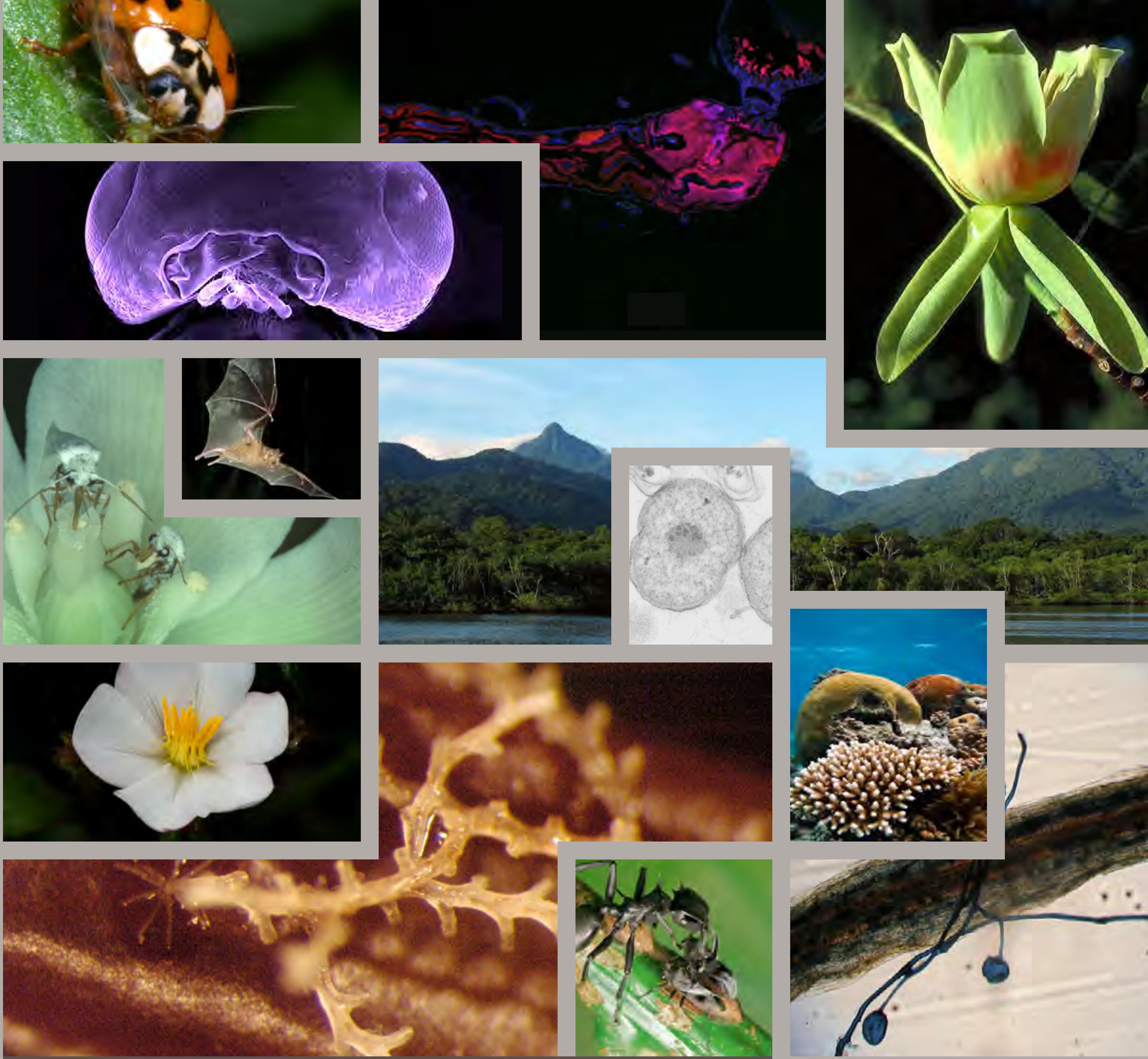

Dimensions of Biodiversity

NATIONAL SCIENCE FOUNDATION

2010 - 2014

PROJECTS

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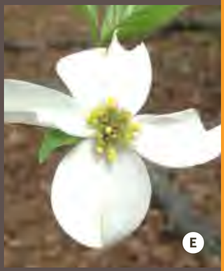

FRONT COVER IMAGES

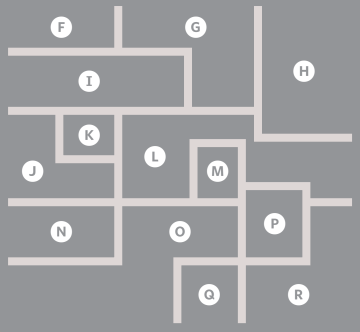

IMAGE CREDIT

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FRONT COVER

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ACKNOWLEDGMENTS

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

We thank Mina Ta, Design Specialist, for her important contributions to the abstract booklet. Finally we are grateful to AAAS Science and Technology Policy Fellows Drs. Sara Chun, Sean M. Watts, and Karen Alroy who were most helpful in the strategic planning for the Dimensions of Biodiversity program and the production of this abstract booklet.

Dimensions of Biodiversity

The Dimensions of Biodiversity program is now in its fifth year of research support to characterize the least-well-known aspects of the diversity of life on Earth. The National Science Foundation (NSF) funded 12 new projects in fiscal year 2014 bringing the total number of funded projects to 67.

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. Recent estimates predict that there may be as many as ~8.7 million eukaryotic species globally, of which ~2.2 million are marine[1]. This suggests that approximately 86% of existing species on Earth and 91% of species in the ocean have yet to be described, and these estimates do not even account for the diversity of prokaryotic organisms.

All species rely on a vast network of mostly invisible and largely unknown life forms, such as bacteria, 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. In addition, the genetic diversity within crop plants and their immediate relatives 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 biodiversity is shaped over time. Utilizing this same historic lens of phylogenetics to investigate ecological, physiological, behavioral, cellular and even molecular patterns and processes both strengthens and advances how we understand biodiversity. Despite centuries of study, we still have much to learn about the origin, maintenance, and function of diversity.

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

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[1] Mora, C., et al. "How many species are there on Earth and in the ocean?" *PLoS Biology* 9.8 (2011): e1001127.

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

APPROACH

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

> *This year's portfolio of projects will accelerate our understanding of biodiversity across disciplines and across scales of time and space. Through this program, we're witnessing a transformation in our ability to bridge scientific approaches and perspectives.*
>
> **Penny Firth**
> Division Director
> NSF Division of Environmental Biology

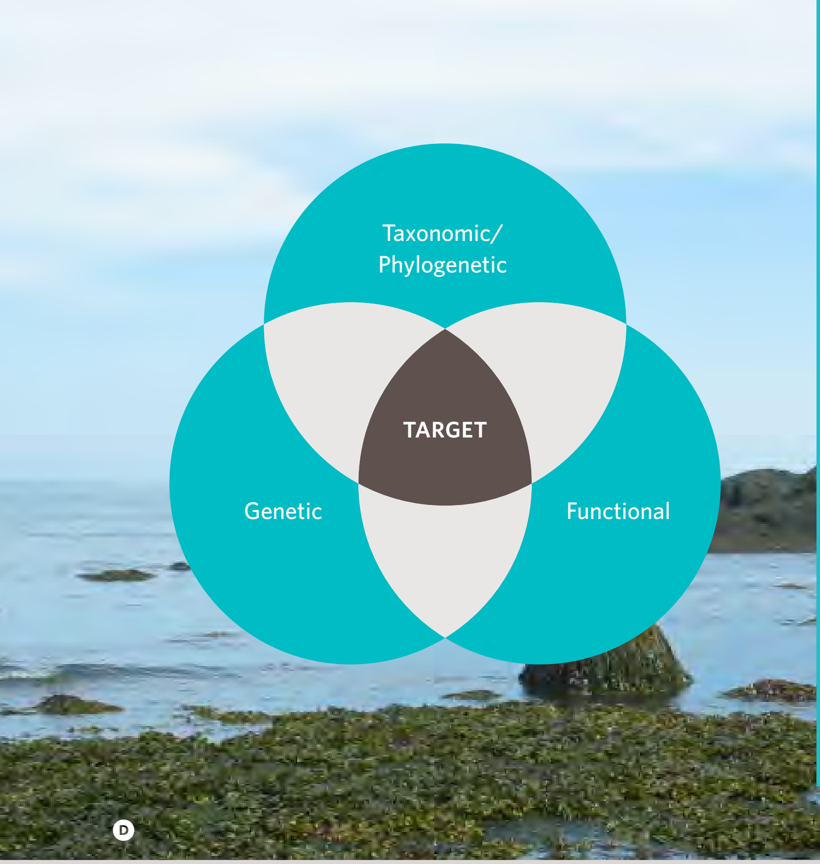
scales. Current international partnerships with the National Natural Science Foundation of China (NSFC) and the Brazilian funding agency [The São Paulo Research Foundation (FAPESP)] support the exchange of students and scientists, joint research projects, university partnerships and the digitization 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.

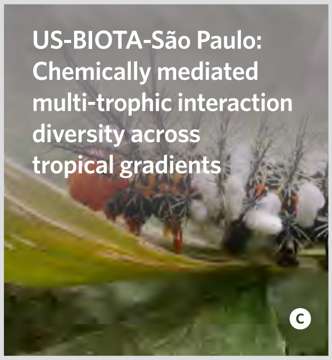
Dimensions of Biodiversity involves five streams of activity. The approach for supporting these activities involves planning and partnering, developing baselines of our current understanding, and assessing progress periodically during the decade in order to align investments with newly-appreciated priorities.

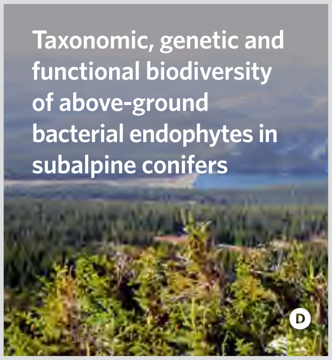
By 2020, Dimensions of Biodiversity is expected to have transformed our understanding of the scope and role of life on Earth and how biodiversity science is conducted. The initial focus of Dimensions has been on the integration of genetic, taxonomic/phylogenetic, and functional aspects of biodiversity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

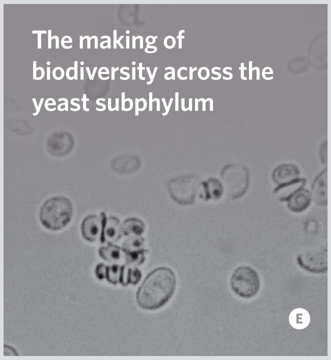
IMAGE CREDIT
Ⓐ Jeffry B. Mitton
Ⓑ Walter S. Judd
Ⓒ Jon Flanders
Ⓓ Susan H. Brawley

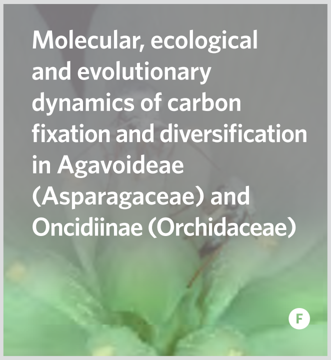


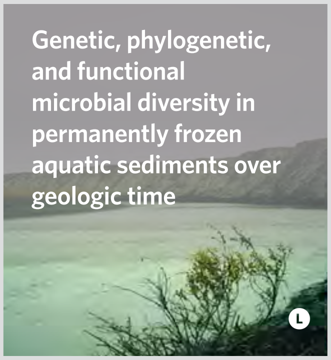
FY 2010	FY 2011	FY 2012	FY 2013	FY 2014	FY 2015
16 projects	12 projects	14 projects	13 projects	12 projects	Partners
US Total ~$25.7M	US Total ~$28.0M	US Total ~$26.4M	US Total ~$25.1M	US Total ~$23M	
BIO $18.9M	BIO $17.5M	BIO $21M	BIO $21.7M	BIO $22M	
Other NSF $6.8M	Other NSF $10.5M	Other NSF $4.7M	GEO $1.0M	GEO $1.0M	
		NASA $0.72M	NASA $2.5M		
NSFC ¥0.8M	NSFC ¥0.6M	NSFC ¥6M	NSFC ¥3M	NSFC ¥3M	NSFC Up to ¥6M
		FAPESP-São Paulo $2.2M	FAPESP-São Paulo $1.8M	FAPESP-São Paulo $2.0M	FAPESP-São Paulo Up to $4M











2014
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IMAGE CREDIT

Ⓐ Susan H. Brawley
Ⓑ Karen E. Sears
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Ⓕ Olle Pellmyr
Ⓖ Sarah Cummins
Ⓗ John Wertz & Alicia Withrow
Ⓘ Klaus Nüsslein
Ⓙ Jenny Xiang
Ⓚ Ryan McMinds & Jerome Payet
Ⓛ E.M. Rivkina

Proj. 1 / 12

The macroalgal microbiome in space and time: Maintaining primary producers in the Atlantic rocky intertidal zone

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

Intertidal macroalgae ("seaweeds") provide habitat, shelter and food to many invertebrates and young fishes. Much is now known about the adaptations and acclimations of intertidal algae to stressful levels of temperature, desiccation, and irradiance at low tide, but little is known about the bacteria associated with these algae or how they affect host function. Previous studies have shown that several intertidal algae lose their multicellular structure after antibiotic treatment; therefore, understanding the interactions between host macroalgae and their bacteria may change our understanding of algal responses to natural and anthropogenic stresses.

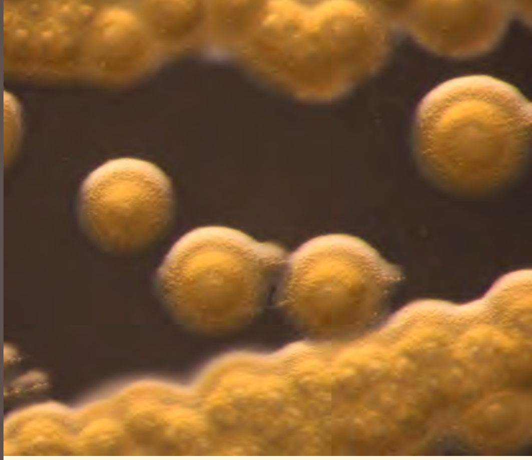
Microbiomes of host algae will be characterized within two prominent genera of the intertidal zone on the Maine shore (*Fucus*, also known as "rockweed" and *Porphyra*, also known as "laver"). A concurrent study comparing microbiomes of the mid-zone *Porphyra umbilicalis* and *Fucus vesiculosus* from the Northwest and Northeast Atlantic range will determine whether compositional changes found over an intertidal stress gradient are mirrored across the Atlantic. The potential to detect microbiome changes over historic time will be assessed using herbarium specimens. Environmental variation associated with microbiome collections will be measured with *in situ* sensors and from archival and real time data available from government climate services (e.g., NOAA).

Additionally, the significance of seasonal or latitudinal changes in the bacteria associated with an intertidal algal host will be examined. This will be done by studying the particular bacterial genes that are present at different sampling times and by studying host genetic responses to inoculations with host-associated bacteria. To study bacteria that are likely to be most critical to the normal structure and function of *Fucus* and *Porphyra*, the researchers will focus on bacterial isolations from algal spores and fertilized eggs. The temperature tolerances of key bacterial taxa will be determined in laboratory experiments, and, in association with genetic and taxonomic biodiversity data. The research will discover whether any key bacteria are inhibited by the environmental extremes found across the intertidal zone or over latitude, especially at the southern borders of the host range where climate change may disturb the bacterial community on the host alga. This research will test whether ecological paradigms developed for larger organisms in the intertidal zone also apply to bacteria (e.g., a stress-tolerant versus a stress-intolerant microbiome).

Trainees will include undergraduate thesis students, a Ph.D. student, a postdoctoral associate, and citizen scientists. Researchers will deposit isolates and voucher specimens into public collections, and, in collaboration with trained citizen scientists, they will provide digital access to all algal materials within the University of Maine Herbarium. This research will provide a baseline of the biodiversity of macroalgal microbiomes.

^ The low zone is uncovered for only an hour on many low tides. Here, a distant ledge is covered by high and mid-zone rockweeds, and the canopy of the low-zone *Fucus distichus* is just becoming exposed.

CREDIT: SUSAN H. BRAWLEY, UNIVERSITY OF MAINE



^ Colonies of an isolate of one of the many different bacteria present in nature on blades of *Porphyra umbilicalis* growing in Maine. This image shows the bacteria growing on solid media in Petri dishes.

CREDIT: SUSAN H. BRAWLEY, UNIVERSITY OF MAINE

^ The rocky intertidal zone on Atlantic shores often appears brown due to its cover by multiple species of brown macroalgae called rockweeds (*Fucus* spp.). These rockweeds shelter many other algae and animals from temperature, light and drying stresses that are present in a sharp gradient from the high to low zones at low tide.

CREDIT: SUSAN H. BRAWLEY, UNIVERSITY OF MAINE

^ The rockweed, *Fucus spiralis*, loses its normal morphology and undergoes disorganized growth without bacteria.

CREDIT: SUSAN H. BRAWLEY, UNIVERSITY OF MAINE

^ This mid-zone rockweed, *Fucus vesiculosus*, is one of the most abundant intertidal macroalgae.

CREDIT: SUSAN H. BRAWLEY, UNIVERSITY OF MAINE

^ The low-zone rockweed, *Fucus distichus*, is especially common on cold temperate shores of the northwest Atlantic.

CREDIT: SUSAN H. BRAWLEY, UNIVERSITY OF MAINE

^ This mid-zone red alga (mass of algae in photo's center), *Porphyra umbilicalis*, is consumed by many invertebrates, as well as humans.

CREDIT: SUSAN H. BRAWLEY, UNIVERSITY OF MAINE

Proj. 2 / 12

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

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This project aims to discover how sensory genes, developmental regulation, and morphological structures influence the ecological and taxonomic diversity of New World noctilionoid bats. These discoveries will illuminate the mechanisms underlying the different sensory abilities of ecological specialists and generalists, as well as the evolution of novel sensory modes.

The forces that enable or constrain adaptation and their influence on the evolution of different species remain unknown for most organisms. When genetic changes in a particular species confer access to new resources, this evolution of innovation is believed to be one of a few proposed mechanisms that enable a population to differentiate and specialize into a new and different species. These key innovations can often include new sensory adaptations that enable access to previously unavailable ecological resources. Sensory adaptations confer great advantages. For example, the keen eyesight of birds of prey allow them to pinpoint their targets with great accuracy, and echolocation in some bats and whales enables orientation and hunting in low-light environments that are lacking in other organisms. These advantages seem so dramatic, they raise an enduring question: why don't species evolve multiple sensory adaptations simultaneously?

This research will integrate toolkits from genomics, evolutionary developmental biology, and evolutionary anatomy to uncover the mechanisms of sensory innovation and specialization in New World noctilionoid bats. New phylogenetic comparative methods will then be used to model the influence of sensory innovations and possible physical limits to innovation on species and ecological diversity. Noctilionoid bats are an ideal system to study the mechanisms of sensory innovation because the approximately 250 species have evolved a wide range of adaptations to multiple sensory challenges. These include constant frequency echolocation (with Doppler-shift compensation) that allows the detection of insect prey in cluttered environments, ultraviolet light perception in one flower-visiting species, olfactory receptors associated with fruit detection in darkness, and the use of chemical receptors for non-volatile molecules that communicate sexual and social status.

