)

Rytas Vilgalys
Duke University
(NSF 1046052)

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

WEBSITE 1: STANFORD.EDU/%7EKPEAY/DOB_HOME.HTML
WEBSITE 2: VDM.SDSU.EDU/IVIREONS

Update

This team's published work has demonstrated spatial and functional patterning differences between ectomycorrhizal and saprobic fungi at local scales. They found that species richness of ectomycorrhizal (EM) fungi and sabropic fungi are correlated with different functional activities in the bulk soil. Additionally, genetic analysis of two fungal individuals from 300km apart showed high rates of heterozygosity, and indicated slight but highly significant genetic differentiation. Overall these results are providing novel insights into the way the soil fungal fraction of pine communities are structured and how they function.

Publications

Talbot, Jennifer M., et al. "Independent roles of ectomycorrhizal and saprotrophic communities in soil organic matter decomposition." *Soil Biology and Biochemistry* 57 (2012):282-291.

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Proj. 3 / 16

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

Bradley Cardinale
University of Michigan Ann Arbor
(NSF 1046121)

Charles F. Delwiche
University of Maryland College Park
(NSF 1046075)

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

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

Update

Genetic sequencing of algae has resulted in the generation of a tremendous amount of data: more than 470,505,945,780 nucleotides. This team developed phylogenomic and bioinformatic tools in order to adequately process and analyze these data. Some of the major findings suggest that evolutionary history does not play any role in controlling species interactions, species coexistence, nor the functioning of ecosystems. As such, Darwin's claim that closely related species compete more strongly and are less likely to coexist may need to be revisited and revised. In addition, we may also need to revisit and revise claims that conservation of evolutionary diversity will insure the future of biodiversity and the functioning of ecosystems that are being subjected to environmental change. Findings from this study have not only resulted in a substantial number of academic publications, but the research findings have percolated into the popular news media, expanding its impact beyond a strictly scientific community.

Publications

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Cardinale, Bradley J., et al. "Biodiversity loss and its impact on humanity." *Nature* 486.7401 (2012): 59-67.

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Cardinale, Bradley J., et al. "Biodiversity simultaneously enhances the production and stability of community biomass, but the effects are independent." *Ecology* 94 (2013): 1697-1707.

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Narwani, Anita, et al. "Experimental evidence that evolutionary relatedness does not affect the ecological mechanisms of coexistence in freshwater green algae." *Ecology Letters* 16.11 (2013): 1373-1381.

Fritschie, Keith Jeffrey, et al. In press "Evolutionary history and the strength of species interactions: testing the phylogenetic limiting similarity hypothesis." *Ecology* (2013).

Undergraduate research assistants sample algae from lab experiment (top) and maintain chemostats (bottom).

CREDIT: BRADLEY CARDINALE

International Research Coordination Network—Diversity and forest change: Characterizing functional, phylogenetic and genetic contributions to diversity gradients and dynamics in tree communities

US TEAM

Stuart Davies
Harvard University
W. John Kress
Smithsonian National Museum of Natural History

Rick Condit
Center for Tropical Forest Science, Smithsonian Tropical Research Institute (STRI)

Nathan G. Swenson
Michigan State University
Helene Muller-Landau
STRI
(NSF 1046113)

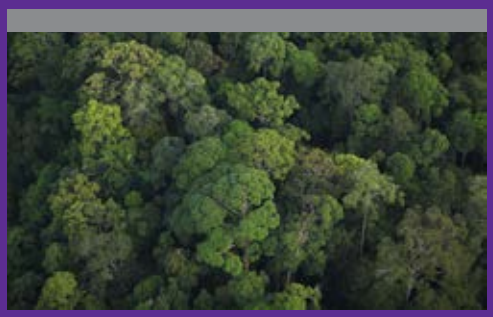
CHINA TEAM

Zhanqing Hao
Institute of Applied Ecology, Chinese Academy of Sciences (CAS)
Keping Ma
Institute of Botany, CAS

Wanhui Ye
South China Botanical Garden, CAS
Jie Li
Xishuangbanna Tropical Botanical Garden, CAS

Xiangcheng Mi
Institute of Botany, CAS
Xugao Wang
Institute of Applied Ecology, CAS

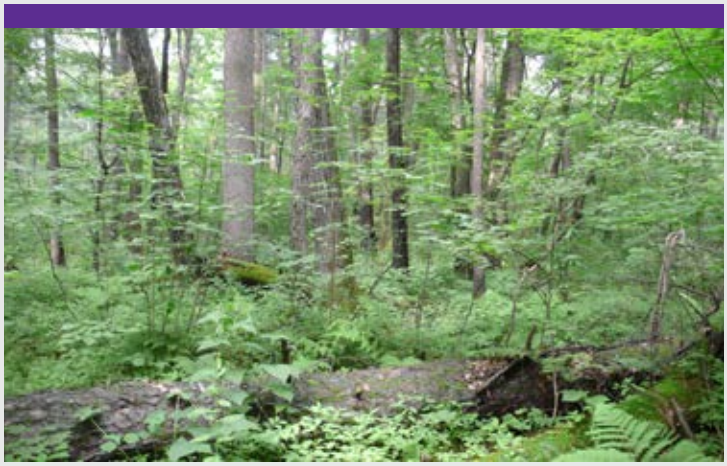
This Dimensions project was the first to be funded by the partnership between NSF and the National Natural Science Foundation of China. A group of forest scientists from the US, China, and other parts of Asia have created an international research coordination network (IRCN) to explore the resilience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



WEBSITE: CTFSNEWS.BLOGSPOT.COM

Update

The Davies et al. research team has, in a short time, published a substantial volume of academic research. Assembling this diverse group of students, post-docs and other researchers in Dimensions funded workshops was critical to enabling this productivity. Many of the Chinese and U.S. participants (and others from around the world) have found that the three-week workshop time was their most intense and productive research time in the year. Many of the dozens of papers published in the past year have been significant, several have received notable mentions in other journals or science media.



Publications

Chang-Yang, Chia-Hao, et al. "Long-term Seedling Dynamics of Tree Species in a Subtropical Rain Forest, Taiwan." *Taiwania* 58.1 (2013): 35-43.

Condit, Richard, Ryan A. Chisholm, and Stephen P. Hubbell. "Thirty Years of Forest Census at Barro Colorado and the Importance of Immigration in Maintaining Diversity." *PloS One* 7.11 (2012): e49826.

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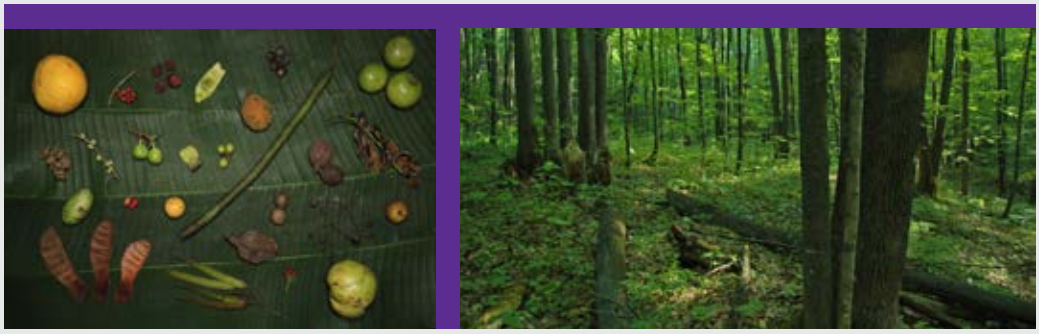
CONTINUE

Left: Temperate Forest at CTFS plot in Changbaishan, China. Above: Canopy of the plot at Lambir, Malaysia.