By analyzing approximately 2000 genes involved in vision, hearing, olfaction and the vomeronasal system in more than 150 bat species, this multidisciplinary international team will find out how genetic variation contributes to sensory adaptation. To discover how some of these genes shape the development of distinct sensory systems, their actions will be studied in the lab. The relative sizes of eyes, inner ears, and chemical sensory structures in the nose will be combined with hypotheses about the relatedness of different species — or evolutionary trees — to evaluate whether total head size limits the evolution of multiple sensory structures. Data on the diet, anatomy and genetic variation of the bats will be integrated with evolutionary trees to model the influence of sensory adaptations on ecological and species diversity through time.

This research will illuminate the main biological forces in the genome, during embryonic development, and in anatomical structures that promote the success of species by adapting to their ever-challenging environment. Genes that determine key sensory adaptations will be identified, along with the timing of events in embryonic development that enables certain species to modify sensory structures. This will allow experimental manipulation of sensory structures and ultimately connect intrinsic biological mechanisms to the ecological demands that organism's experience. These mechanistic insights will provide a template for future studies with similarly diverse groups of mammals and other vertebrates.

Jamaican fruit bat, *Artibeus jamaicensis*, in flight. Along with closely related frugivorous bats of the New World, Jamaican fruit bats have a distinctive olfactory repertoire likely associated with the perception of volatile compounds from fruits.

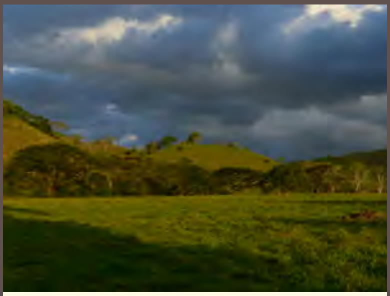
CREDIT: KAREN E. SEARS, UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN

Using mutliharmonic sweeps, the Antillean ghost-faced bat, *Mormoops blainvillei*, is able to feed at the forest edge.

CREDIT: JON FLANDERS, UNIVERSITY OF BRISTOL

The Fishing bat, *Noctilio leporinus*, uses echolocation over the surface of the water to detect fish.

CREDIT: JON FLANDERS, UNIVERSITY OF BRISTOL



Specialized sensory systems allow noctilionoid bats to travel between pastures and forest remnants and maintain plant population connectivity.

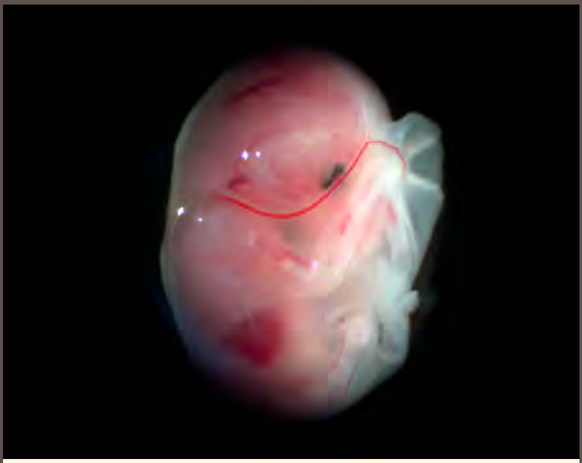
CREDIT: LAUREL R. YOHE, STONY BROOK UNIVERSITY

Cochleae from micro-CT scans. *Mormoops megalophylla* (left) and *Pteronotus parnellii* (right) differ dramatically in their echolocation calls.

CREDIT: STEPHEN ROSSITER, QUEEN MARY UNIVERSITY

Common vampire bat, *Desmodus rotundus*, in flight. Vampire bats have a distinctive set of sensory adaptations associated with their unique diet of vertebrate blood, including infrared sensors on the noseleaf.

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



Embryo of Seba's short-tailed bat, *Carollia perspicillata*. Tracking gene activity as sensory systems develop will allow investigators to discover the mechanisms that generate these diverse sensory systems.

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

Micro computerized tomography (CT) of the skull of adult Seba's short-tailed bat, *Carollia perspicillata*, showing highly opaque cochleae.

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

Noctilionoid bats contribute to the maintenance of this forest ecosystem on Hispaniola island.

CREDIT: LAUREL R. YOHE, STONY BROOK UNIVERSITY

Proj. 3 / 12

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

(CO-FUNDED WITH FAPESP)

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

The diversity of interactions among plants, insects, and their predators makes up a significant proportion of overall biodiversity and is a key component of ecosystem health. This is especially true for tropical forests, where ecologists are only beginning to understand the nature and complexity of these interactions.

Recent advances in chemistry and molecular biology provide the opportunity to understand the diversity of plant-insect interactions at three different levels (chemical, genetic, and taxonomic), how these different measures of diversity are shaped by environmental gradients and disturbances, and how this diversity affects insect outbreaks, forest stability, and productivity. The comprehensive sampling and methods used in this project will likely result in the discovery of new species of plants and insects as well as new biologically active molecules. An ancillary goal of this research is to deliver new tools and approaches that have powerful applications in agriculture and medicine. The international and multi-disciplinary research project provides copious research opportunities to K-12 students, science teachers, and citizen scientists, and the work is fully integrated with the volunteer-driven biodiversity research funded by Earthwatch Institute. Discoveries will be rapidly communicated to the public via websites, and scientific and popular publications.

This project is focused on plants in the diverse pepper genus, *Piper* (Piperaceae), associated herbivores, and parasitic wasps and flies. The research links measures of interaction diversity to genetic diversity and plant chemical diversity, and includes the following approaches: 1) Large scale sampling of herbivores and their parasitic wasps and flies on diverse *Piper* species across an array of sites to assess effects of environmental gradients on interaction biodiversity and ecosystem services. 2) Field experiments in which taxonomic, genetic, and interaction diversity are manipulated along with other environmental factors to strengthen inferences from the observational approaches. 3) Systematic analyses of plants, herbivores, and parasitic wasps and flies using traditional and genomic methods to document and describe new taxa, understand their relationships, and reveal hidden diversity. 4) Genetic analyses of plants, herbivores, and parasitic flies to understand how geography, plant evolutionary history and chemistry influence plants and their associated insects. 5) Characterization of chemical diversity of *Piper* species to examine how diversity in plant chemistry varies and how this variation affects entire communities.

The combination of quantitative sampling along elevational gradients and a large scale experimental framework will enable testing emerging hypotheses about relationships between plant chemistry, and different dimensions of diversity. This will contribute to understanding how large global changes in biodiversity and climate will affect plant-insect-predator interactions and how taxonomic and genetic diversity of plants and insect predators can affect outbreaks and control of harmful insects.

Teenage volunteers from Earthwatch Institute making extracts from *Piper* plants for analysis with Nuclear Magnetic Resonance spectroscopy (NMR). This process produces a metabolomic fingerprint for each plant species, allowing the project to quantify the diversity of defensive chemistry in each plant that is studied.

CREDIT: LEE DYER, UNIVERSITY OF NEVADA

Teenage volunteers from Earthwatch Institute working with adult moths collected from *Piper* plants. The volunteers are learning to pin the specimens, so that they can be identified and new species can be described. Legs from the moths are removed for genetics, and in some instances, the entire specimen is utilized for chemical and genetic analyses.

CREDIT: LEE DYER, UNIVERSITY OF NEVADA

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

CREDIT: LEE DYER, UNIVERSITY OF NEVADA

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

CREDIT: LEE DYER, UNIVERSITY OF NEVADA

Proj. 4 / 12

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

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The goal of this project is to determine the evolutionary and ecological significance of a novel symbiosis between pine trees and bacteria living inside their foliage as endophytes. A deeper understanding of how taxonomic, genetic and functional biodiversity of endophytes affects the capability of forest conifers to use nitrogen from the atmosphere has the potential to significantly improve our understanding of the nitrogen cycle and help solve a long-standing ecological mystery: where does the nitrogen come from in conifer forests?

Nitrogen is essential to all life on Earth, but is a growth-limiting nutrient in most ecosystems. For a long time, the only important pathways for nitrogen input to terrestrial ecosystems were thought to be microbes that live in the soil or in a symbiotic relationship with legumes, alders and a few other plants. Recent findings using DNA sequencing indicate that symbiotic endophytes living inside the foliage of high-elevation pines can fix atmospheric nitrogen.

The goal of this research is to investigate how the diversity of endophytes in pine foliage affects the amount of atmospheric nitrogen fixed within the tree. The research focuses on limber pine, a species with a wide climatic, elevational and geographic range. Limber pine grows in the Rocky Mountains from Alberta to New Mexico; in the Great Basin states of Nevada and Utah; and in the Sierra Nevada in California. To understand how endophyte diversity is shaped by the environment and how it shapes the nitrogen cycle in subalpine forests, the investigators will examine the biodiversity of endophytes in limber pine and co-occurring pine species across the limber pine range. Like most bacteria, the endophytes cannot be cultured in the lab. Therefore, cutting-edge methods including DNA sequencing and genome analysis will be integrated with established and highly sensitive methods for detecting and visualizing nitrogen fixing activity inside limber pine tissue.

The research has the potential to radically change our perspective on how some plants acquire nitrogen, and also our understanding of the terrestrial nitrogen cycle. Temperate and boreal coniferous forests accumulate more nitrogen in soil and vegetation than can be explained by known sources of nitrogen, suggesting an unknown biodiversity of nitrogen fixing bacteria exists in these ecosystems. Moreover, a better characterization of this symbiosis could influence crop and plantation management, enabling plants to get their nitrogen from symbiotic bacteria rather than from synthetic fertilizers. The experiments will take place at a small university that serves a high proportion of underrepresented minority and low-income students. Additionally, the research will engage teachers, administrators and students from a public K-8 school in a rural, low-income community in California.

View of the subalpine forest from treeline at Niwot Ridge on the Rocky Mountain's western slope, Colorado.

CREDIT: ANDREW MOYES, UNIVERSITY OF CALIFORNIA, MERCED

Ancient limber pine growing on a rocky slope.

CREDIT: JEFFRY B. MITTON, UNIVERSITY OF COLORADO

Testing for nitrogen fixation in the field. Bags are filled with gas that has a high concentration of the stable nitrogen isotope ^{15}N rather than ^{14}N, the dominant nitrogen isotope in the atmosphere. Microbes in the plant fix the $^{15}N_2$, which can then be detected in dried and ground plant material using spectrometric methods to measure the relative abundance of isotopes.

CREDIT: ANDREW MOYES, UNIVERSITY OF CALIFORNIA, MERCED

Measurements of nitrogen fixation in the lab.

CREDIT: ANDREW MOYES, UNIVERSITY OF CALIFORNIA, MERCED

Proj. 5 / 12

The making of biodiversity across the yeast subphylum

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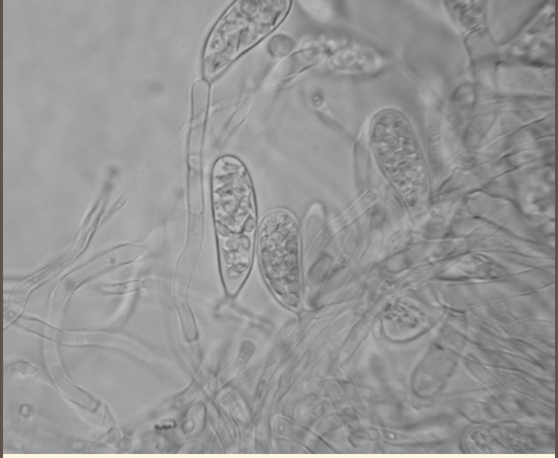
Yeasts of the ancient fungal subphylum Saccharomycotina inhabit every continent and every major aquatic and terrestrial habitat, and yet little is known about the place that most of these species fill in nature. A key factor of yeast ecological dominance is their impressive diversity of resource utilization abilities and strategies. This project seeks to understand the diversification of yeasts by using information written in their genome.

Among the yeasts, the bread, beer, and wine yeast *Saccharomyces cerevisiae* is the best known of these unicellular fungi and is also one of the best model organisms for molecular genetics research. In contrast to this well-known fermenter, the metabolisms of the other ~1,000 known species in this subphylum vary widely. Several of these yeasts are emerging pathogens, some can produce oil, many can metabolize xylose (the second most abundant monosaccharide in woody plant material), and most actually prefer cellular respiration, instead of fermentation. Some traits have evolved a handful of times, while others have evolved independently dozens of times, providing rich systems for the study of historical contingency and convergent evolution, respectively. The yeasts are more genetically and metabolically diverse than the vertebrates, but the genomic and ecological functions of most species remain unexplored.

To illuminate the genetic and ecological factors that drive yeast diversification and generate biodiversity, the research team will create the first comprehensive catalog of genetic and functional diversity for any high-level taxonomic rank by generating high-quality and richly annotated genome sequences for all known yeast species, inferring their definitive phylogeny and taxonomy, and tracing the evolution of genome content and traits. Overlaying quantitative physiological data will enable a broad integration of genetic and ecological functions across yeast history. The gain and loss of genes and traits will be correlated to each other, ecological niches, and rates of diversification. This project will test the relative predictive values of phylogenetic history, genome content, and physiology for traits that are relevant to niche, pathogenicity, and biotechnology. The investigators will create a hierarchical, integrated web-based interface for researchers, clinicians, teachers, and students to explore genome sequence and trait data.

Despite the importance of many yeast species to biotechnology and biomedical research, many species are represented by a single isolate, and dozens of new species are described every year. The Yeast Exploration and Analysis Science Team (YEAST) will train high school and undergraduate students in microbiology by engaging them in genuine biodiversity research to isolate new genetic and taxonomic diversity from the wild, including samples submitted by citizen scientists. Metagenomic and genome-based approaches will be incorporated to improve computational training and lay the groundwork for genomics to become a central and integrated part of taxonomic and ecological research in the yeasts and beyond.



Ascoidea asiatica.

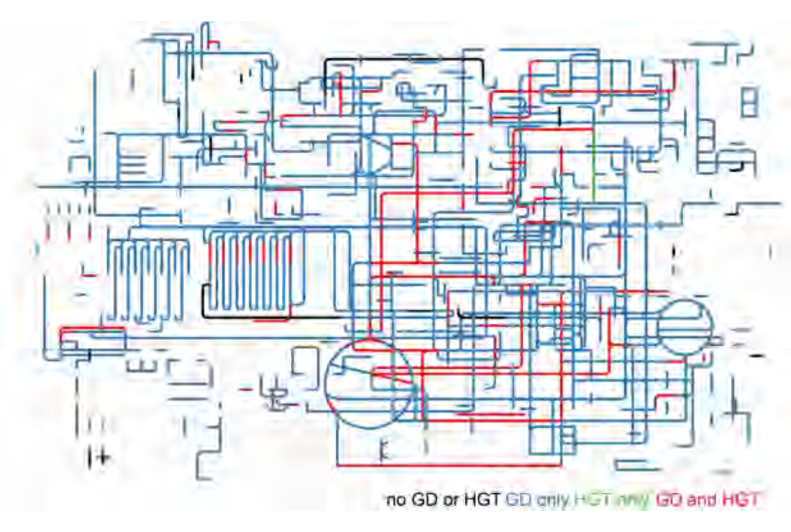
CREDIT: C. P. KURTZMAN, USDA

Yeasts from the genera *Saccharomyces, Kluyveromyces, Zygosaccharomyces, Candida, Kazachstania, Pichia,* and *Dekkera (Brettanomyces)* are critical to produce bread, beer, wine, kefir, soy sauce, sourdough, lambics, kimchi, dietary supplements, probiotics, and some cheeses.

CREDIT: A. B. HULFACHOR

Undergraduate Daniel Rodriguez isolating yeasts.

CREDIT: A. B. HULFACHOR



Incidence of gene duplication (GD) and horizontal gene transfer (HGT) mapped onto the yeast global metabolism network.

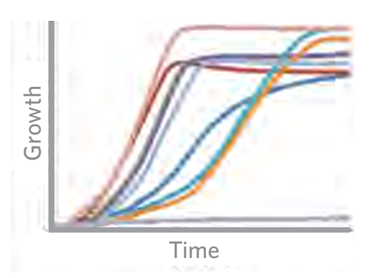
CREDIT: JENNIFER WISECAVER AND ANTONIS ROKAS, VANDERBILT UNIVERSITY

Cyberlindnera amylophila.

CREDIT: C. P. KURTZMAN, USDA

Pachysolen tannophilus.

CREDIT: C. P. KURTZMAN, USDA



Yeast galactose metabolism varies widely among species.

CREDIT: M. KUANG AND C. T. HITTINGER

Eremothecium gossypii.

CREDIT: C. P. KURTZMAN, USDA

Proj. 6 / 12

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

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Photosynthesis is a fundamental biological process supporting the vast majority of life on Earth. In water-limited environments, many plants have evolved alternative metabolism strategies. This project aims to understand the molecular basis of physiological adaptations to water limitation in agaves, yuccas and epiphytic orchids and the impact of these adaptations on diversification. Genomic analyses will identify changes that enabled evolutionary shifts from typical photosynthesis to CAM (*Crassulacean Acid Metabolism*).

For plants living under water-limited conditions, the productivity of photosynthesis can be greatly reduced by hotter and drier climatic conditions. To counteract these conditions, some plants utilize forms of photosynthesis that increase the efficiency with which they use water. One such innovation seen in plants growing in deserts or other water-limited habitats is *Crassulacean Acid Metabolism* or CAM. CAM has evolved independently across diverse plant lineages and it is typically associated with stem (e.g. cacti) or leaf (e.g. agaves, some orchids) succulence. This research project will use several approaches to address fundamental questions about how plants use CAM, how genes involved in performing CAM are regulated in response to varying environmental conditions, and how the evolution of CAM facilitates diversification in water-limited habitats. To achieve these aims, the project will focus on the independent evolution of CAM in the orchid and agave plant families, both of which have species known for their ability to thrive in water-limited environments. This research will provide a foundation for understanding the genetic basis of CAM pathways and contribute to ongoing efforts to introduce CAM to economically important plants for improved water use efficiency when growing under drought conditions.

This project will use an integrated research strategy to investigate the evolution of CAM in epiphytic orchids and members of the agave plant family living in arid habits. Comparative genomic and experimental approaches will be used to illuminate the mechanisms that link ecological, genetic and molecular dimensions of CAM evolution and its consequences for the origin and maintenance of biodiversity. The proposed project will combine ecological, physiological, phylogenetic, genetic and genomic approaches to address fundamental questions about how plants use CAM and how genes involved in performing CAM are regulated in response to varying environmental conditions. The study systems for this project are the species-rich Agavoideae (Asparagaceae) and Oncidiinae (Orchidaceae) lineages, both of which include CAM, C_3 (the typical form of photosynthesis) and facultative or weak CAM species. Comparisons of gene content and expression in these two plant groups will help researchers unravel the interacting molecular and environmental factors driving evolutionary shifts between C_3 photosynthesis and CAM and how these shifts have influenced the origin and maintenance of species diversity.

Undergraduate students will contribute to this research through course-based research projects and more traditional research internships, both aimed at assessing the timing and mode of carbon assimilation for plants growing under various environmental conditions. To gauge the impact of these course and internship based research experiences, the principle investigators will compare student understanding of physiological ecology, evolution, comparative genomics and scientific reasoning from each group.

Yucca moths (*Tegeticula* spp.), obligate pollination mutualists yuccas, are seen pollinating (moth on left) and injecting eggs into a yucca flower (moth on right). Yucca moths are hypothesized to have transferred pollen between C_3 and CAM yucca species, forming intermediate hybrids such as Spanish dagger.

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

The Spanish dagger (*Yucca gloriosa*) plant growing in coastal dunes, is a hybrid species with varying ability to perform CAM-based carbon assimilation.

CREDIT: DAVID ALTHOFF

Oncidium sotoanum (above) and *Oncidium sphacelatum* (below). Both are epiphytic C_3 species.