CREDIT: STUART DAVIES (LEFT), CHRISTIAN ZIEGLER (ABOVE)



Left: Seeds from the plot at Huai Kha Khaeng, Thailand. Right: Understory in the plot at Wabikon Lake Forest, USA.

CREDIT: STUART DAVIES

Detto, Matteo, and Helene C. Muller-Landau. "Fitting Ecological Process Models to Spatial Patterns Using Scalewise Variances and Moment Equations." *The American Naturalist* 181.4 (2013): E68-E82.

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Lutz, James A., et al. "Ecological importance of large-diameter trees in a temperate mixed-conifer forest." *PloS One* 7.5 (2012): e36131.

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Liu, Xiaojuan, et al. "Covariation in plant functional traits and soil fertility within two species-rich forests." *PloS One* 7.4 (2012): e34767.

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Proj. 5 / 16

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

Richard Lankau
University of Georgia
(NSF 1045977)

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

Update

The Lankau research team has conducted substantial sampling efforts across 12 sites around the Eastern United States as well as large greenhouse experiments testing local adaptation of plants to soil communities. The greenhouse experiments have yielded significant results on how plant adaptation is impacted by soil microbial communities. Genetic sequencing efforts are ongoing and the Lankau research team has additionally been reaching out broadly to engage community members via citizen science projects.

Proj. 6 / 16

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

Carol Lee
University of Wisconsin Madison
(NSF 1046372)

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

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

Update

In the first years of the study, the research team successfully refined methods for sampling the copepod microbiome and distinctly sampling microbes from the surrounding water. The research team has collected samples from a multitude of copepod populations and has finalized a protocol for the *de novo* assembly of the transcriptome in the absence of a reference genome, using the Trinity assembler. In the process, these researchers have also contributed to the newly released version of the Trinity assembler software, published earlier in 2013.

Publications

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Metzger, B.P., et al. "Direct sequencing of haplotypes from diploid individuals through a modified emulsion PCR-based single-molecule sequencing approach." *Mol Ecol Resour* 13.1 (2013): 135-43.

Lee, C.E., et al. "Feasting in fresh water: impacts of food concentration on freshwater tolerance and the evolution of food × salinity response during the expansion from saline into fresh water habitats." *Evol Appl* 6.4 (2013): 673-689.

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

Anne Arnold
University of Arizona
(NSF 1045766)

Ignazio Carbone
North Carolina State University
(NSF 1046167)

Georgiana May
University of Minnesota Twin Cities
(NSF 1045608)

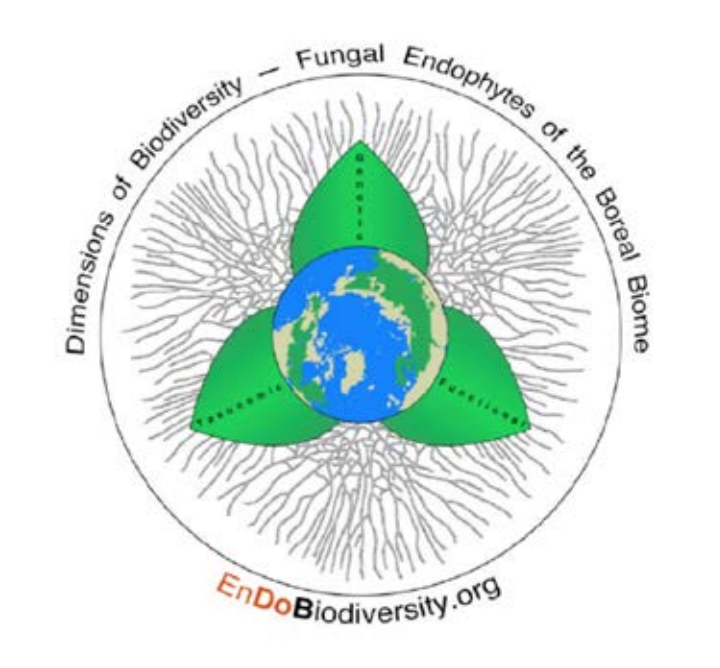
Francois Lutzoni
Duke University
(NSF 1046065)

This project investigates a diverse and poorly described group of endophytic fungi with symbiotic relationships to boreal vascular plants and lichens.