CREDIT: KATIA SILVERA

Erycina crista-galli (above) is an epiphytic obligate C_3 photosynthesis orchid species. It is closely related to *Erycina pusilla* (below), a CAM species.

CREDIT: KATIA SILVERA

Proj. 7 / 12

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

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

For centuries, scientists have been cataloging the biodiversity of our planet, often with the naked eye. Each year, the list of plant and animal species grows longer when a few cryptic taxa are found deep within a tropical rainforest or at the bottom of the ocean. These discoveries capture the curiosity of scientists and the public alike, but pale in comparison to the exponentially growing inventory of microbial biodiversity. It is assumed that microbial communities obey some of the same ecological rules as plant and animal communities, but many fundamental questions regarding the generation and maintenance of microbial biodiversity remain unanswered. In this project, such questions are addressed through a focus on seed banks and the processes of dormancy that regulate them.

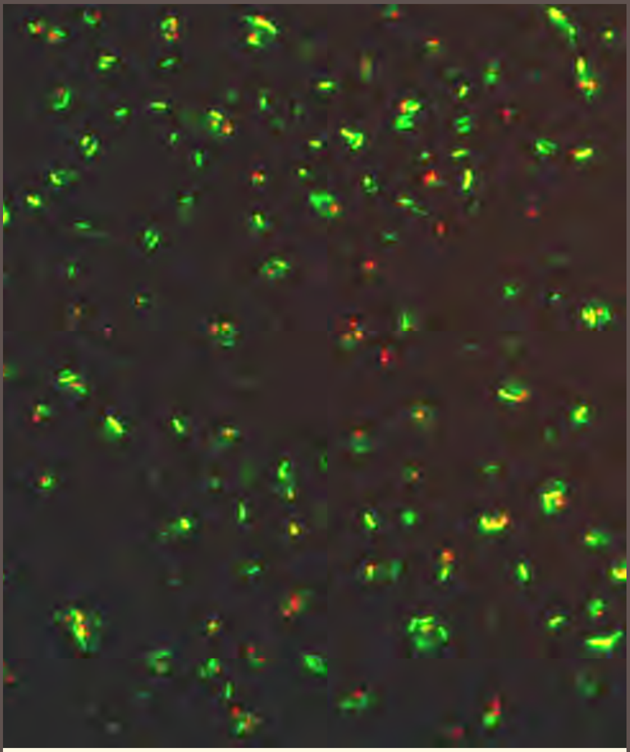
The investigators are exploring how dormancy contributes to the size, composition, and functionality of microbial seed banks, which may represent one of the largest reservoirs of biodiversity on Earth. The project integrates ideas and approaches from theoretical ecology, microbiology, protein chemistry, comparative genomics, and biogeography. Results will provide novel insight into the life history strategies and biogeographic processes that influence the dynamics of beneficial and pathogenic microbes.

This project develops a seed bank framework for understanding the biodiversity of microbial communities. The major objectives are to: 1) quantify survivorship during dormancy in a diverse collection of soil bacteria and link this to phylogeny, functional traits, and trade-offs, 2) focus on the effects of resuscitation on the diversity and function of seed banks by manipulating signaling processes that regulate dormancy, and 3) develop and test ecological theory for the influence of seed banks on geographic patterns of taxonomic and phylogenetic diversity.

The scientific findings will shed light on how seed banks influence microbial biodiversity and the stability of managed and natural ecosystems. The educational impacts of the project will include the development of a capstone-research experience for students from Transylvania University, a primarily undergraduate institution (PUI), in addition to providing research opportunities for underrepresented high school and undergraduate students through STEM Summer Scholars Institute and the Lilly Scholars Program at Indiana University. Dissemination will include the development and release of an open-source individual-based modeling software package combined with public outreach through engagement with a local science museum.

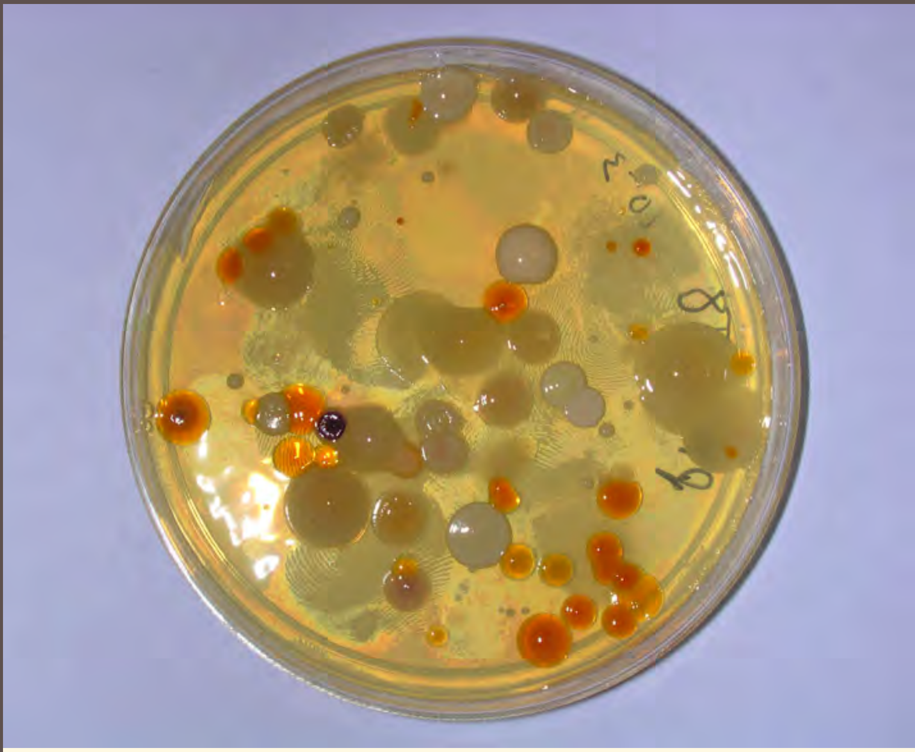
^ Agricultural landscape at the Kellogg Biological Station Long-Term Ecological Research site.

CREDIT: KURT STEPNITZ



^ Variation in the metabolic activity of a bacterial population (*E. coli*) exposed to an environmental stressor (ethanol).

CREDIT: SARAH CUMMINS



^ Bacteria cultured from an agricultural soil sample.

CREDIT: JAY T. LENNON

Proj. 8 / 12

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

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This project explores how the diversity and functional integration of social animals and their bacterial gut symbionts are shaped by historical and contemporary environmental interactions. Lessons learned from this unique system will help us to understand the rules governing one of nature's most ubiquitous but still poorly understood partnerships — animal symbioses with gut bacteria.

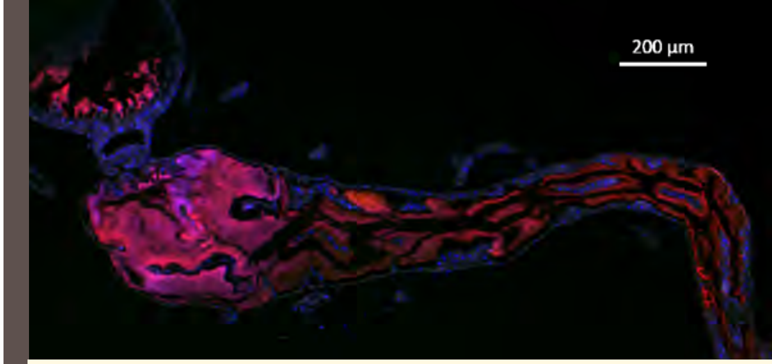
Although individuals have long been considered the fundamental unit of evolution, we now know that animals are really co-dependent collections of host and microbes: many, perhaps most, depend on gut bacteria to access essential nutrients. We can consider these integrated collections of host and symbiont cells as a single unit, called a "holobiont." Increasingly, we are discovering that biodiversity is perhaps best viewed and understood by looking at interactions across different levels of biological organization. Can we more fully explain global patterns of biodiversity — long a central challenge in the fields of ecology and evolutionary biology — in light of holobiont interactions?

To untangle the importance of such partnerships for hosts and symbiotic gut bacteria, the research team plans to study a diverse and ecologically successful social animal group, the turtle ants. The team will use state-of-the-art molecular and genomic methods, and extensive geographical and ecological sampling to investigate the history of turtle ant bacteria symbioses, the bacterial function in host health, and the mechanisms by which the microbes are acquired and maintained. By studying this diverse and tractable system, this research will explore the relationships between symbiosis and the dimensions of holobiont biodiversity with unprecedented clarity. In pursuit of these goals, the research will address: 1) the roles of time, biogeography, and habitat in host diversification; 2) variation in gut microbial communities across host phylogeny, geography, habitat, and ecology; 3) the extent of codiversification for core, microbial symbiont lineages, and the impacts of host phylogeny, geography, and ecology on symbiont transfer; 4) variation in microbial genome evolution and innovation across varying degrees of codiversification and genes with varying function; and 5) symbiont function in light of symbiont genome evolution, host-symbiont codiversification, and host phylogeny, geography, and ecology.

As social organisms, ants resemble humans in how they acquire helpful and harmful bacteria. This project will not only advance our understanding of the ecological and evolutionary processes that structure animal gut microbial communities, but will also provide authentic, hands-on research experiences for high-school and undergraduate students. Through targeted research opportunities we will provide training in interdisciplinary scientific approaches for women and minorities in the STEM fields. Finally, educational materials related to this research will be developed for K-12 students, aligned to the Next Generation Science Standards (NGSS), and shared with teachers/educators throughout the Chicago area reaching hundreds of homes and classrooms.

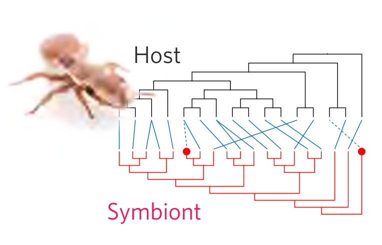
Cephalotes grandinosus turtle ant worker (top) and soldier (bottom). *Cephalotes* turtle ant workers are protected by their shell-like armor while they forage in the canopy, and soldiers use their large, rounded heads to block entrances to their colony's arboreal nests.

CREDIT: JON G. SANDERS



Fluorescence micrograph of the *Cephalotes* hindgut illustrating the extraordinary abundance of bacteria found there. In this image, host ant nuclei are blue, and bacterial symbionts are stained in red/magenta. The size and complex structure of the hindgut differentiate *Cephalotes* from most other ants, which typically have simple, tube-like hindguts.

CREDIT: PIOTR ŁUKASIK



Tanglegram shows the correlation of turtle ant (top) and gut bacterial symbiont (bottom) evolutionary trees. Lines connect symbionts to their hosts and dots indicate cultured isolates.

CREDIT: JON G. SANDERS

Bird droppings are a rich source of nitrogen and gut microbes help to utilize it. *Cephalotes maculatus* (top right) and two *Cephalotes eduarduli* feed at a fresh bird dropping.

CREDIT: SCOTT POWELL

Cephalotes atratus worker tending sap-feeding insects in Madre de Dios, Peru. Sugary honeydew excreted by these insects is an important food source for tree-dwelling ants, but as it is very low in nitrogen, must be complemented by other food sources or microbial symbionts.

CREDIT: JON G. SANDERS

Transmission electron micrograph of a gut bacterial symbiont isolated from *Cephalotes varians*. This isolate is representative of a new genus and species of bacteria, only found within the guts of turtle ants.

CREDIT: JOHN WERTZ, CALVIN COLLEGE, AND ALICIA WITHROW, MICHIGAN STATE UNIVERSITY

Two *Cephalotes borgmeieri* workers in the Brazilian cerrado share nectar after one has finished feeding at a nearby extrafloral nectary (round plant structure to left). Extrafloral nectar is an abundant, sugar-rich food source in the canopy of most tropical habits.

CREDIT: SCOTT POWELL

Proj. 9 / 12

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

(CO-FUNDED WITH FAPESP)

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This project focuses on how the widespread deforestation of tropical forests for agriculture affects the production and consumption of methane, a potent greenhouse gas. The goal of this research is to identify the microorganisms involved in methane production and consumption, their physiologies and genetics, and how together they determine the flow of methane from Amazon rainforest soils to the atmosphere. This project will provide a new understanding of how converting tropical forests into farms affects the biodiversity of microorganisms and the ecosystem functions they mediate.

The Amazon forest is the largest biological reservoir of animal and plant species on Earth. However this ecosystem is among the least studied with regard to microbial biodiversity. This is of concern because increasing demand for food, fiber, and biofuel has accelerated the conversion of the Amazon rainforest to agriculture, creating a vast frontier of deforestation. The effects of this conversion on microorganisms, and the essential functions they perform, are poorly understood.

One function performed by microorganisms is the production and consumption of the gas methane. Methane is a greenhouse gas more than 20 times as powerful as carbon dioxide. Although production and consumption of methane is common to all soils, we do not yet understand why some soils tend to pump methane into the atmosphere, while others tend to draw methane out of the atmosphere. This is especially true of tropical rainforests, where conversion to agriculture often results in soils changing from net methane consumers to net methane producers. This research combines recent advances in microbiology, genomics, environmental chemistry and ecosystem modeling to provide a detailed understanding of which species produce and consume methane, how they do it, and how they are affected by conversion of rainforests into farms. This study has the potential to better inform climate change models, resulting in more accurate predictions of the effect of tropical deforestation on global climate. It will also increase our understanding of how human activity alters microorganisms and the functions they provide.

This research addresses a critical question in global change biology, through characterizing soil microbial diversity and activity at the level of entire ecosystems. It will enable wide-ranging interdisciplinary training of K-12, undergraduate and graduate students, as well as postdoctoral researchers. The project is highly collaborative, with Brazilian and American scientists working in close cooperation, and it will provide students and postdoctoral scientists with the international experience and cross-cultural training necessary to succeed in a global economy.

PIs Rodrigues, Bohannan and Nüsslein at the primary Amazon rainforest site, Rondonia, Brazil.

CREDIT: KLAUS NÜSSLEIN, UNIVERSITY OF MASSACHUSETTS

PI Brendan Bohannan sampling Amazon rainforest soil with Brazlian colleagues.

CREDIT: KLAUS NÜSSLEIN, UNIVERSITY OF MASSACHUSETTS

Primary rainforest in the Amazon Basin, Rondonia, Brazil.

CREDIT: KLAUS NÜSSLEIN, UNIVERSITY OF MASSACHUSETTS

PI Bohannan sampling from pasture converted from primary rainforest, Rondonia, Brazil.

CREDIT: KLAUS NÜSSLEIN, UNIVERSITY OF MASSACHUSETTS

Secondary forest developed fifteen years after pasture abandonment.

CREDIT: KLAUS NÜSSLEIN, UNIVERSITY OF MASSACHUSETTS

An old pasture slowly returning to forest.

CREDIT: KLAUS NÜSSLEIN, UNIVERSITY OF MASSACHUSETTS

Soil sampled from primary rainforest, Rondonia, Brazil.

CREDIT: KLAUS NÜSSLEIN, UNIVERSITY OF MASSACHUSETTS

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

CREDIT: KLAUS NÜSSLEIN, UNIVERSITY OF MASSACHUSETTS

Proj. 10 / 12

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

(CO-FUNDED WITH NSFC)

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In this collaborative project, US and Chinese scientists are conducting novel analyses of plant and microbial diversity in forests in the US and China to discover those factors that shape biodiversity through space and time.

Biodiversity is multidimensional, composed of genetic, phenotypic, ecological, and geographic variation within and among species. Less frequently considered is the role of evolutionary history in shaping current patterns of biodiversity. That is, how does history constrain or enhance biodiversity? The forests of eastern Asia and eastern North America were once connected and have a shared evolutionary and ecological history. They therefore offer an excellent opportunity to study the drivers of biodiversity across geographic space and through evolutionary time. Within forests, plants grow in association with soil bacteria and fungi (collectively referred to as microbes), but little is known about how these associations vary within and among forests and how they generate biodiversity. Do forests in the eastern US and eastern China share evolutionary and ecological features that trace to their common ancestry, or have they followed separate paths since they diverged million of years ago? Do plants and microbes reveal the same patterns, suggesting their histories remain tightly linked, or do these patterns vary geographically?

This multidisciplinary project integrates phylogenomics, biogeography, and plant and microbial evolution and ecology to address novel questions on the origins and functional consequences of biodiversity. The research team will reconstruct evolutionary histories for key plant groups shared between eastern North America and eastern China using cutting-edge genetic methods and will evaluate spatial patterns of diversity within and between continents. This exploration of microbial diversity across spatial scales — from individual plant microbiomes to communities and continents — will yield new discoveries of biodiversity and plant-microbial interactions, enabling investigation of co-diversification of plants and associated microbes. Ecosystem function, inferred from analysis of plant functional traits and remotely sensed canopy properties, will be quantified at all sites and linked to analyses of microbial function. Innovative analytical methodologies will lead to new discoveries in evolutionary and functional diversity of plants and microbes at community and regional scales. Integration of historical connections, current patterns, and future species distribution models will lead to more holistic views of the drivers of biodiversity and a better understanding of our planet's ecosystems, how to conserve them, and how to represent them in global climate-carbon models that inform national and international climate and energy policies.

The research team will conduct joint fieldwork in both the US and China. The team has already developed an extensive education and training program for students at various levels, a highlight of which is a cyber-enabled course for Chinese and US participants.

Liriodendron (tulip tree) exhibits the classic Eastern Asia – Eastern North American floristic disjunction, with *L. chinense*, shown here, in China and *L. tulipifera* in Eastern North America.

CREDIT: PAMELA S. SOLTIS, UNIVERSITY OF FLORIDA

Liriodendron tulipifera from eastern North America, whose sister species is *L. chinense* from central and southern China, showing its beautiful tulip-like flower.

CREDIT: WALTER S. JUDD, UNIVERSITY OF FLORIDA

Qiyunshan, a national park in Anhui Province in eastern China, exhibits a mixed temperate deciduous forest typical of natural areas in eastern Asia and eastern North America, with many plants showing the classic disjunction with North American relatives. Qiyunshan itself (Mount Qiyun) is one of the four most sacred Taoist mountains in China.

CREDIT: JENNY XIANG, NORTH CAROLINA STATE UNIVERSITY

Cornus (dogwoods) comprises nearly 60 species, most of which are distributed in temperate and subtropical regions of the Northern Hemisphere. Within *Cornus*, several species groups exhibit the Eastern Asia – Eastern North American disjunction. Shown here is *C. florida*, with its head-like inflorescences subtended by four large, white bracts and young leaves.

CREDIT: JENNY XIANG, NORTH CAROLINA STATE UNIVERSITY

Liquidambar (sweetgum) also exhibits the Eastern Asia – Eastern North American disjunction, comprising four species, two of which occur in China, one in eastern North America, and one in the eastern Mediterranean. *Liquidambar formosana*, shown here, from Tianmushan National Nature Reserve in Zhejiang Province, China.