WEBSITE: ENDOBIODIVERSITY.ORG

Update

The EnDoBiodiversity team has sampled lichens and plants from around the world, including in Siberia, Sweden, Quebec and Alaska. More than 11,520 tissue segments have been processed to isolate endophytic and endolichenic fungi and more than 23,040 segments have been processed for high-throughput, culture-free analysis. This team has established methods for reinoculation of endophytes with endohyphal bacteria and has expanded phenotype evaluations. A publicly available culture library with as many as 6,800 strains of previously unknown boreal endophytic fungi and their associated endohyphal symbionts is being constructed. To disseminate this quickly growing wealth of information, a website highlighting the project and a Duke University course called Symbiosis have been created.



Logo for project on fungal endophytes of the boreal biome.

CREDIT: FRANCOIS LUTZONI & BETSY ARNOLD, DUKE UNIVERSITY & UNIVERSITY OF ARIZONA

Publications

Arnold, A. E., Carbone, I., Lutzoni, F. and May, G., "A multidimensional study of endophytic fungal diversity." *IMA Fungus* 2.1 (2011): 2-4.

Bascom-Slack, C., Arnold, A. E., Strobel, S. A. "Student-directed discovery of the plant microbiome and its products." *Science* 338 (2012): 485-486.

Gazis, R., et al. "Culture-based study of endophytes associated with rubber trees in Peru reveals a new class of Pezizomycotina: Xylonomycetes." *Molecular Phylogenetics and Evolution* 65 (2012): 294-304.

May, G. and Nelson, P. "Defensive mutualisms: do microbial interactions within hosts drive the evolution of defensive traits?" *Functional Ecology* (2013) doi: 10.1111/1365-2435.12166.

Monacell, J. T. and Carbone, I. "Mobyle SNAP Workbench: A web-based analysis portal for population genetics and evolutionary genomics." *Bioinformatics* (2014) doi: 10.1093/bioinformatics/btu055.

Olarte, R. A., et al. "Effect of sexual recombination on population diversity in aflatoxin production by Aspergillus flavus and evidence for cryptic heterokaryosis." *Molecular Ecology* 21 (2012): 1453-1476.

U'Ren, J. M. et al. "Host and geographic structure of endophytic and endolichenic fungi at a continental scale." *American Journal of Botany* 99 (2012): 898-914.

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

CREDIT: AE ARNOLD

Biological controls in the ocean: The Redfield Ratio

Adam Martiny
Steven Allison
University of California Irvine
(NSF 1046297)

Michael Lomas
Bigelow Laboratory for Ocean Sciences
(NSF 1303287)

Benjamin Van Mooy
Bermuda Institute of Ocean Sciences
(NSF 1045966)

Simon Levin
Princeton University
(NSF 1046001)

Kun Zhang
University of California San Diego
(NSF 1046368)

The Redfield ratio is the ratio of nitrogen to phosphorus in seawater. Understanding how biodiversity regulates the Redfield ratio will provide important insights for understanding the role of biodiversity in regulating global nutrient cycles.

WEBSITE: BCO-DMO.ORG/PROJECT/2178

Update

Data from this study illustrate potential flaws with one of the central tenets in marine biogeochemistry, the Redfield Ratio. Based on a global dataset of particulate elemental measurements and new elemental nutrient data for individual surface plankton populations, the Martiny research team found that surface plankton nutrient ratios exhibit large spatial variation with a global average higher than the canonical Redfield Ratio. This study has provided direct observational evidence that the coupling between oceanic carbon, nitrogen, and phosphorus cycles is more dynamic than previously considered. In addition to numerous academic publications, this project has produced a novel theoretical model for conceptualizing elemental ratios in phytoplankton populations, as well as a new methodology for metagenomic sequencing on as few as 1,000 cells for characterizing diversity.