CREDIT: PAMELA S. SOLTIS, UNIVERSITY OF FLORIDA

Proj. 11 / 12

Coevolution of scleractinian corals and their associated microorganisms

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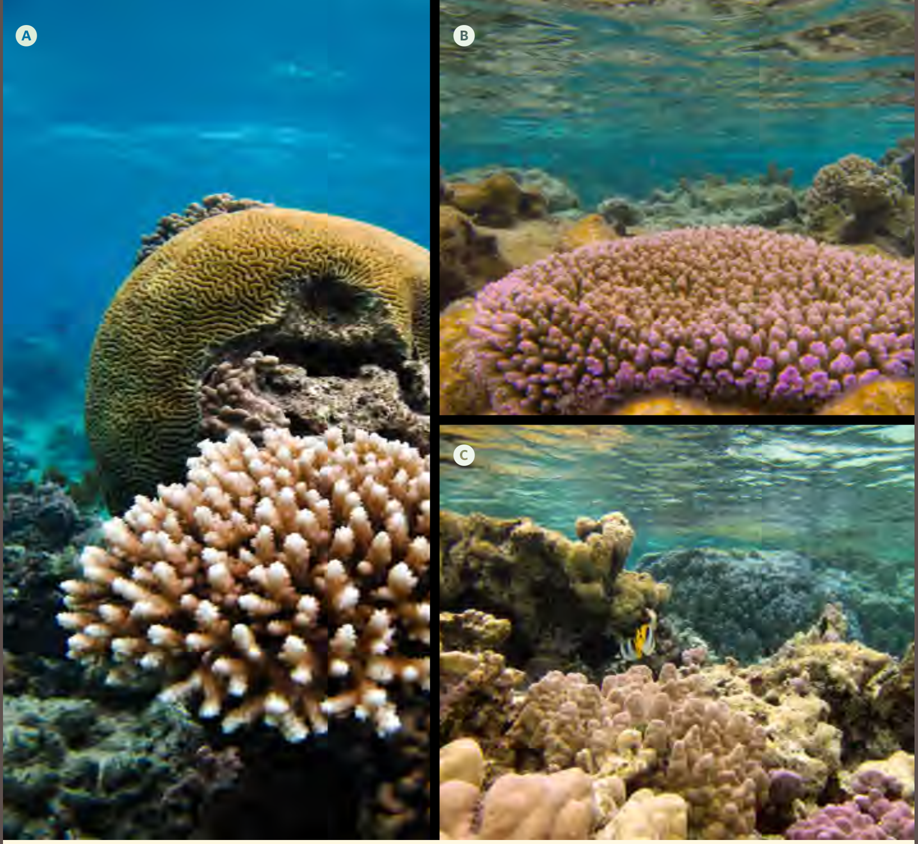
Coral reefs are among the most biodiverse marine ecosystems on the planet, and provide substantial economic and ecological benefits to coastal communities. This project aims to describe microbial diversity across all major groups of reef-building corals in each of several distinct ecosystems across the globe, to determine the genome sequences and metabolic capabilities of key coral bacteria, and to test whether the composition of coral microbial communities helps to explain the overall vulnerability or resistance of different coral species to stress or disease.

Corals are composed of both the Cnidarian animal host and complex communities of unique and underexplored microbial organisms. Today these natural wonders are in global decline, threatened by the intersecting effects of multiple stressors including overfishing, pollution, and climate change. These stressors can alter coral microbial communities in ways that may make corals more susceptible to disease or algal competition. Therefore understanding the relationships between corals and their microbiota may be useful for efforts to combat coral disease and preserve reef ecosystems. While much effort is underway to understand coral reef ecosystems and help steward them for future generations, most studies of the microbial communities present on corals have focused on a relatively small portion of coral diversity, in terms of both the locations in which it has been studied and the evolutionary linages of the corals. As a result the microbial diversity of coral species in many diverse and ancient groups remains unexplored. Understanding these communities will help to extend the knowledge gained in well-studied corals to diverse reefs worldwide.

Coral species differ in their susceptibility to bleaching and disease, but these differences are only partially explained by coral phylogeny. Therefore this project will test the extent to which incorporating the microbiota (or their contributed genes) better predicts these and other traits. Recent technological advances will allow us to examine the role of more complex microbiomes in shaping the life history, physiology, and evolution of their multicellular hosts (e.g., the human microbiome). The use of newly developed DNA sequencing techniques will allow a more complete exploration of microbial diversity than has previously been feasible, while advanced computational methods will help to maximize the value of sequenced bacterial genomes. Improved predictive models that incorporate both coral phylogeny and microbial function will help inform conservation strategies and yield predictive biomarkers for coral vulnerability to disease or bleaching. Relating the diversity of corals to the diversity of their microbes will also provide important insights into how intimate symbiotic associations with microorganisms arose and are maintained in diverse animals.



Pictures of different coral taxa from three coral reefs around the world. A) Australia and B, C) Moorea.

CREDIT: RYAN MCMINDS AND JEROME PAYET

Images of microbial isolates from coral. This project will culture and sequence the genomes of key coral symbionts such as these.

CREDIT: AKI OHDERA AND MONICA MEDINA

Map of proposed sampling sites and their coral diversity. Letters represent locations for site sampling and numbers represent areas where collaborators will conduct sampling:

A) Hawaii
B) Moorea
C) Gulf of Mexico
D) Western Florida
E) Florida Keys
F) Panama
G) Curacao
H) Saudi Arabia
I) Madagascar
J) Reunion Island
K) Andaman Islands
L) Singapore
M) Western Australia
N) Okinawa
O) Northern Great Barrier Reef
P) Southern Great Barrier Reef

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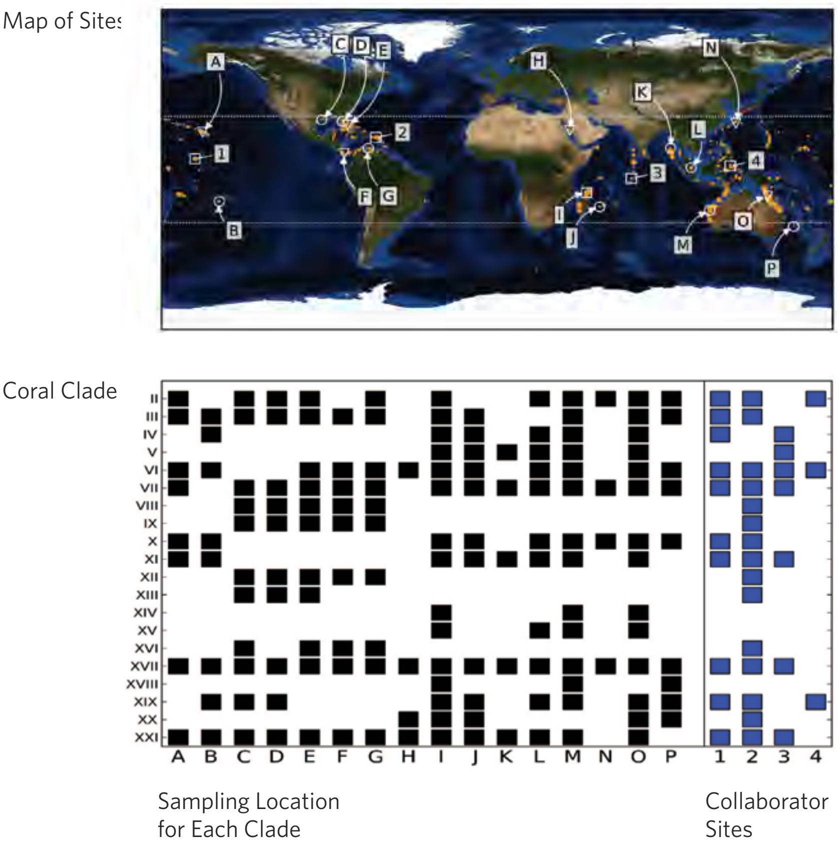
1) Line Islands
2) St. John, US Virgin Islands
3) Chagos
4) Indonesia

Boxes in the lower panel represent coral groups (clades) present at each location according to the Census of Marine Life OBIS database.

CREDIT: JESSE ZANEVELD, MONICA MEDINA AND REBECCA VEGA THURBER



	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	1	2	3	4
II	■		■	■	■		■		■			■	■	■	■	■	■	■		■
III	■	■	■	■	■	■	■		■	■			■		■	■	■	■		
IV		■							■	■		■	■		■		■		■	
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VI	■	■			■	■	■	■	■	■		■	■		■	■	■	■	■	■
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Sampling Location for Each Clade

Collaborator Sites

Proj. 12 / 12

Genetic, phylogenetic, and functional microbial diversity in permanently frozen aquatic sediments over geologic time

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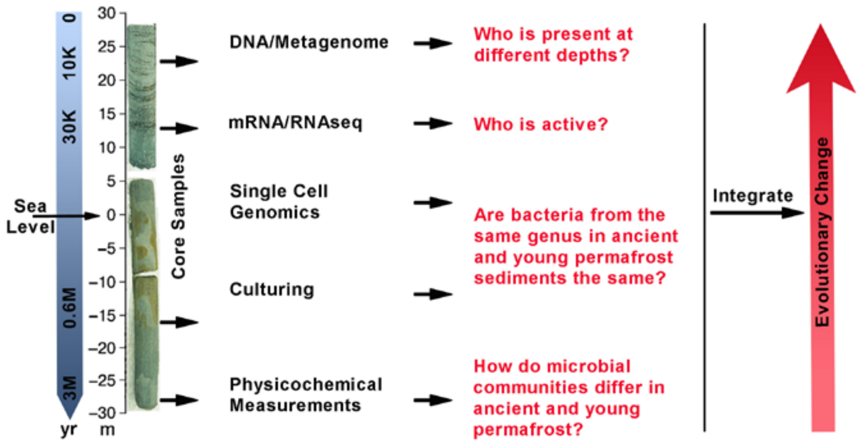
This project addresses the unresolved question of whether microbes embedded in permafrost sediments are dead (or fossils), representing ancient communities preserved through time, or living, thriving communities that have been evolving since becoming buried.

Permafrost, or permanently frozen sediments and soils, are believed to provide snapshots of ancient biological communities and represent fossil archives for plants and animals present at the time of deposition. However, in contrast to animals and plants, microbes can survive extreme conditions including cold, pressure and lack of oxygen, so it is possible that some microbes in permafrost are not fossils but rather are alive. The current literature presents contradictory interpretations, with many studies based on the premise that samples from deep, permanently frozen sediments represent a fossil archive of past surface communities, whereas others assume these samples include microbes with active metabolism at subzero temperatures. The resolution of this debate is critical for determining past versus present microbial diversity in deep sediments and also in determining evolutionary changes within bacterial taxa.

This project will study permafrost collected from the oldest known sediments in the Northern Hemisphere, located in Siberia, Russia to determine how long microbial communities can live in permafrost. The permafrost in the Kolyma-Indigirka Lowland contains sediments of lake-alluvial or marine origin approximately 5,000 to 3 million years old. These permafrost sediments have never completely thawed since becoming frozen and represent an archive of the Arctic ecosystem including plant and animal fossils as well as microorganisms trapped at the time of deposition.

The research employs multiple state-of-the-art techniques including metagenomics, metatranscriptomics, single cell genomics, and bioinformatics and will add considerable value to our understanding of the dynamics of the permafrost ecosystems, paleoecology, microbial evolution and permafrost degradation. The age and physical-chemical characteristics of sediments will be used to study the functional biodiversity of the living fossils and for paleoecological reconstruction of extinct and extant microbial communities.

To perform this study, a collaborative team has been formed with scientists from the University of Tennessee, Princeton University, and the Institute of Physicochemical and Biological Problems in Soil Science of the Russian Academy of Science (IPBPSS). The international nature of this project provides a platform to expand a network of collaborative permafrost research with open system data management, sharing and training. This project will provide high-quality research opportunities for young scientists and students, and engage high school teachers through the molecular biology workshops.



A schematic overview of the approaches that will be employed in this project.

CREDIT: T. A. VISHNIVETSKAYA AND A.C. LAYTON, UT, KNOXVILLE, USA

The young and ancient permafrost samples will be obtained from sediments of lake-alluvial and marine origin.

CREDIT: T. A. VISHNIVETSKAYA, UT, KNOXVILLE, USA

Permafrost core samples will be collected using sterile drilling techniques.

CREDIT: E.M. RIVKINA, IPBPSS, PUSHCHINO, RUSSIA

Numerous rivers flowing into the East Siberian Sea are relatively short with a high right bank.

CREDIT: E.M. RIVKINA, IPBPSS, PUSHCHINO, RUSSIA

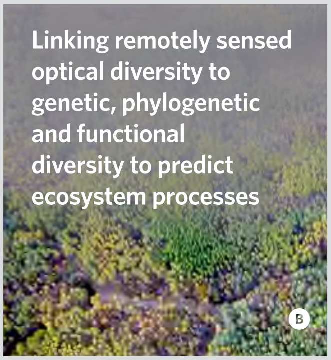
Study site is located in the Kolyma-Indigirka Lowland in the northeastern part of Russia.

CREDIT: T. A. VISHNIVETSKAYA, UT, KNOXVILLE, USA

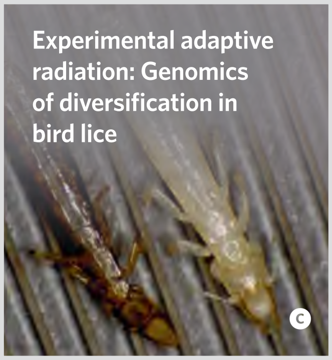
An Aerial view of the Kolyma-Indigirka Lowland. This area occupies tens of thousands of square kilometers and remains virtually unexplored.

CREDIT: E.M. RIVKINA, IPBPSS, PUSHCHINO, RUSSIA

US-BIOTA-São Paulo: A multidisciplinary framework for biodiversity prediction in the Brazilian Atlantic forest hotspot p. 34



Linking remotely sensed optical diversity to genetic, phylogenetic and functional diversity to predict ecosystem processes p. 35



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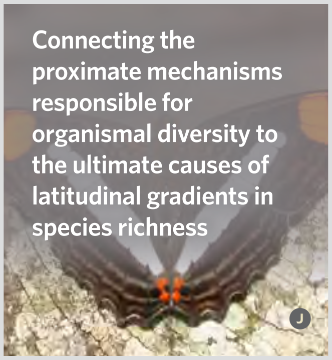

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Landscapes of Linalool-scent mediated diversification of flowers and moths across western North America p. 43

Symbiont and transcriptomic niche dimensions of long-term coexistence in *Trifolium* communities p. 44

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2013 updates

IMAGE CREDIT

Ⓐ Ivan Prates
Ⓑ Michael Madritch
Ⓒ S.E. Bush & D.H. Clayton
Ⓓ Joe Craine
Ⓔ Kevin Kohl
Ⓕ Audrey T. Paterson
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US-BIOTA-São Paulo: A multidisciplinary framework for biodiversity prediction in the Brazilian Atlantic forest hotspot

(CO-FUNDED WITH NASA AND FAPESP)

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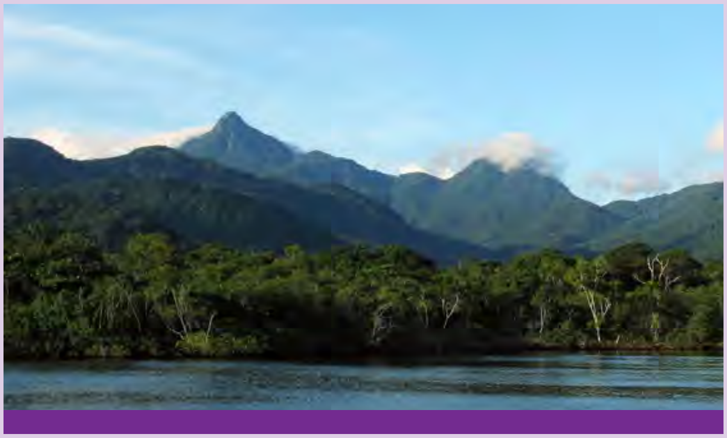
This project aims to develop a framework for predicting spatial patterns of biodiversity in the highly diverse environment of the Brazilian Atlantic Forest. This model is being constructed by integrating numerous types of data including remote sensing, meteorological, locality, phylogenetic, functional,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

Update

Many activities took place in the first year of this project. In January and February of 2014 the herpetology group sampled amphibians and reptiles, and the geomorphology and paleoclimatology groups sampled cave deposits. The team additionally established a methodological approach to the genomic component of the project. All collaborating investigators came together for an all hands grant meeting that was held in February in São Paulo, Brazil. Lastly, several papers were published as a result of this work, including one published in the British journal *Proceedings of the Royal Society B*. In this paper, Carnaval and colleagues reported on their newly developed biodiversity metric called “phylogeographic endemism”. This measure quantifies the degree to which genetic variation is restricted to a particular geographic space. It is anticipated that this metric could be applied to other regions to help advance biodiversity prediction and conservation in tropical hotspots worldwide.



^ View of the Brazilian Atlantic Forest in Ubatuba, São Paulo.
CREDIT: IVAN PRATES, CITY COLLEGE OF CUNY

Publications

Batalha-Filho, H., et al. “Phylogeny and historical biogeography of gnateaters (Passeriformes, Conopophagidae) in the South America forests.” *Molecular Phylogenetics and Evolution* 79 (2014): 422-432.

Carnaval, A.C., et al. “Prediction of phylogeographic endemism in an environmentally complex biome.” *Proceedings of the Royal Society B: Biological Sciences* 281.1792 (2014): 20141461.

Chan, Y.L., et al. “Detecting concerted demographic response across community assemblages using hierarchical approximate Bayesian computation.” *Molecular Biology and Evolution* (2014): msu187.

Dantas, G.P.M., et al. “Population genetic structure of the Atlantic Forest endemic *Conopophaga lineata* (Passeriformes: Conopophagidae) reveals a contact zone in the Atlantic Forest.” *Journal of Ornithology* (2014): 1-15.

Robinson, J.D., et al. “ABC inference of multi-population divergence with admixture from unphased population genomic data.” *Molecular Ecology* 23.18 (2014): 4458-4471.

Waltari, E., et al. “Bioclimatic variables derived from remote sensing: assessment and application for species distribution modeling.” *Methods in Ecology and Evolution* (2014): doi: 10.1111/2041-210X.12264.

Zuntini, A.R., Lohmann, L.G. “Synopsis of *Martinella Baill* (Bignonieae, Bignoniaceae), with the description of a new species from the Atlantic Forest of Brazil.” *PhytoKeys* 37 (2014): 15-24.

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

(CO-FUNDED WITH NASA)

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

Update

Major activities for this team have focused on the diversity of optical images gathered from remote sensing data. Significant advances were made in developing project infrastructure at the Cedar Creek test site, including the set up of a robotic platform — tram system to obtain proximal hyperspectral images. Cavender-Bares and colleagues have been examining how changes in scale, resolution, seasonal variation and year-to-year variation impact these remotely sensed data. Preliminary results have already shown optical differences with increases in species richness. Additionally, populations from the same genus of plants but grown in different geographic locations and under differing stress levels are also showing significant optical differences in the remotely sensed data. The research group is planning an upcoming airborne campaign to take measurements from aircraft and from low-flying hexacopters.

^ 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: JOHN A. GAMON, UNIVERSITY OF ALBERTA & UNIVERSITY OF NEBRASKA (LINCOLN)

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

CREDIT: MICHAEL MADRITCH

Proj. 3 / 13

Experimental adaptive radiation: Genomics of diversification in bird lice

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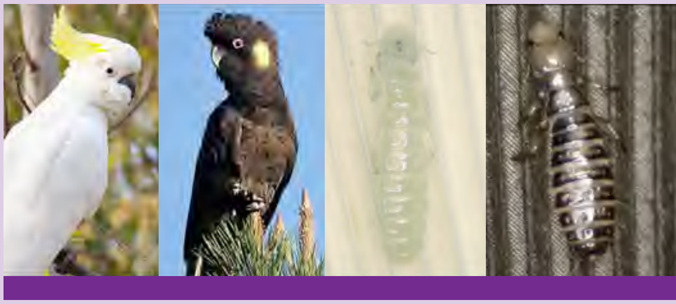
The goal of this project is to expand the understanding of adaptive radiation by utilizing bird-specific ectoparasites as a model system. The researchers are conducting experimental studies that link phylogenetic, phenotypic, and functional data in order to clarify how micro-and macro-evolutionary processes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

Update

In the first year of this project, Clayton and colleagues have focused their efforts on optimizing their methodology and beginning genetic analysis. Two pigeon genomes were sequenced and the genetic data are undergoing further analysis and gene assembly. DNA extraction techniques for single lice ectoparasites have been refined in an attempt to sequence only individuals and minimize population level genetic differences. In the next year, the team plans on sequencing additional host and parasite genomes and identifying orthologous genes (genes believed to be descendants of the same ancestral speciation event).