Members of PI A. Martiny and co-PI S. Allison laboratories at the sampling site at Newport Pier, Calfornia.

CREDIT: ADAM MARTINY, UNIVERSITY OF CALIFORNIA, IRVINE

Publications

Freitas, Sara, et al. "Global distribution and diversity of marine Verrucomicrobia." *The ISME Journal* 6.8 (2012): 1499-1505.

Martiny, Adam C., Kathleen Treseder, and Gordon Pusch. "Phylogenetic conservatism of functional traits in microorganisms." *The ISME Journal* 7.4 (2013): 830-838.

Allison, Steven D., et al. "Fine-scale temporal variation in marine extracellular enzymes of coastal southern California." *Frontiers in Microbiology* 3 (2012): 1-10.

Lomas, M.W., et al. "Effect of ocean acidification on cyanobacteria in the subtropical North Atlantic." *Aquatic Microbial Ecology* 66 (2012): 211-222.

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

Nancy Moran
University of Texas at Austin
(NSF 1415604)

Jay Evans
USDA ARS
(NSF 1046153)

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

Update

Through this research, Moran et al. have begun to establish a firm foundation of the taxonomy, function and genetics of the bacterial microbiota of honey bees and bumble bees. The distribution and abundance of the major bacterial species present in the guts of these bee groups has been established and this team has begun to provide formal taxonomy for the bee gut species. These efforts will greatly enhance the field by enabling different researchers to refer to known strains. Additional *in situ* hybridization studies have shown that the microbiota members have characteristic locations in the bee gut. The importance of honey bees and bumble bees to agricultural pollination means that these results will have significance for agricultural systems. In addition, there are many parallels between the bee gut microbiota and human gut microbiota, so these results may have relevance to understanding human gut bacteria in both health and disease.

Top: Bumble bee at a flower *(Bombus sonorus)*. Above: Honeybee workers and queen on the hive *(Apis mellifera)*.

CREDIT: NANCY MORAN, UNIVERSITY OF TEXAS AT AUSTIN (TOP), JAY EVANS, USDA (ABOVE)

Publications

Martinson, Vincent G., Jamie Moy, and Nancy A. Moran. "Establishment of characteristic gut bacteria during development of the honeybee worker." *Applied and Environmental Microbiology* 78.8 (2012): 2830-2840.

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Sabree, Zakee L., Allison K. Hansen, and Nancy A. Moran. "Independent studies using deep sequencing resolve the same set of core bacterial species dominating gut communities of honey bees." *PLoS One* 7.7 (2012): e41250.

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Tian, Baoyu, et al. "Long-term exposure to antibiotics has caused accumulation of resistance determinants in the gut microbiota of honeybees." *mBio* 3.6 (2012): 1-7.

Engel, Philipp, and Nancy A. Moran. "Functional and evolutionary insights into the simple yet specific gut microbiota of the honey bee from metagenomic analysis." *Gut microbes* 4.1 (2013): 60-65.

Cornman, R. Scott, et al. "Pathogen webs in collapsing honey bee colonies." *PloS One* 7.8 (2012): e43562.

Dimensions of Biodiversity Distributed Graduate Seminar

Julia Parrish
University of Washington
(NSF 1050680)

A distributed graduate seminar is serving as a baseline for the planned 10-year program. A synthesis of the current understanding of the dimensions of biodiversity is posted on a wiki, crowd-sourced regularly, and "frozen" periodically to allow assessment of progress.

WEBSITE 1: DBDGS.ORG
WEBSITE 2: BIODIVERSEPERSPECTIVES.COM

Update

The Dimensions of Biodiversity Distributed Graduate Seminar (DBDGS) has been very successful, and to date has included collaborations with 4 NGOs, 15 countries, and 85 partners. A student run blog on Biodiversity "BioDiverse Perspectives," which was launched in January 2013, has established a model for graduate student engagement in the field of Biodiversity. There have been more than 51 posts, 200 comments written, and more than 30,000 page views. Furthermore, biodiversity baselining efforts, encompassing more than 19,000 papers within the field of biodiversity, have yielded fascinating preliminary data and network analyses.