Crypsis in feather lice: according to host species the lice are able to evade detection through camouflage.
CREDIT: FIR0002/FLAGSTAFFOTOS, DAVID COOK, S. E. BUSH AND D. H. CLAYTON

Proj. 4 / 13

The biogeography and evolution of drought tolerance in grasses

(CO-FUNDED WITH NASA)

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Lynn Clark
Iowa State University
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Northern Illinois University
(NSF 1342782)

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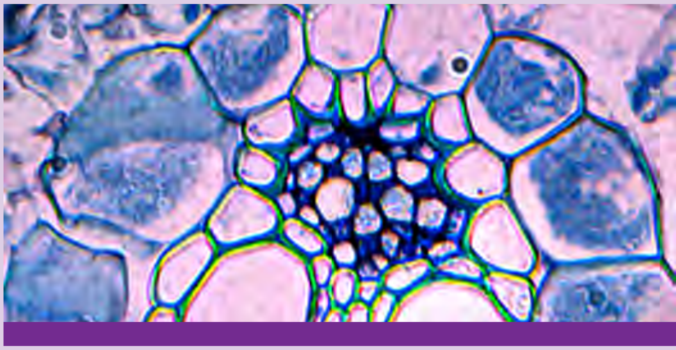
Oregon State University
(NSF 1342703)

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.

Update

Research for this project began in January of 2014. Ungerer and colleagues assembled seeds from over 1200 grass species. The team is currently beginning to screen these species for their drought tolerance and ecophysiological traits. All the investigators met in May of 2014 at the Konza Prairie for a research coordination meeting. Genetic material will next be prepared for next generation sequencing. By assembling this genetic, taxonomic and functional data on drought tolerance in grasses, the team is aiming to answer two primary questions 1) how has drought-tolerance evolved in difference species of grasses and 2) if drought conditions result in gene expression compatibility among different grasses.



Xylem within these vascular bundles undergoes strong selection for physiological drought tolerance.
CREDIT: JOE CRAINE

Biodiversity of the gut microbiome of herbivorous woodrats

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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 disease, the metabolism of toxic compounds, and how gut flora controls the host's digestion of variable diets.

Update

Dearing and colleagues have begun evaluating microbial communities in herbivorous woodrats through feeding trials and by conducting microbial inventories in different sections of the woodrat gastrointestinal track. It has been hypothesized for many years that the microbiome of certain species can serve a function to the host mammal by detoxifying particular foods within their diet. The Dearing research team demonstrated that this is the case, and that gut microbes do allow mammals to consume plant toxins. The research team has performed a number of microbial transplants between animals, and they have effectively transferred this detoxification function by doing so. Furthermore, they have found that woodrats lose their microbial diversity as they enter a captive environment, which has major relevance for conservation biology. Their research has been highlighted by several popular science media sources, including Science Magazine. In the upcoming year the research team plans to more specifically investigate how microbe-microbe and host-microbe interactions are involved in maintaining oxalate-degrading bacteria and their associated function.

Publications

Kohl, K.D., et al. "Captivity results in disparate loss of gut microbial diversity in closely related hosts." *Conservation Physiology* 2.1 (2014): cou009.

Kohl, K.D., et al. "Gut microbes of mammalian herbivores facilitate intake of plant toxins." *Ecology Letters* 17.10 (2014): 1238-1246.

Kohl, K.D., et al. "Herbivorous rodents (*Neotoma* spp.) harbor abundant and active foregut microbiota." *Environmental Microbiology* 16.9 (2014): 2869-2878.

Miller, A.W., et al. "The Gastrointestinal Tract of the White-Throated Woodrat (*Neotoma albigula*) Harbors Distinct Consortia of Oxalate-Degrading Bacteria." *Applied and Environmental Microbiology* 80.5 (2014): 1595-1601.

Miller, A.W., Dearing, D. "The Metabolic and Ecological Interactions of Oxalate-Degrading Bacteria in the Mammalian Gut." *Pathogens* 2.4 (2013): 636-652.

^ The desert woodrat (*Neotoma lepida*) with a branch of the creosote bush (*Larrea tridentata*). The desert woodrat consumes creosote foliage regularly in the wild, even though creosote is heavily defended by plant secondary compounds, including tannins.

CREDIT: KEVIN KOHL, UNIVERSITY OF UTAH

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

CREDIT: KEVIN KOHL, UNIVERSITY OF UTAH

Functional diversity of chemosymbiosis in lucinid bivalves from coastal biomes

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Laurie Anderson
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Barbara Campbell
Clemson University
(NSF 1342763)

Endosymbionts are the organisms that live within another species. Bivalves, a type of mollusk, are capable of hosting endosymbionts that offer chemical nutrients to the host, in a relationship called chemosymbiosis. This project investigates the genetic, taxonomic, and functional diversity of modern lucinid bivalve chemosymbioses from uncharacterized coastal marine biomes and tests for ways to characterize lucinid-bacteria biodiversity from the geologic past.

Update

Engel and colleagues finished their first field season in Florida, characterizing in detail the mangrove habitat of *Phacoides pectinatus* and the seagrass habitat of *Stewartia floridana*. In total, almost 600 lucinid and other molluscan specimens were collected for morphometrics, geochemical analyses, and molecular gene surveys for hosts and endosymbionts. This was accompanied by over 230 sediment samples at various depths and spatial distances, as well as from different vegetation types. The high-density spatial sampling scheme has provided a substantial biogeographic understanding of lucinid and endosymbiont diversity in shallow marine habitats affected by anthropogenic activities. Four new graduate students joined the team, each focusing on different aspects of lucinid life history, sediment biogeochemistry, and endosymbiont diversity and metabolism.

Close-up of lucinid *Stewartia floridana* from Pine Island, Florida.

CREDIT: AUDREY T. PATERSON, UNIVERSITY OF TENNESSEE

Top: The research team from the University of Tennessee, South Dakota School of Mines and Technology, and Clemson University in July 2014, prior to sampling lucinid bivalves, *Phacoides pectinaus*, in Wildcat Cove, Florida.

CREDIT: LUCY RIORDAN

Bottom: Two graduate students collecting sediment samples associated with the lucinid *Phacoides pectinaus*, in Wildcat Cove, Ft. Pierce, Florida.

CREDIT: ANNETTE SUMMERS ENGEL, UNIVERSITY OF TENNESSEE

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

(CO-FUNDED WITH NSFC)

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CHINA TEAM	**Ming-jian Yu** Zhejiang University **Zhihong Xu** Zhejiang Agriculture and Forestry University	**Jianbo Lu** Hangzhou Normal University **Xiao-yong Chen** East China Normal University

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

Update

In the first year of this project, the research team made excellent progress. They completed plant surveys on 20 islands. All plants in the survey plots with a diameter at breast height (DBH) of >1cm were tagged, mapped, measured for DBH and height and identified to the species level. Habitat diversity was measured for 9 islands. Plant functional traits were documented for 61 species. Leaf litter of common plant species was collected and is being analyzed for chemical composition. A total of ~2000 arthropod individuals were collected from 16 islands. Microsatellite genetic markers have been identified for four plant species, and population genetic analyses are being conducted for one species. Information from the plant data generated from this collection is already informing ecological theory.

Publications

Ding, Y.Y., et al. "Development of polymorphic microsatellite loci in *Lithocarpus harlandii* (Fagaceae)." *Conservation Genetics Resources* 6 (2014): 755-757.

Zhang, L.Y., et al. "Isolation and characterization of thirteen polymorphic microsatellite loci for *Lithocarpus glaber*." *Biochemical Systematics and Ecology* 55 (2014): 10-13.

^ A tagged and marked tree on one of the Thousand-Island Lake islands.

CREDIT: MINGJIAN YU, ZHEJIANG UNIVERSITY

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

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James Birch
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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.

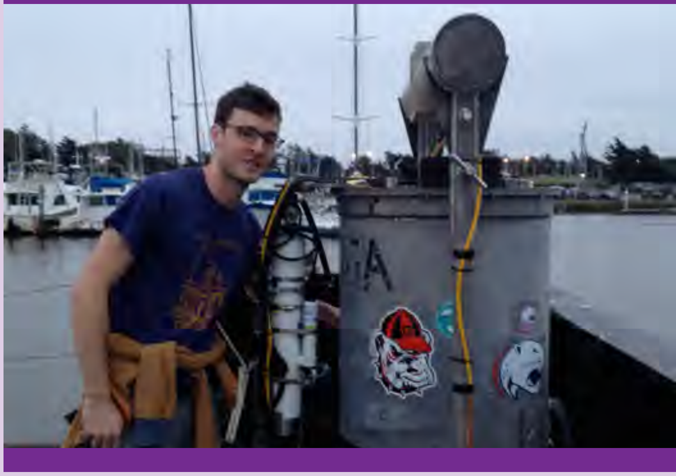
Update

Moran and colleagues have made great strides during their first year of the project. A microcosm experiment was initiated in August 2014 with three model marine microorganisms (dinoflagellate *Alexandrium tamarense*, diatom *Thalassiosira pseudonana*, and bacterium *Ruegeria pomeroyi*) in which a shift in the dominant primary producer (from dinoflagellate to diatom) was induced at the mid-point of the 6-week experiment. Phytoplankton community composition is hypothesized to influence the pathway by which marine bacteria degrade DMSP. In turn, the bacterial degradation pathway affects sulfur release from the ocean to the atmosphere. In these experiments, gene transcription patterns, DMSP concentrations, and DMSP turnover rates were measured and evaluated, providing insights into bacterial regulation of DMSP transformation pathways. In addition to these experiments, the Environmental Sample Processor (ESP), an autonomous instrument capable of molecular biology assays and sample collection at sea, was deployed in Monterey Bay in September 2014. It was tasked to collect daily replicated samples for bacterial gene expression analysis. The ESP is concentrating microbial cells from 1-liter seawater samples onto collection filters and preserving and storing the filters until recovery at the end of the month-long deployment. The microbial cells are slated for metagenomic and metatranscriptomic analyses, and resulting gene expression patterns will provide data on the oceanic conditions regulating bacterial DMSP degradation in the ocean.

Metal pucks loaded with sample filters are used in water filtration and cell preservation on the ESP.
CREDIT: M.A. MORAN, UNIVERSITY OF GEORGIA

Publication

Yarza, P., et al. “Uniting the classification of cultured and uncultured bacteria and archaea using 16S rRNA gene sequences.” *Nature Reviews Microbiology* 12.9 (2014): 635-645.



Top: The ESP goes through final pre-deployment checks at the Monterey Bay Aquarium Research Institute.
CREDIT: M.A. MORAN, UNIVERSITY OF GEORGIA
Bottom: University of Georgia graduate student Brent Nowinski stands next to the ESP on the morning of deployment.
CREDIT: JESSIE MOTARD-CÔTÉ, UNIVERSITY OF SOUTH ALABAMA

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

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Shikha Sharma
West Virginia University
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This project has three goals: to broadly characterize the diversity of microbes living at deep shale interfaces, to identify the microbial origin of these lineages within geologic time, 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.

Update

Research activities during the past year have focused on methods development for extracting biomass from shale, the construction of high pressure/high temperature devices for biomass enrichments, and the testing of methods used for tracing microbial and chemical contaminants during sample collection and handling. In order to identify the state-of-the art knowledge in this area, the research team coordinated a February 2014 workshop in Columbus, Ohio to discuss "Trends and Challenges in Sampling the Deep Subsurface." The workshop included presentations from nine eminent and emerging scientists with experience in coring and genomics analysis of deep biosphere samples, along with 50 other attendees from academia, state agencies, and industry, as well as citizen activists who engaged in discussions. The workshop outcomes were summarized in a perspective article (Wilkins et al., 2014) and were incorporated into project sampling plans. Analysis has also begun on the Marcellus and Utica shale core to test methodological improvements and refine genomic and chemical analysis techniques before pristine core samples are collected from the OSU and WVU shale energy field laboratories. This project was highlighted in a special issue of *Science* in June 2014 entitled "The Shale Gas Surge" (*Science*, 344: 6191).

Publications

Arthur, M.A., Cole, D.R. "Unconventional Hydrocarbon Resources: Prospects and Problems." *Elements* 10.4 (2014): 257-264.

Wilkins, M.J., et al. "Trends and future challenges in sampling the deep terrestrial biosphere." *Frontiers in Microbiology* 5 (2014): doi: 10.3389/fmicb.2014.00481.

^ Lipid extractions from Marcellus and Utica Shale.
CREDIT: P. MOUSER, OSU

^ Student sampling a Marcellus core in the WVU Stable Isotope Laboratory.
CREDIT: S. SHARMA, WVU

^ Student collecting gas samples from the well-head of a producing well.
CREDIT: S. SHARMA, WVU

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

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(NSF 1342706)
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University of Chicago
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Keith Willmott
University of Florida
(NSF 1342705)
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This project connects the genetic, molecular and cellular mechanisms underlying adaptive variation within species to the ultimate causes of higher-order species diversity. Utilizing the radiation of neotropical *Adelpha* butterflies as a model system, this team integrates novel phylogenetic and genomic insights about the evolution of adaptive traits (e.g. vision, color taste and smell) with data from the ecology and natural history of the butterflies to test hypotheses about what is driving the development of biodiversity.

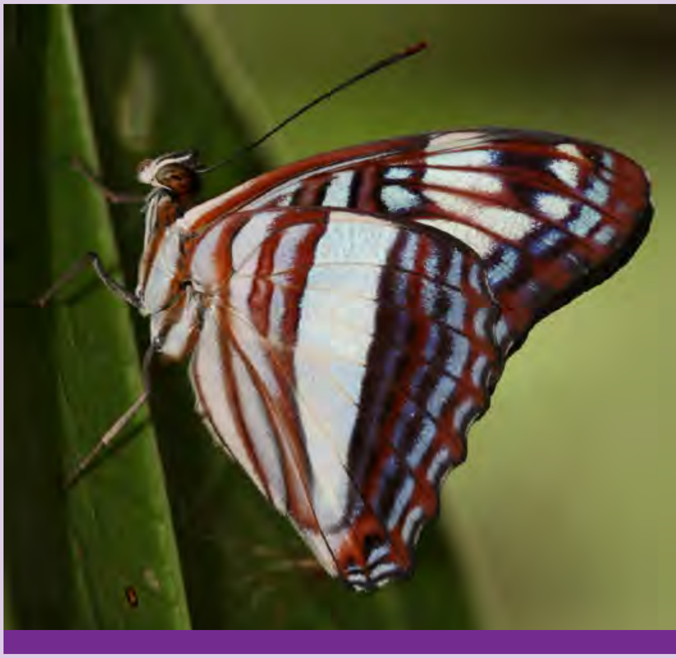
Update

Mullen and colleagues have made substantial progress in the first year towards completing their research aims. Major activities have focused on the phylogeny reconstruction, reference genome assembly, and the initiation of field experiments. The team is currently in the process of assembling this enormous data set. Field experiments have commenced in the Yasuni preserve in lowland Ecuador, at several locations within the Guanacaste Region of Costa Rica, and several sites in California and New Hampshire. Mark and recapture studies are ongoing and model-based predation experiments are planned for 2015.

Publication

Gallant, J.R., et al. "Ancient homology underlies adaptive mimetic diversity across butterflies." *Nature Communications* 5 (2014): doi: 10.1038/ncomms5817.

^ 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: RYAN HILL, UNIVERSITY OF THE PACIFIC



^ A male *Adelpha capucinus* dries its wings after emerging from its pupa at the Napo Wildlife Center in the east Ecuadorian Amazon.
CREDIT: KEITH WILLMOTT, UNIVERSITY OF FLORIDA

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

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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.

HTTP://ONAGMOTH.ORG
HTTPS://WWW.YOUTUBE.COM/WATCH?V=8IPQTS0CFQW

Update

Skogen and colleagues launched their research efforts with a project planning and coordination meeting held in February 2014 at the Chicago Botanic Garden. Following the initial meeting, the team conducted extensive fieldwork in Arizona, California, Colorado, Nevada, New Mexico, Texas, and Utah. A total of 20 populations were studied in 2014, with data collected on floral morphology, scent and phenology, and herbarium vouchers were prepared for of all focal and co-flowering species. In the upcoming year, field collections will focus on 16 species in particular, with a goal of sampling 5 populations for each species. Efforts to sequence the genome of *Oenothera harringtonii*, the flagship genome of the project, are underway, as are RNA-Seq experiments that will expand transcriptomic resources broadly across Onagraceae. Additionally, this Dimensions project has been featured in numerous media and outreach forums, including the internet series "Plants Are Cool, Too" where host Dr. Chris Martine joined investigator Krissa Skogen in the field for an interview.

Publication

Rhodes, M.K., et al. "Local Topography Shapes Fine-Scale Spatial Genetic Structure in the Arkansas Valley Evening Primrose, *Oenothera harringtonii* (Onagraceae)." *Journal of Heredity* (2014): esu051.

O. harringtonii — scented, white, night-opening flowers.
CREDIT: KRISSA SKOGEN, CHICAGO BOTANIC GARDEN

O. capillifolia — unscented, yellow, day-opening flowers.
CREDIT: KRISSA SKOGEN, CHICAGO BOTANIC GARDEN

Top: Manduca quinquemaculata hawkmoth drinking nectar from *Oenothera harringtonii* at dusk.
CREDIT: KRISSA SKOGEN, CHICAGO BOTANIC GARDEN
Bottom: Lasioglossum sp. bee robbing pollen from *O. harringtonii* at dawn.
CREDIT: SADIE LUNA TODD, CHICAGO BOTANIC GARDEN

Proj. 12 / 13

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)

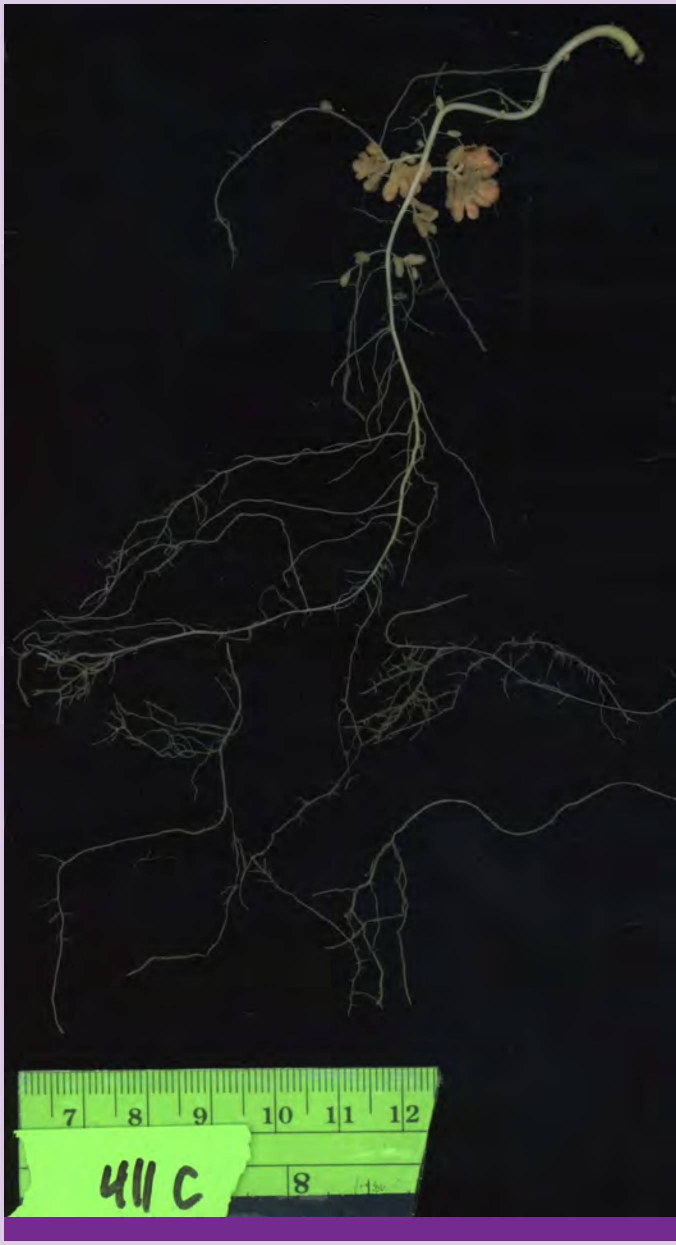
This project expands on a long-term record of clover (*Trifolium*) species' distributions to examine the role of genetic variation in rhizobial root symbionts in biological nitrogen fixation and clover coexistence.