Publications

Wolf, Jeffrey A., et al. "Plant Species Richness is Associated with Canopy Height and Topography in a Neotropical Forest." *Remote Sensing* 4.12 (2012): 4010-4021.

Podgaiski, Luciana R., et al. "Spider Trait Assembly Patterns and Resilience under Fire-Induced Vegetation Change in South Brazilian Grasslands." *PloS One* 8.3 (2013): e60207.

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Collage representing dimensions of biodiversity with images contributed by student participants of the DBDGS program.

CREDIT: JES COYLE, DAVID GONTHIER, JONATHAN MOORE AND THE BROOKHAVEN NATIONAL LAB, GRAPHIC DESIGN BY CATHY SCHWARTZ

Proj. 11 / 16

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

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

Alexander Flecker
Kelly Zamudio
Cornell University
(NSF 1045960)

Steven Thomas
University of Nebraska Lincoln
(NSF 1045991)

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

WEBSITE: EEB.CORNELL.EDU/EVOTRAC/WELCOME.HTML

Update

Major sampling efforts, referred to by the team as a "Bioblitz" have taken place in both Colorado and Ecuador, resulting in the collection of thousands of aquatic organisms. Specimens have been identified based on morphology and DNA barcoding and the team is nearly 75% complete with the species discovery/taxonomy portion of the project. The work thus far has contributed to the understanding of how taxa are distributed across temperate and tropical elevational gradients, discovery of cryptic diversity in stream insects and frogs, and the diversity patterns along elevational gradients in these tropical and temperate stream systems.

Publications

Heinold, Brian D., et al. "Recent collection and DNA barcode of the rare coffee pot snowfly Capnia nelsoni (Plecoptera: Capniidae)." *Illiesia* 9.2 (2013) 14-17.

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Coloma, Luis A., et al. "Molecular phylogenetics of stream treefrogs of the Hyloscirtus larinopygion group (Anura:Hylidae), and description of two new species from Ecuador." *Zootaxa* 3364 (2012): 1-78.

Gill, Brian A., et al. "Morphological taxonomy, DNA barcoding, and species diversity in southern Rocky Mountain headwater streams." *Freshwater Science* 33.1 (2013): 288-301.

Proj. 12 / 16

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

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

This project examines virus diversity on coral reefs along a gradient of human-caused effects at both regional and global scales.

WEBSITE 1: VDM.SDSU.EDU
WEBSITE 2: VDM.SDSU.EDU/IVIREONS

Update

Numerous publications, as well as two websites, have resulted so far from this project. The Rohwer research team has also developed several computational tools including an improved prophage finding program and more neural network programs capable of predicting function. The programs PhySpy, iVIREONS, and many other software resources have been developed by this team, and will be used by the scientific community far beyond the lifetime of this project. It is anticipated that the methods being developed by Rohwer et al. will impact many computational, ecological, as well as biomedically related disciplines.

Publications

Edwards, Robert A., et al. "Real Time Metagenomics: Using k-mers to annotate metagenomes." *Bioinformatics* 28.24 (2012): 3316-3317.

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Kelly, L.W., et al. "Black reefs: iron-induced phase shifts on coral reefs." *ISME Journal* 6 (2012): 638-649.

Aziz, R.K., et al. "SEED servers: high –performance access to the SEED genomes, annotations, and metabolic models." *PLOS One* 7.10 (2012).

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

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

Andrew Latimer
University of California Davis
(NSF 1045985)

Justin Borevitz
University of Chicago
(NSF 1046251)

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

WEBSITE: DARWIN.EEB.UCONN.EDU/WIKI/INDEX.PHP/PARALLEL_EVOLUTIONARY_RADIATIONS_IN_PROTEA_AND_PELARGONIUM_IN_THE_GREATER_CAPE_FLORISTIC_REGION

Update

This study has involved major taxonomic sampling, which is nearly complete. Fieldwork has been conducted at greater than 95 sites across South Africa's Greater Cape Floristic Region. The field team collected trait data from 275 species at Hangklip, 273 species at Langeberg, and 241 species at Cederberg. For each species sampled, traits on five individuals—for a total of over 3,900 replicates—were collected. Thus far the study has verified the initial prediction that separate clades within the genus *Pelargonium* have distinct strategies of water use. Not only have several publications resulted from this project, but the researchers have also been engaged with regional conservation efforts in association with the Fynbos Forum to utilize Proteaceae to enhance conservation efforts.

Top: *Pelargonium peltatum*. Bottom: *Pelargonium crithmifolium*.

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

Publications

Carlson, Jane E., and Kent E. Holsinger. "Direct and indirect selection on floral pigmentation by pollinators and seed predators in a color polymorphic South African shrub." *Oecologia* 171 (2013): 905-919.

Carlson, Jane E., and Kent E. Holsinger. "Developmental Plasticity in Protea as an Evolutionary Response to Environmental Clines in the Cape Floristic Region." *PloS One* 7.12 (2012): e52035.

Martínez-Cabrera, Hugo I., et al. "Low levels of climate niche conservatism may explain clade diversity patterns in the South African genus Pelargonium (Geraniaceae)." *American Journal of Botany* 99.5 (2012): 954-960.

Significance of nitrification in shaping planktonic biodiversity in the ocean

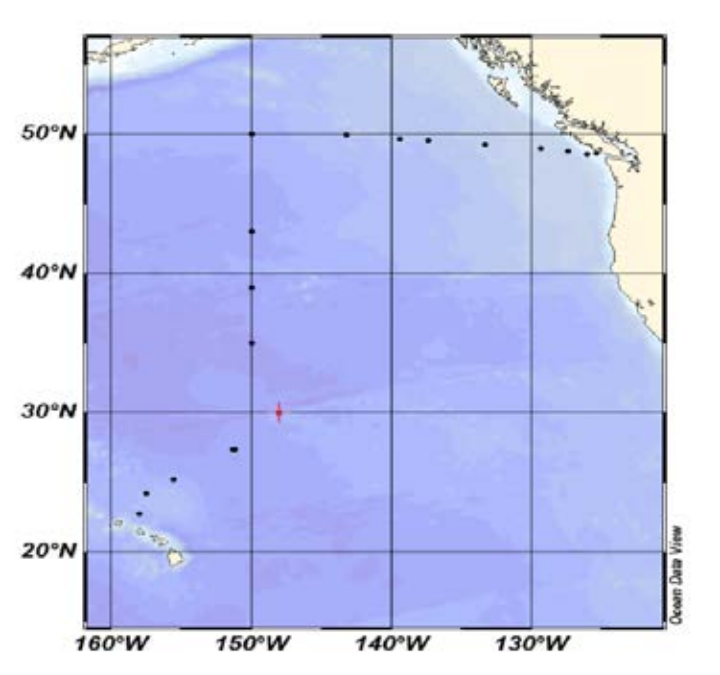
David Stahl
E. Virginia Armbrust
Allan Devol
Anitra Ingalls
University of Washington
(NSF 1046017)

James Moffett
University of Southern California
(NSF 1046098)

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

Update

Stahl's research team has conducted repeated collections from the Hood Canal in Washington State, and conducted a major sampling cruise from Seattle to Hawaii. This work has been followed by molecular characterization and analytic chemistry in order to evaluate the significance of ammonia oxidizing populations in shaping water chemistry and the population structure of plankton in the upper water column. Initial data showed that the addition of copper to ammonia oxidizing Archea (AOA) stimulates nitrification rates by 20 fold. These findings suggest that copper limitation in the euphotic zone may limit AOA and thus contribute to the observed reduction in nitrification rates in this zone.