Update

This research team made great advances on their project, despite facing significant challenges outside of their control. They surveyed 150 long-term plots at Bodega Bay but due to extreme drought conditions in California, it yielded only 4 *Trifolium* individuals. Thus, they focused efforts on (1) greenhouse experiments in field soils, (2) bulking seed in the greenhouse for field experiments and (3) microbiome sequencing. They analyzed microbiome data from nodules of six species grown experimentally in six soils and discovered a rare community of bacterial taxa that is structured both by soil, *Trifolium* species, and interactions between soil and species. They also completed an experiment manipulating the microbial community factorially with conspecific and heterospecific competition. Overall, they found that the small soil fraction, which only contained bacteria, differentially increased growth in home soil, but not in away soils. This suggests that specific strains of rhizobia or other bacteria cultivated by a *Trifolium* species may increase its own performance. The research team is currently analyzing root architecture from digital images to examine nodulation patterns in this experiment. Finally, they have improved their *de novo* transcriptome assembly of *Trifolium fucatum* and started collaborating with an international group that generated a *Trifolium subterraneum* genome. Analysis of these transcriptomes identified multiple differentially expressed genes across competitive environments, including those involved in phytohormone signaling and symbiosis.

^ Searching for *Trifolium* individuals at Bodega Bay during the 2013-2014 California drought — only 4 plants were found.

CREDIT: MAREN FRIESEN, MICHIGAN STATE UNIVERSITY



^ Digitized image of a *Trifolium fucatum* root showing abundant nodulation from an experiment manipulating soil microbial community and plant competition.

CREDIT: MAREN FRIESEN, MICHIGAN STATE UNIVERSITY

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 Urbana-Champaign
(NSF 1342876)

This project investigates 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 clarify the ways in which viruses influence the composition of microbial communities.

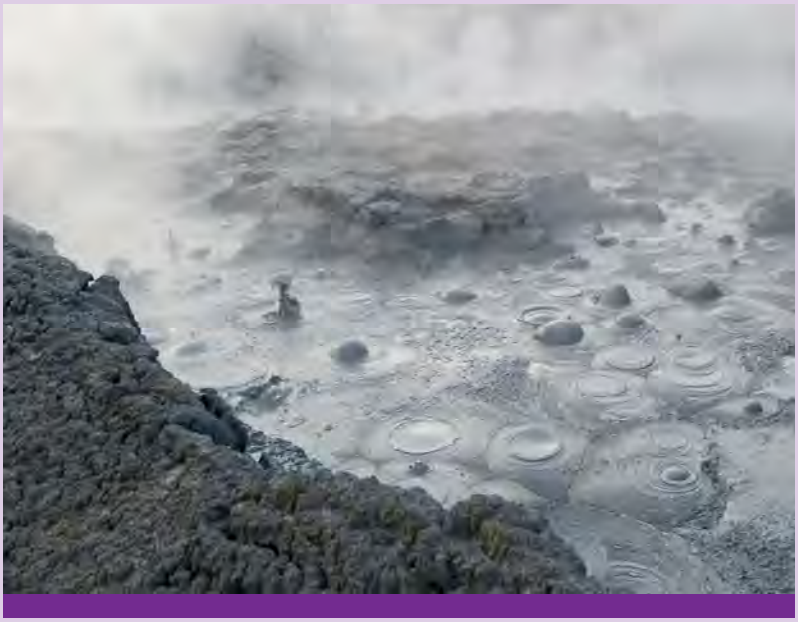
Update

The research team embarked on several activities during the first year of their Dimensions award. Young, Whitaker, Weitz and members of their labs met for a 2-day planning meeting in Bozeman, Montana. Over the year they conducted three winter sampling trips and an intensive 10-day sampling trip to Yellowstone National Park, which entailed host and viral sampling every 4-6 hours. In the laboratory, major advances have taken place in the development and optimization of qPCR assays and florescence *in situ* hybridization assays, as well as experimental evolution of virus-host pairs. The team has already isolated 40 novel host strains and 30 novel virus strains from the hot spring study sites and they are characterizing their genomes and infection traits in the laboratory. Additionally, the Illinois team led a workshop called Project Microbe that taught a six-week curriculum in microbiology to teachers from 30 Chicago Public High and Middle Schools. In the next year, the team plans to initiate developing a model for describing the host-virus interactions that integrates parameters of host and virus variation that have been determined in the lab.

Publications

Childs, L.M., et al. “CRISPR-Induced Distributed Immunity in Microbial Populations.” *PLoS One* 9.7 (2014): e101710.

Dellas, N., et al. “Archaeal Viruses: Diversity, Replication, and Structure.” *Virology* 1 (2014): 399-426.



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

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

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

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Research on Airborne Ice Nucleating Species (RAINS)

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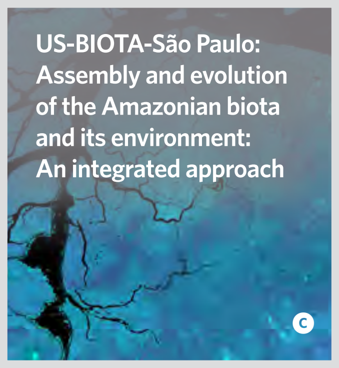

US-BIOTA-São Paulo: Assembly and evolution of the Amazonian biota and its environment: An integrated approach

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Do parallel patterns arise from parallel processes?

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

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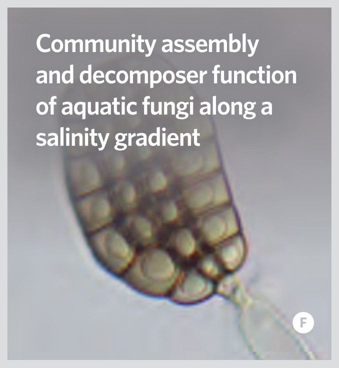

Community assembly and decomposer function of aquatic fungi along a salinity gradient

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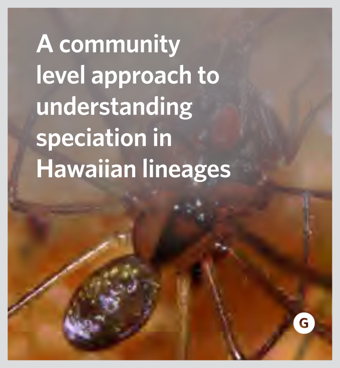

A community level approach to understanding speciation in Hawaiian lineages

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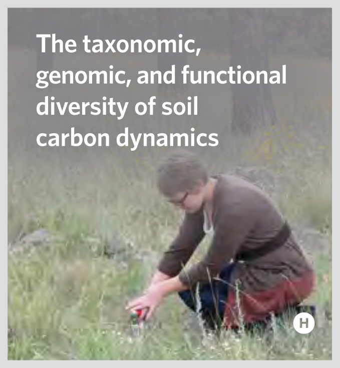

The taxonomic, genomic, and functional diversity of soil carbon dynamics

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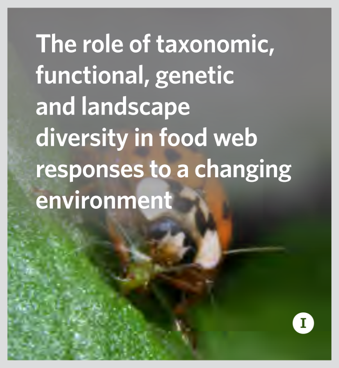

The role of taxonomic, functional, genetic and landscape diversity in food web responses to a changing environment

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The role of biodiversity for microbial adaptation to anthropogenic perturbations

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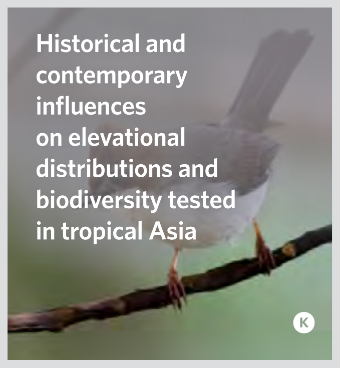

Historical and contemporary influences on elevational distributions and biodiversity tested in tropical Asia

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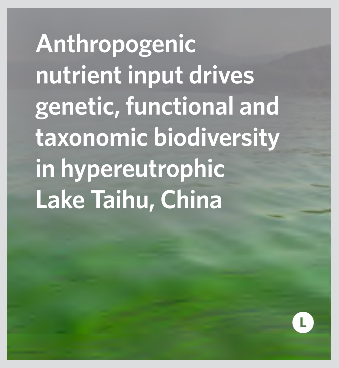

Anthropogenic nutrient input drives genetic, functional and taxonomic biodiversity in hypereutrophic Lake Taihu, China

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2012 updates

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

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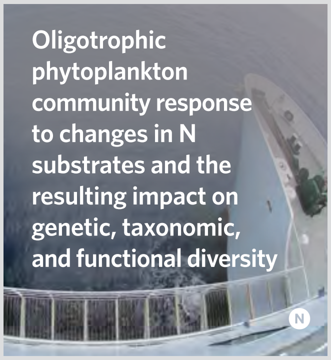

Oligotrophic phytoplankton community response to changes in N substrates and the resulting impact on genetic, taxonomic, and functional diversity

p. 59

IMAGE CREDIT

Ⓐ Arlo Midgett
Ⓑ Cindy E. Morris
Ⓒ Joel Cracraft
Ⓓ Michael N. Dawson
Ⓔ Jeremy Herren & John Jaenike
Ⓕ A. Ferrer
Ⓖ Karl Magnacca
Ⓗ Paul Dijkstra
Ⓘ Anthony R. Ives
Ⓙ K. Konstantinidis & D. Tsementzi
Ⓚ T. E. Martin
Ⓛ Hans Paerl
Ⓜ Nathan Swenson
Ⓝ Paul Lethaby

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

(CO-FUNDED WITH NSFC)

US TEAM	**Tia-Lynn Ashman** University of Pittsburgh (NSF 1241006)	**Aaron I. Liston** Oregon State University (NSF 1241217)	**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

Polyploid species have undergone recent whole genome duplications. This project examines the role that polyploidy has played in the evolution of strawberry species growing in the U.S. and in China.

HTTP://WILDSTRAWBERRY.ORG

Update

In 2013, Ashman and colleagues coordinated major collections of *Fragaria* populations in North America, Europe, China and Japan. The collections were made by the project investigators and by approximately 50 different collaborators. An average of 50-60 seeds per plant and 18-21 plants per population were collected from roughly 250 sites. This resulted in >200,000 seeds. This global collection will serve as the foundation for the team's research into the role of polyploidy in generating biodiversity. This collection will also serve as a community resource for ecological and evolutionary studies in strawberry.

Publication

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

Johnson, A.L., et al. "Bioclimatic evaluation of geographical range in *Fragaria* (Rosaceae): consequences of variation in breeding system, ploidy and species age." *Botanical Journal of the Linnean Society* 176.1 (2014): 99-114.

Liston, A., et al. "*Fragaria*: A genus with deep historical roots and ripe for evolutionary and ecological insights." *American Journal of Botany* 101.10 (2014): doi: 10.3732/ajb.1400140.

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

CREDIT: AARON LISTON, OREGON STATE UNIVERSITY

Bottom: *Fragaria* collecting in Oregon. Aaron Liston and Junmin Li.

CREDIT: TIA-LYNN ASHMAN, UNIVERSITY OF PITTSBURGH

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

CREDIT: TIA-LYNN ASHMAN, UNIVERSITY OF PITTSBURGH

Research on Airborne Ice Nucleating Species (RAINS)

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

HTTPS://SITES.GOOGLE.COM/A/ISU.EDU/CFWEBERLAB/RESEARCH/AMOEBA-AND-RAINS-JOIN-FORCES-TO-ACCOMPLISH-DISCOVERY-BASED-RESEARCH-IN-BIOLOGY-101
HTTPS://BIOICE.WORDPRESS.COM

Update

The RAINS research team has invested much effort into precipitation sampling with a variety of methods and different technologies. They have also developed and optimized a DNA extraction protocol for rain and snow samples and have begun screening bacterial cultures for ice nucleation. As an educational and outreach endeavor, the RAINS team has joined forces with AMOEBA (Authentic Mentoring of Engaged Biologist Alliance) at Idaho State University. Nine AMOEBA undergraduate students worked closely with the RAINS research team and the highlights of these activities are summarized at the Weber lab's website. An international early-career workshop on "Microbes at the Interface of Land-Atmosphere Feedbacks" (MILAF) was held in October 2014 as part of the training activities of the RAINS research project. To elucidate the environmental contexts in which bioprecipitation could have a major role in rainfall, interdisciplinary research will be essential. Engagement of stakeholders and the public at large will also be necessary to eventually influence bioprecipitation in view of mitigating drought. The objective of the MILAF workshop was to foster the interdisciplinary community that is needed for this challenge and to increase awareness of the role of stakeholders in translating the research challenges into practical solutions for societal and environmental problems.

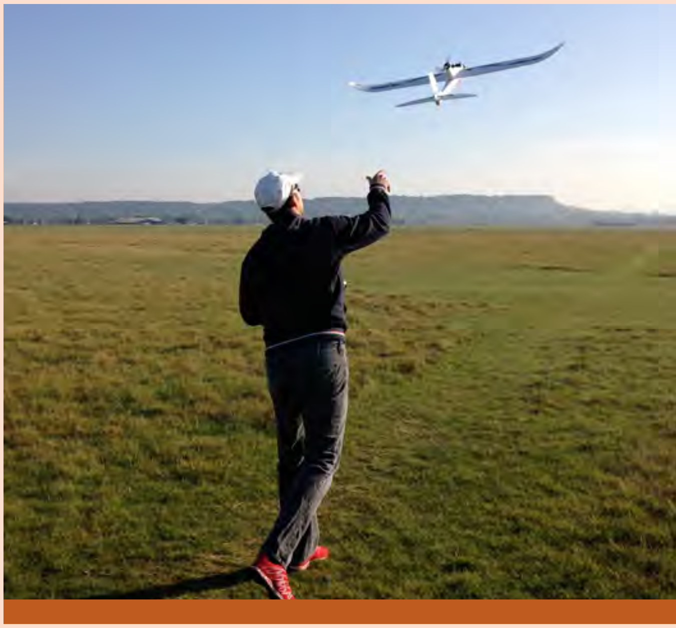
Participants of the 2014 MILAF workshop held 13-17 October 2014 in Sainte-Maxime France.
CREDIT: BRENT CHRISTNER, LSU

Publication

Cameron, K.A., et al. "Diversity and potential sources of microbiota associated with snow on western portions of the Greenland Ice Sheet." *Environmental Microbiology* (2014): doi: 10.1111/1462-2920.12446.

Michaud, A.B., et al. "Biological ice nucleation initiates hailstone formation." *Journal of Geophysical Research: Atmospheres* 119 (2014). doi:10.1002/2014JD022004.

Morris, C.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* 20.2 (2014): 341-351.



A hand-launched drone taking off for an atmospheric sampling mission in Pujaut, France. The drone is equipped with a device to sample microorganisms in the lower atmosphere.
CREDIT: DAVID SCHMALE, VIRGINIA TECH

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

(CO-FUNDED WITH NASA AND FAPESP)

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Diogo Meyer
Francisco Cruz
Universidade de São Paulo

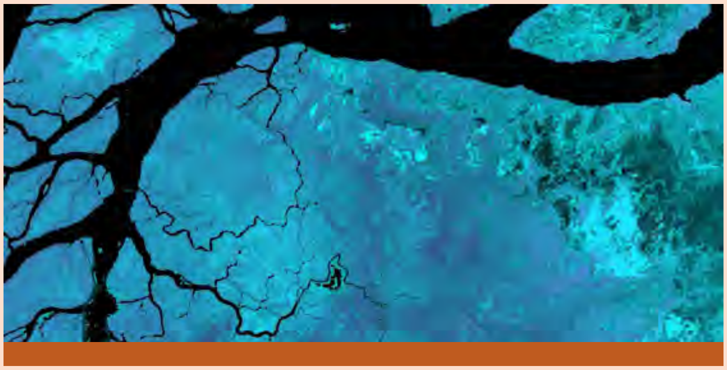
Andre Freitas
Universidade Estadual de Campinas

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.

HTTP://WWW.AMAZONIABIODIVERSITY.ORG

Update

In the first and second years of the award, coordination efforts for this large multi-institution project included a workshop at FAPESP in Brazil, the São Paulo Research Funding agency, and a meeting at INPA, the Brazilian National Institute for Amazonian Research. Research activities have been comprehensive and span a wide range of efforts. Major field work was conducted in the Brazilian State of Roraima where every passable road was traversed in search of outcrops to evaluate geomorphology, in addition, significant efforts were put towards advancing the Amazonian avian phylogenies, georeferencing and mapping the Amazonian plant species, and developing an on-line biodiversity data portal. Planning has already begun for the 2015 collaborators meeting, slated to take place in the state of Para, Brazil.



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

CREDIT: JOEL CRACRAFT, AMERICAN MUSEUM OF NATURAL HISTORY

Publications

Brower, A.V.Z., et al. "Phylogenetic relationships of ithomiine butterflies (Lepidoptera: Nymphalidae: Danainae) as implied by combined morphological and molecular data." *Systematics and Biodiversity* 12.2 (2014): 133-147.

Brower, A.V.Z., "Transformational and taxic homology revisited." *Cladistics* (2014): doi: 10.1111/cla.12076.

Figueiredo, W., et al. "A molecular phylogeography of the uacaris (*Cacajao*)." *Evolutionary Biology and Conservation of Titis, Sakis and Uacaris* (2013): 23-30.

Garzón-Orduña, I.J., et al. "Timing the diversification of the Amazonian biota: butterfly divergences are consistent with Pleistocene refugia." *Journal of Biogeography* 41.9 (2014): 1631-1638.

Lohmann, L.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.

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

Rocha, L.A., et al. "Collecting biological specimens is essential in science and conservation." *Science* 344.6186 (2014): 814-816.

CONTINUE >

Hoffmann's two-toed Sloth (*Choloepus hoffmanni*) is distributed in rainforests of lower Central America, northwestern South America, and western Amazonia. Usually hidden in the canopy during the day, they eat vast quantities of leaves at night and slowly digest them with the aid of symbiotic bacteria.

CREDIT: JOEL CRACRAFT, AMERICAN MUSEUM OF NATURAL HISTORY

Rodrigues N., et al. "Neogene-Quaternary sedimentary and paleovegetation history of the eastern Solimões Basin, central Amazon region." *Journal of South American Earth Sciences* 46 (2013): 89-99.

Sigurðsson, S., Cracraft, J. "Deciphering the diversity and history of New World nightjars (Aves: Caprimulgidae) using molecular phylogenetics." *Zoological Journal of the Linnean Society* 170.3 (2014): 506-545.

Tello, J.G., et al. "Reassessment of the systematics of the widespread Neotropical genus *Cercomacra* (Aves: Thamnophilidae)." *Zoological Journal of the Linnean Society* 170.3 (2014): 546-565.

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

Proj. 4 / 14

Do parallel patterns arise from parallel processes?

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

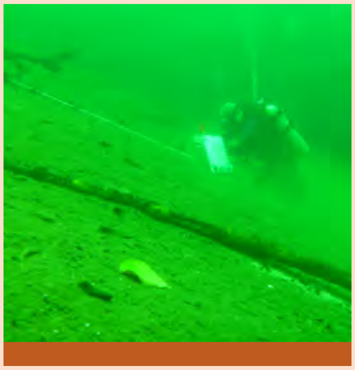
Julian P. Sachs
University of Washington
(NSF 1241247)

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' 'natural experiments' to evolve independently under similar environmental conditions.

HTTP://MARINELAKES.UCMERCED.EDU

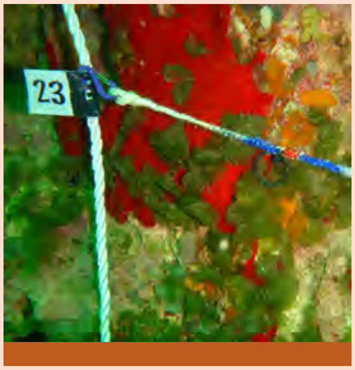
Update

Dawson and colleagues have now led two successful years of fieldwork in Palau – one in 2013, and most recently in June & July of 2014. These field trips involve survey and collection of marine microbes, invertebrates, fishes, and algae samples. Over 15 lakes are being surveyed for all species, and 21 species of macrobiota have been sampled in detail for genetic information. To find out how communities have changed through time, coring operations were initiated in Fall 2013. Analysis has begun on the core samples, using visual imagery, x-radiography, and x-ray fluorescence. Initial data are already yielding intriguing results.



Surveys at ~25 m depth have an eerie ambience.

CREDIT: MICHAEL N. DAWSON, UNIVERSITY OF CALIFORNIA, MERCED



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

CREDIT: MICHAEL N. DAWSON, UNIVERSITY OF CALIFORNIA, MERCED

Publications

Nelson, D.B., Sachs, J.P. "The influence of salinity on D/H fractionation in dinosterol and brassicasterol from globally distributed saline and hypersaline lakes." *Geochimica et Cosmochimica Acta* 133 (2014): 325-339.

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

CREDIT: MICHAEL N. DAWSON, UNIVERSITY OF CALIFORNIA, MERCED

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

Update

In this project, Douglas and colleagues are utilizing molecular tools to gain insight into the significance of animal hosts as drivers of microbial diversity as well as to understand how interactions with the bacteria affect various traits of the animal host, including food processing, habitat choice, competition, and interactions with parasites, all of which can potentially drive animal diversification. In addition to making substantial progress in the laboratory, the research team has had the opportunity to interact with various audiences to promote an appreciation and understanding of biodiversity, at scales from an individual human body to the global biosphere. In 2014 and early 2015, the research team is sponsoring a photographic exhibition open to the general public entitled "Shifting Paradigms: Microbes as Animal-Helpmates," in order to demonstrate the importance of microbial diversity in the lives of animals. Additionally, the team has led hands-on training sessions on *Drosophila* taxonomy and field monitoring. Science Saturday meetings for the general public at the Rochester Museum and Science Center are planned to illustrate that animal-associated microbes include not only pathogens, but also species important for the well-being and normal ecological functioning of animals.

Publications

Douglas, A.E. "The Molecular Basis of Bacterial–Insect Symbiosis." *Journal of Molecular Biology* (2014): doi: 10.1016/j.jmb.2014.04.005.

Douglas, A.E. "Symbiosis as a General Principle in Eukaryotic Evolution." *Cold Spring Harbor Perspectives in Biology* 6.2 (2014): a016113.

Douglas, A.E. "Microbial brokers of insect-plant interactions revisited." *Journal of Chemical Ecology* 39.7 (2013): 952-961.

^ A live trap and associated lure used to collect *D. melanogaster* and *D. suzukii* adults in the field.
CREDIT: GREG LOEB, CORNELL UNIVERSITY

^ *Drosophila suzukii* on a raspberry.
CREDIT: H. BURRACK, NORTH CAROLINA STATE UNIVERSITY

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 looks 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.

HTTP://PUBLISH.ILLINOIS.EDU/AQUATICFUNGI

Update

Ferrer and colleagues have now completed 5 censuses of wood samples set out in the decomposition experiment in Panama. This work has been followed by the morphological characterization of the fungal community. The team has identified over 300 species of aquatic fungi and they are currently conducting the molecular characterization of these species (DNA barcoding and identifying functional genes). The chemical and structural characterization of the wood has begun, which will eventually link fungal community composition to the process of wood decay. In addition, the researchers have been able to grow a large fraction of fungal isolates in the laboratory and have contributed these to a screening program to assess them for potential antimicrobial activity and activity against tropical diseases. Lastly, in addition to the research developments stemming from this project, the team has made great strides in training the next generation of biodiversity scientists. Three Latin American biologists were trained in the Ferrer lab, two of which are currently applying for graduate school in molecular biology and mycology.

Spore of the aquatic fungus *Canalisporium* sp.
CREDIT: A. FERRER

Sampling in the Playa Hermosa River, Coiba Island.
CREDIT: A. FERRER

Top: A block of replicate wood samples incubating in the Playa Hermosa River.
Middle: Mangroves at the entrance of the Santa Cruz River, Coiba Island.
Bottom: Playa Hermosa River, Coiba Island.
CREDIT: A. FERRER

Proj. 7 / 14

A community level approach to understanding speciation in Hawaiian lineages

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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.

Update

Over the past two years Gillespie and colleagues have focused on establishing protocols for ecological sampling, field collecting, and gathering molecular data. Planning meetings took place in December 2012 and July 2013. Fieldwork subsequently began in the summer of 2013. Geographic information systems with remote sensing laser data (LiDAR) were utilized for field site selection. The team has chosen to sample 6 plots from each of the 9 proposed sites, resulting in a total of 54 sampling locations, and a proposed 100,000 specimens for collection. In conducting this project, the team hopes to develop theoretical tools for predicting biodiversity response in the face of species invasions, extinctions and other impacts of societal relevance including climate change and urbanization.

Publications

Brewer, M.S., et al. "New sequencing technologies, the development of genomics tools, and their applications in evolutionary arachnology." *Journal of Arachnology* 42.1 (2014): 1-15.

A Hawaiian carnivorous caterpillar, *Eupithecia palikea*.
CREDIT: KARL MAGNACCA

Proj. 8 / 14

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

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

Update

The central hypothesis of this research project is that microbial biodiversity plays a role in modulating carbon cycling. This hypothesis is often referred to as the "priming effect". Thus far, the research team has completed two major experiments examining the relationship between microbial biodiversity and priming effects. Early findings indicate that the priming effect is associated with an increase in microbial biodiversity and that no single specific organism can be identified as largely responsible for the priming effect. A manuscript describing this research is currently in preparation. Collaborations between Northern Arizona University and Translational Genomics Research Institute have resulted in practical web-based bioinformatics tools that will have widespread impact for scientists worldwide.

Publications

Schwartz, E., et al. "Accelerated microbial turnover but constant growth efficiency with warming in soil." *Nature Climate Change* (2014): doi: 10.1038/NCLIMATE2361.

Collecting soil for microbial diversity analysis.
CREDIT: PAUL DIJKSTRA, NORTHERN ARIZONA UNIVERSITY

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

(CO-FUNDED WITH NASA)

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University of Georgia
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Jason Harmon
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(NSF 1241031)

Ives and colleagues are examining how genetic, taxonomic, ecological and landscape diversity influence the control of agricultural pests by their natural enemies.

Update

This project is advancing in each of its four dimensions to understand the role of bacterial-aphid symbiotic relationships in the ecology and evolution of aphids. Newly developed genetic techniques are being used to rapidly determine which bacterial symbionts are contained within an aphid, and which of these symbionts are linked with providing increased heat tolerance. These techniques are being used to follow the evolution of aphids and their symbionts in real time. A citizen science project involving more than 100 individuals and K-12 classrooms is generating a large library of aphids from across the continental USA, which will give unprecedented insights into the diversity of bacterial symbionts. Finally, field experiments have shown the potential for complex interactions among aphids, symbionts, and predators to determine the outcome of climate change on aphid populations. Ongoing work with satellite imaging is extrapolating these experimental results to landscape scales.

Publication

Harmon, J.P., Barton, B.T. "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.

Meisner, M.H., et al. "Temperature effects on long-term population dynamics in a parasitoid-host system." *Ecological Monographs* 84.3 (2014): 457-476.

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

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

The role of biodiversity for microbial adaptation to anthropogenic perturbations

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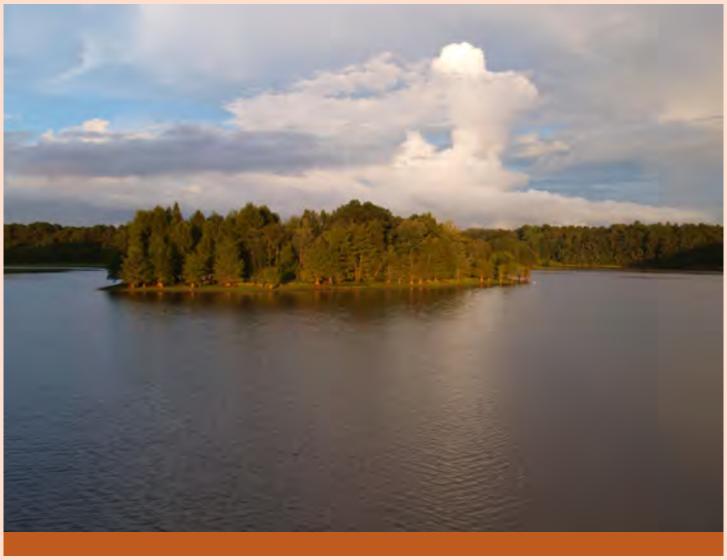
(NSF 1241046)

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

HTTP://ENVE-OMICS.CE.GATECH.EDU

Update

Konstantinidis and colleagues have developed new bioinformatics algorithms and pipelines to analyze the genetic data generated for this project. These algorithms and useful analysis tools have been published on-line for free public access. These tools have become very popular, with more than 500 visitors per month routinely visiting the site to use the tools for their own projects and data. The research team has made additional progress in their laboratory experiments, establishing mesocosms of their model system environment, Lake Lanier (Atlanta, GA). Fieldwork continues year round at Lake Lanier, and the team currently has three years worth of summer samples from four additional lake sites in the Southeastern United States. The preliminary results from the laboratory mesocosms show that rare genes and species frequently underlie community adaptation to perturbations and that horizontal gene transfer is more frequent than previously thought during adaptation. The analysis of field data revealed strong biogeographic patterns for several planktonic populations, with specific populations in the northern lakes being replaced by close relatives in the more southern lakes. The underlying mechanisms for the latter observation are currently under investigation using a combination of metagenomics, mathematical modeling and metabolomics techniques.



^ Photo of Lake Eufaula, Alabama.

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

Publication

Caro-Quintero, A., Konstantinidis, K.T. “Inter-phylum HGT has shaped the metabolism of many mesophilic and anaerobic bacteria.” *The ISME Journal* (2014): doi:10.1038/ismej.2014.193.

Luo, C. et al. “A User’s Guide to Quantitative and Comparative Analysis of Metagenomic Datasets.” *Methods in Enzymology* 531 (2013): 525-547.

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

Oh, S., et al. “Microbial community degradation of widely used quaternary ammonium disinfectants.” *Applied and Environmental Microbiology* 80.19 (2014): 5892-5900.

Poretsky, R., et al. “Strengths and Limitations of 16S rRNA Gene Amplicon Sequencing in Revealing Temporal Microbial Community Dynamics.” *PloS One* 9.4 (2014): e93827.

Rodriguez-R, L.M., Konstantinidis, K.T. “Bypassing Cultivation To Identify Bacterial Species.” *Microbe* 9.3 (2014): 111-118.

Rodriguez-R, L.M., Konstantinidis, K.T. “Estimating coverage in metagenomic data sets and why it matters.” *The ISME Journal* (2014): doi: 10.1038/ismej.2014.76.

Rodriguez-R, L.M., and Konstantinidis, K.T. “Nonpareil: a redundancy-based approach to assess the level of coverage in metagenomic datasets.” *Bioinformatics* 30.5 (2013): 629-635.

Tsementzi, D., et al. “Evaluation of metatranscriptomic protocols and application to the study of freshwater microbial communities.” *Environmental Microbiology Reports* (2014): doi: 10.1111/1758-2229.12180.

Weigand, M.R., et al. “Genome sequencing reveals the environmental origin of enterococci and potential biomarkers for water quality monitoring.” *Environmental Science & Technology* 48.7 (2014): 3707-3714.

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

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

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

Arriero, E., et al. “Ontogeny of constitutive immunity: maternal vs. endogenous influences.” *Functional Ecology* 27.2 (2013): 472-478.

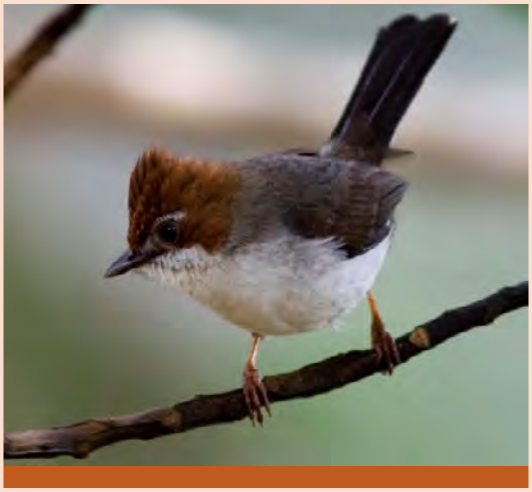
Ghalambor, C.K., et al. “Plasticity of parental care under the risk of predation: how much should parents reduce care?” *Biology Letters* 9.4 (2013): doi: 10.1098/rsbl.2013.0154.

Martin, T.E. “A Conceptual Framework for Clutch-Size Evolution in Songbirds.” *The American Naturalist* 183.3 (2014): 313-324.

Martin, T.E., et al. “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.

Martin, Thomas E., et al. “Postnatal Growth Rates Covary Weakly with Embryonic Development Rates and Do Not Explain Adult Mortality Probability among Songbirds on Four Continents.” *The American Naturalist* 185.3 (2015): 380-389.

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



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

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

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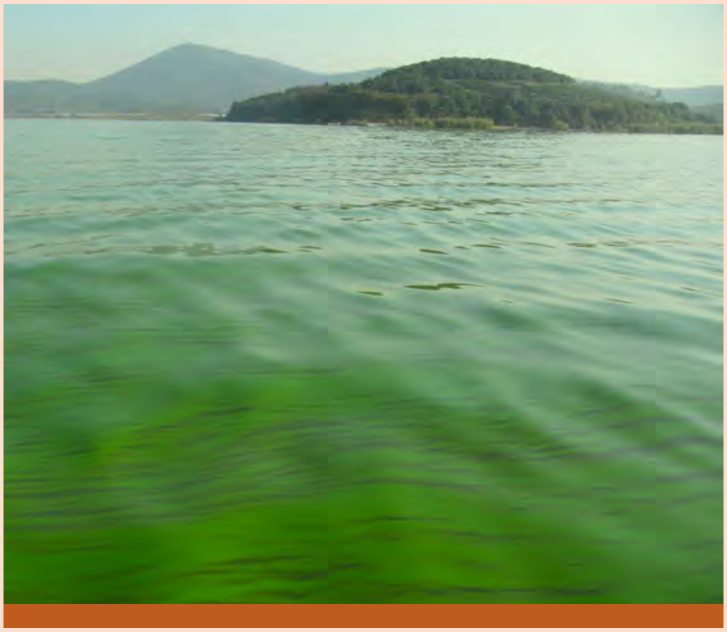
Paerl and colleagues are examining the species and genetic diversity of microbes in a lake that experiences massive blooms of toxic cyanobacteria. They are linking that diversity to the processing of nitrogen that is the cause of the toxic blooms.

HTTP://WWW.UNC.EDU/IMS/PAERLLAB/RESEARCH/TAIHU

Update

2014 was a productive year for Paerl and colleagues. The principal investigators, graduate students, and post-doctoral fellows made several research trips to Lake Taihu in China to examine seasonal patterns of nitrogen cycling. In the spring of 2014, the team established a mesocosm experiment to investigate the effects of temperature increases and nutrient enrichment on cyanobacterial blooms. A masters student on the team, embarked on a side project testing the hypothesis that the production of toxins (microcystin) is driven by the need to neutralize reactive oxygen species (ROS). ROS constitute a group of chemical compounds that cause oxidative stress and damage in a variety of organisms. Cyanobacterial blooms in large lake ecosystems can have negative impacts to drinking water supplies, human and animal health, fisheries, tourism, and recreational use. This research has already yielded interesting early results, which have been recently published, with implications for nutrient input reduction strategies in this and other eutrophic, bloom-impacted lake systems.



^ View of toxic cyanobacterial bloom on Lake Taihu, China.

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

Publications

Deng, J., et al. "Earlier and warmer springs increase cyanobacterial (*Microcystis* spp.) blooms in subtropical Lake Taihu, China." *Freshwater Biology* 59.5 (2014): 1076-1085.

Ma, J. et al. "Environmental factors controlling colony formation in blooms of the cyanobacteria *Microcystis* spp. in Lake Taihu, China." *Harmful Algae* 31 (2014): 136-142.

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.

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

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Scott, J.T., 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.

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

Steffen, M.M., et al. "Status, causes and controls of cyanobacterial blooms in Lake Erie." *Journal of Great Lakes Research* 40.2 (2014): 215-225.

Steffen, M.M., et al. "Taxonomic assessment of a toxic cyanobacteria shift in hypereutrophic Grand Lake St. Marys (Ohio, USA)." *Harmful Algae* 33 (2014): 12-18.

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

Zhu, M., et al. "The role of tropical cyclones in stimulating cyanobacterial (*Microcystis* spp.) blooms in hypertrophic Lake Taihu, China." *Harmful Algae* 39 (2014): 310-321.

Proj. 13 / 14

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

(CO-FUNDED WITH NSFC)

US MEMBERS		CHINA MEMBERS	
	Nathan Swenson Michigan State University (NSF 1241136)		**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.

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

CREDIT: NATHAN SWENSON, MICHIGAN STATE UNIVERSITY

Update

In the summers of 2013 and 2014, Swenson et al focused their efforts on developing drought experiments and optimizing greenhouse methods. From these experiments, genetic samples were processed and analyzed to extrapolate information on gene expression and transcriptomic similarity. Under the direction of Dr. Ma, similar work is being conducted in parallel in Gutianshan, China.