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

Publications

Merbt, Stephanie N., et al. "Differential photoinhibition of bacterial and archaeal ammonia oxidation." *FEMS Microbiology Letters* 327.1 (2012): 41-46.

Stahl, David A., and José R. de la Torre. "Physiology and diversity of ammonia-oxidizing archaea." *Annual Review of Microbiology* 66 (2012): 83-101.

Yan, Jia, et al. "Mimicking the oxygen minimum zones: stimulating interaction of aerobic archaeal and anaerobic bacterial ammonia oxidizers in a laboratory-scale model system." *Environmental Microbiology* 14.12 (2012): 3146-3158.

Amin, Shady A., et al. "Copper requirements of the ammonia-oxidizing archaeon Nitrosopumilus maritimus SCM1 and implications for nitrification in the marine environment." *Limnol Oceanogr* 58.6 (2013): 2037-2045.

Horak, Rachel EA, et al. "Ammonia oxidation kinetics and temperature sensitivity of a natural marine community dominated by Archaea." *The ISME Journal* 7 (2013): 2023-2033.

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Metcalf, William W., et al. "Synthesis of methylphosphonic acid by marine microbes: a source for methane in the aerobic ocean." *Science* 337.6098 (2012): 1104-1107.

Proj. 15 / 16

The role of viruses in structuring biodiversity in methanotrophic marine ecosystems

David Valentine
University of California
Santa Barbara
(NSF 1046144)

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

WEBSITE: EXPLORATIONNOW.ORG/ATLANTIS

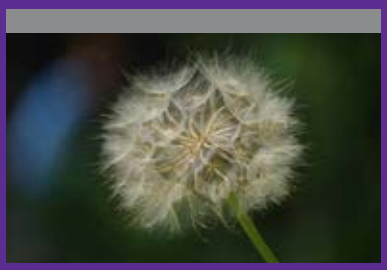
Update

The Valentine et al. research team has already made strides in enabling new techniques to visualize sea floor methane seep environments in three dimensions. Major efforts this past year were focused on the preparation and execution of the SEEPS research expedition, which took place aboard the RV Atlantis in September and October of 2013. Six undergraduate students joined the team on this research voyage. In preparation for the 2013 cruise, this team also focused major efforts towards the design for retrieval of *in situ* incubation devices. Incubators for *in situ* cultivation and manipulation of microbes in deep ocean cold seep environments will have major contributions to the field.

Proj. 16 / 16

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

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



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

WEBSITE: BOTANY.WISC.EDU/DOB

Update

The Waller research team has extended major efforts towards data compilation and database sharing, and they have made substantial strides in the genetic sequencing of barcode loci. Preliminary studies indicate that climate has indeed played a role in shaping both the distribution and abundance of species over the past 50 years. Additionally, the Waller research team has worked closely with the biotechnology corporation, Promega, to develop new techniques for extracting DNA from plants.

Above Image: *Tragopogon sp*, a typical example of wind-dispersed species.

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

Publications

Waller, Donald M., et al. "Wisconsin Vegetation Database–plant community survey and resurvey data from the Wisconsin Plant Ecology Laboratory." Vegetation databases for the 21st century. Edited by J. Dengler, M. Chytrý, J. Ewald, M. Finckh, F. Jansen, G. Lopez-Gonzalez, J. Oldeland, RK Peet, and JHJ Schaminée. *Biodiversity and Ecology* 4 (2012): 255-264.

Bai, Chengke, et al. "New reports of nuclear DNA content for 407 vascular plant taxa from the United States." *Annals of Botany* 110.8 (2012): 1623-1629.

Henss, Jillian M., et al. "Spatial scales of genetic structure and gene flow in Calochortus albus (Liliaceae)." *Ecology and Evolution* 3.6 (2013): 1461-1470.

Dimensions of Biodiversity

NATIONAL SCIENCE FOUNDATION
4201 WILSON BOULEVARD
ARLINGTON, VIRGINIA 22230
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