Proj. 14 / 14

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

In late summer of 2014, Zehr and colleagues conducted a month long expedition named NEMO (Nutrient Effects on Marine microOrganisms). The objective of the NEMO research cruise was to investigate the role of nitrogen in shaping phytoplankton biodiversity and physiology in the central North Pacific Ocean. Starting from San Diego, CA, they characterized the nutrient rich dynamic waters of the California Current System, followed by an extensive phytoplankton bloom in the middle of North Pacific Ocean, low-nutrient waters and a large *Trichodesmium* bloom near Hawaii. By taking various physicochemical and biological measurements along the transect, and conducting nutrient manipulation experiments, they examined how different forms of nitrogenous substrates together with phosphorus and iron alter microbial community structure, physiology and the rates of phytoplankton photosynthesis. In addition to the NEMO cruise, the investigators led a demo-program on how genomics is used to study marine phytoplankton as part of National Geographic BioBLITZ-2014 hosted by the San Francisco Exploratorium.

^ Science team on the research vessel New Horizon at the end of the NEMO cruise.

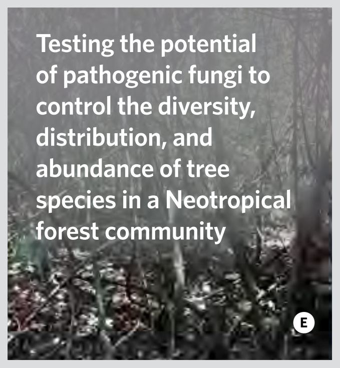
CREDIT: G. VAN DIJKEN, STANFORD UNIVERSITY

Diversity and symbiosis: Examining the taxonomic, genetic, and functional diversity of amphibian skin microbiota p. 62

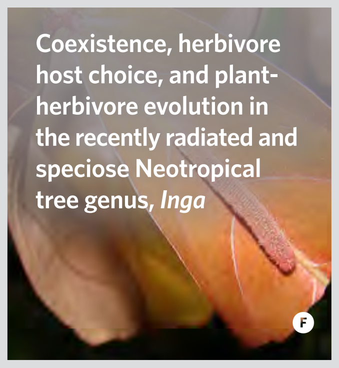
Integrating genetic taxonomic and functional diversity of tetrapods through extinction risk p. 63

US-China: International Research Coordination Network: A research coordination network for biodiversity of ciliates p. 65

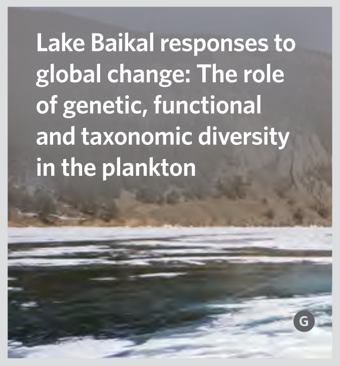
Pattern and process in marine bacterial, archaeal, and protistan biodiversity, and effects of human impacts p. 66



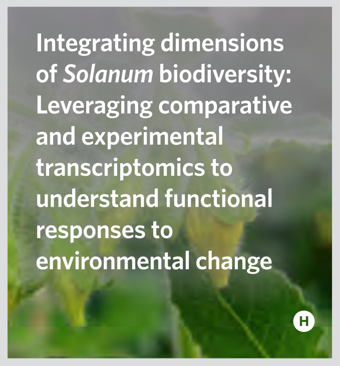
Testing the potential of pathogenic fungi to control the diversity, distribution, and abundance of tree species in a Neotropical forest community p. 68



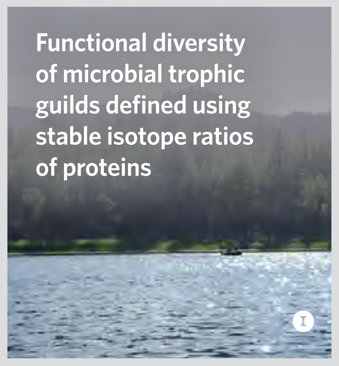
Coexistence, herbivore host choice, and plant-herbivore evolution in the recently radiated and speciose Neotropical tree genus, *Inga* p. 69



Lake Baikal responses to global change: The role of genetic, functional and taxonomic diversity in the plankton p. 70

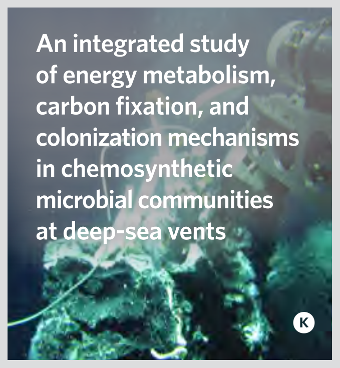


Integrating dimensions of *Solanum* biodiversity: Leveraging comparative and experimental transcriptomics to understand functional responses to environmental change p. 71

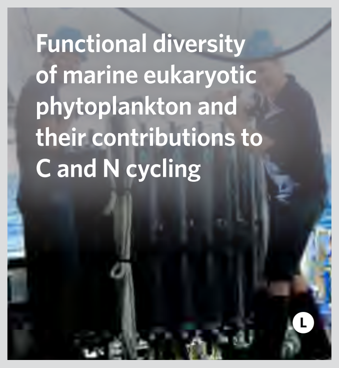


Functional diversity of microbial trophic guilds defined using stable isotope ratios of proteins p. 71

The climate cascade: Functional and evolutionary consequences of climatic change on species, trait, and genetic diversity in a temperate ant community p. 72



An integrated study of energy metabolism, carbon fixation, and colonization mechanisms in chemosynthetic microbial communities at deep-sea vents p. 74



Functional diversity of marine eukaryotic phytoplankton and their contributions to C and N cycling p. 75

2011 updates

IMAGE CREDIT

Ⓐ Jenifer Walke
Ⓑ Geoffrey A. Hammerson
Ⓒ John C. Clamp
Ⓓ Jed Fuhrman
Ⓔ Gregory S. Gilbert
Ⓕ Tom Kursar
Ⓖ Paul Wilburn
Ⓗ David Haak
Ⓘ Jennifer Glass
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Diversity and symbiosis: Examining the taxonomic, genetic, and functional diversity of amphibian skin microbiota

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This project investigates the diverse microbial communities on the skin of amphibian species and their role in controlling a critical disease that threatens amphibian biodiversity in the Neotropics.

Update

In 2012, a field survey of three amphibian species at four sites in Panama resulted in skin bacterial community data and metabolite profiles for 138 individual amphibian hosts. Initial results suggest that these frog species have distinct skin bacterial communities and that metabolite profiles of these communities are highly variable. In 2013, laboratory experiments were conducted to evaluate these microbial communities before and after the exposure to the pathogenic chytrid fungus. The team is currently finalizing analyses of these datasets, and developing a new statistical application to examine potential drivers of differences among complex communities. The Belden research team received a Dimensions Broadening Participation REU supplement and hosted two undergraduates from the University of Puerto Rico who conducted both field collections and lab experiments in the summer of 2014. Major outreach efforts have involved contributions to a permanent amphibian exhibit at the Punta Culebra Nature Center in Panama.

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

CREDIT: JENIFER WALKE, VIRGINIA TECH

Publication

Becker, M.H., et al. “The effect of captivity on the cutaneous bacterial community of the critically endangered Panamanian golden frog (*Atelopus zeteki*).” *Biological Conservation* 176 (2014): 199-206.

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Umile, T.P., et al. “Nonlethal amphibian skin swabbing of cutaneous natural products for HPLC fingerprinting.” *Analytical Methods* 6.10 (2014): 3277-3284.

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Integrating genetic taxonomic and functional diversity of tetrapods through extinction risk

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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

Major strides were made in the compilation of extinction risk and distribution data during a 2013 workshop in collaboration with NatureServe, the Colombian Association of Herpetology (Asociación Colombiana de Herpetología) and the International Union for Conservation of Nature (IUCN) and a 2013 workshop on Brazilian lizards. Following these workshops, the research teams have focused their work on analysis and mapping. In the last year, the team published numerous research articles describing their most recent data and findings.

Top: *Aspidoscelis sexlineata* six-lined racerunner, Colorado, USA.
Bottom: *Thamnophis elegans* terrestrial gartersnake, Washington, USA.
CREDIT: GEOFFREY A. HAMMERSON

Publication

Araújo, C.B., et al. “The importance of biotic interactions in species distribution models: a test of the Eltonian noise hypothesis using parrots.” *Journal of Biogeography* 41.3 (2014): 513-523.

Barrio-Amoros, C.L., et al. “A new tuberculated *Pristimantis* (Anura, Terrarana, Strabomantidae) from the Venezuelan Andes, redescription of *Pristimantis pleurostriatus*, and variation within *Pristimantis vanadisae*.” *Zootaxa* 3647.1 (2013): 043-062.

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Colston, T.J., et al. “Molecular systematics and historical biogeography of tree boas (*Corallus* spp.).” *Molecular Phylogenetics and Evolution* 66.3 (2013): 953-959.

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Mccranie, J.R., Hedges, S.B. “A new species of *Phyllodactylus* (Reptilia, Squamata, Gekkonoidea, Phyllodactylidae) from Isla de Guanaja in the Honduran Bay Islands.” *Zootaxa* 3694.1 (2013): 051-058.

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Mccranie, J.R., Hedges, S.B. “Two additional new species of *Sphaerodactylus* (Reptilia, Squamata, Gekkonoidea, Sphaerodactylidae) from the Honduran Bay Islands.” *Zootaxa* 3694.1 (2013): 40-50.

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

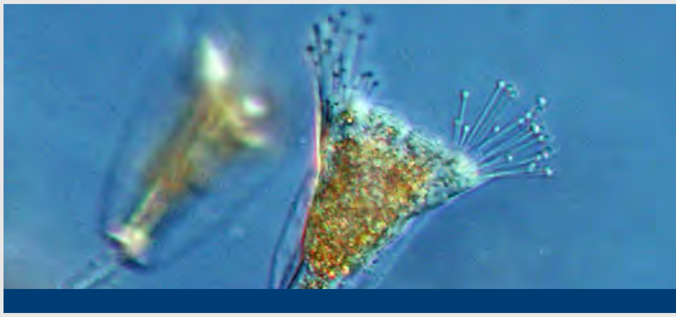
CREDIT: GEOFFREY A. HAMMERSON

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

(CO-FUNDED WITH NSFC)

US TEAM	**John Clamp** North Carolina Central University (NSF 1136580)	**Laura Katz** Smith College (NSF 1136580) **Chris Lobban** University of Guam (NSF 1136580)	**Micah Dunthorn** University of Kaiserslautern Germany (NSF 1136580)
CHINA TEAM	**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** Pontificia Universidade Católica do Rio Grande do Sul Brazil	

This project, jointly supported by the National Natural Science Foundation of China (NSFC), establishes an international research coordination network (IRCN) for the biodiversity of ciliates. The network includes researchers from the United States, China, the United Kingdom, and Brazil and broadens exploration of these important protists.



Acineta tuberosa.

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

HTTP://IRCN-BC.ORG

Update

After the success of the 2012 workshop on ciliate biodiversity, the IRCN has organized three subsequent workshops — two in Vancouver British Columbia following the XIV International Congress of Protistology in the summer of 2013 and one at the University of London in the United Kingdom in fall of 2014. These three workshops have focused on ciliates as model organisms, ciliates and the rare biosphere, and lastly new standards for documenting biodiversity of ciliates and strategies for accessing and sharing data. The collaborative research of this international group of scientists has within the last year, resulted in several publications. Planning for the next workshop is already underway, and is slated to take place in Qingdao, China in 2015.

Diophrys sp, a hypotrich.

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

Publication

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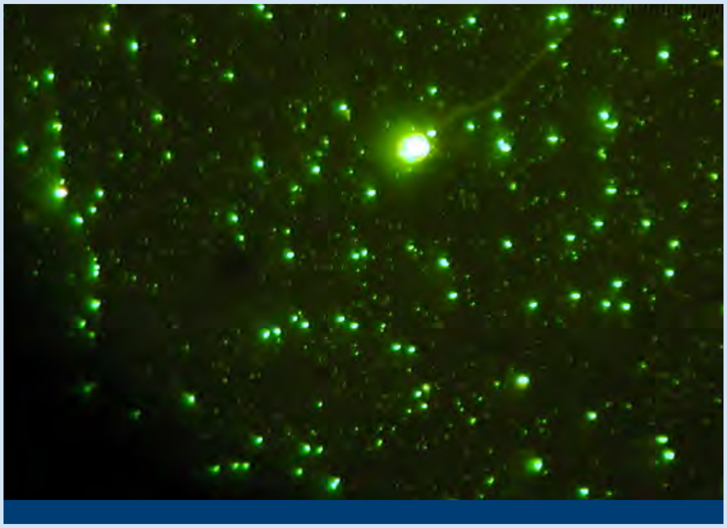
Pattern and process in marine bacterial, archaeal, and protistan biodiversity, and effects of human impacts

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, rate and cell abundance measurements, as well as DNA sequence-based studies covering viruses, bacteria, archaea, and protists have yielded a substantial amount of data for this research team. The port area has higher biomass and activity, as well as substantially different microbial community composition, suggesting selection for high nutrient and contaminant tolerant organisms there. The genetic bases of such selection is being evaluated by metagenomic and metatranscriptomic approaches, with our team of microbiologists and computational biologists currently evaluating several billion bases of sequence data and developing new approaches to do so. 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). The ongoing surface- to-bottom microbial time series continues to yield valuable insights about seasonality and long-term interannual variability of microbial processes in response to oceanographic and other drivers. Numerous publications have already resulted from this research.



^ An epifluorescence microscopy image of viruses (tiniest dots), bacteria (medium sized dots) and protists (larger ones) from the USC Microbial Observatory.
CREDIT: JED FUHRMAN, UNIVERSITY OF SOUTHERN CALIFORNIA

Publications

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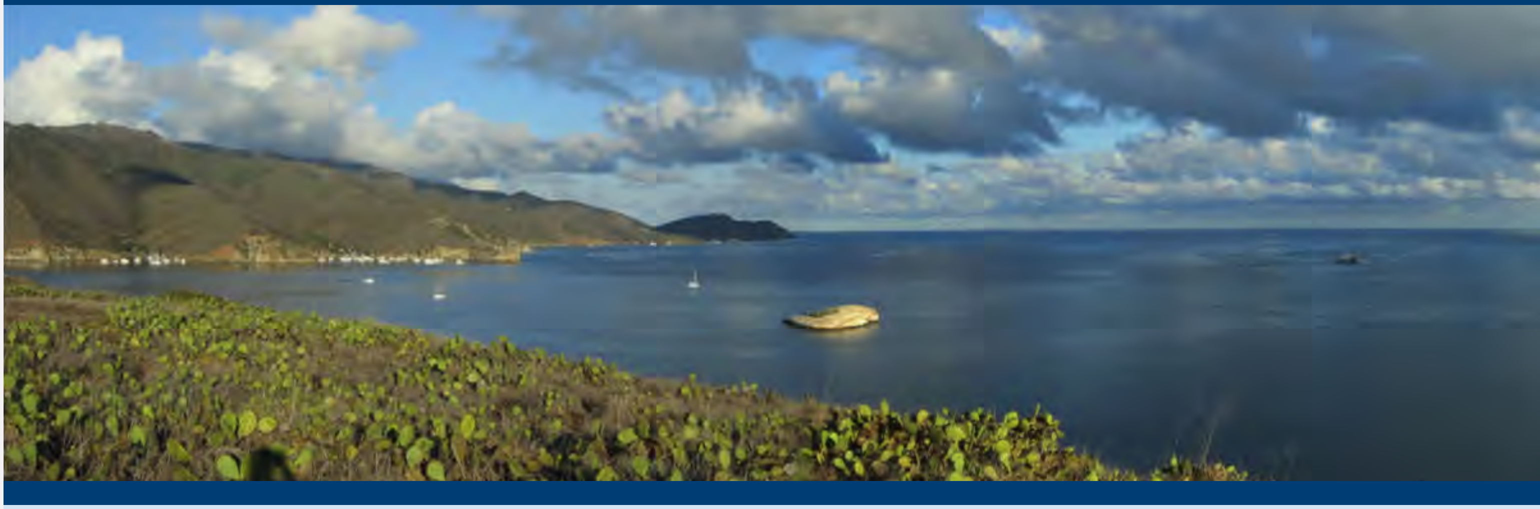

^ ***Top:*** Sampling from a small boat near Catalina Island.
Bottom: Looking out to sea in the general direction of the USC Microbial Observatory from Catalina Island, near the USC Wrigley Marine Science Center.

CREDIT: JED FUHRMAN, UNIVERSITY OF SOUTHERN CALIFORNIA

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

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The 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.

HTTP://WWW.YOUTUBE.COM/WATCH?V=02CGGQVM29M

Update

This research team is testing the Enemy Susceptibility Hypothesis that rare tree species are more susceptible to fungal attack than common tree species, and consequently they are rare because they have fewer safe places to grow and avoid infection. Hubbell and colleagues have made great strides in conducting topographic scans of common and rare tree species in the Barro Colorado Island plot in Panama to determine which trees are infected with the heart-rot fungal pathogen. Over 1700 individual trees representing 98% of all species in the plot have been scanned. The data has shown interesting patterns of infection: larger trees of either rare or common species are most likely in the plot to have the heart-rot fungus. However, of the smaller trees (≤40 cm diameter at breast height), rare species are more likely to have heart rot than the common tree species. Although scientists have suspected that fungi play some role in the maintenance of plant diversity, this research is the first to provide a specific mechanism for how fungi might do this for mature rainforest trees. See the link above for a video highlighting the team's research produced by the Smithsonian Tropical Research Institute, Panama.

Publications

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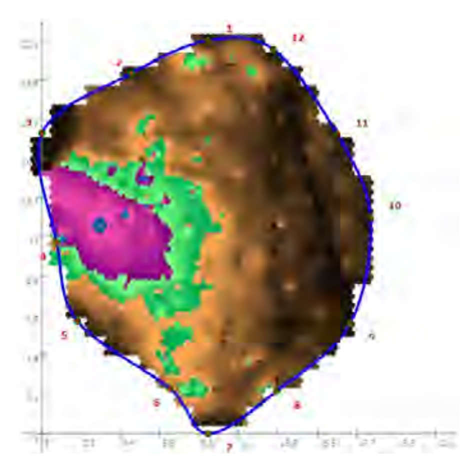
^ A crew of project interns collecting data on internal decay of mature living trees.
CREDIT: GREGORY S. GILBERT, UC SANTA CRUZ



^ A tomographic image showing internal decay in the trunk of a living rainforest tree.
CREDIT: GREGORY S. GILBERT, UC SANTA CRUZ

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

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 is shedding light on the coevolution of plants and herbivores and its influence on the ecology of the most diverse forest communities on Earth.

Update

Kursar and colleagues conducted fieldwork in the summer and fall of 2014 at the Tiputini Biodiversity Station in the Yasuni Biosphere Reserve of Ecuador. This was the second and last field season at this site. They found an extremely high diversity of *Inga* species, with over 50 species of *Inga* in one area 2 x 3 km in size. This was substantially more species than what has been identified at other comparable field sites in Brazil, French Guiana and Peru. During this fieldwork, over 750 herbivore specimens for sequencing and 800 *Inga* samples were collected for analysis of secondary metabolites. The research group has concurrently made great strides in their phylogenetic analysis of *Inga*. They previously faced major technical challenges due to the inherent low level of genetic divergence among species in the *Inga* genus, however, colleagues in Edinburgh have mastered a new approach that entails enriching for specific nuclear genes and then sequencing with next-generation methods. Preliminary analyses for herbivores collected in Peru suggest that, in general, herbivore host choice relies more on the chemical similarity of hosts than on the phylogenetic relationships of the hosts.

Top & Bottom: An inflorescence of *Inga punctata* at Los Amigos, Peru.
CREDIT: TOM KURSAR, UNIVERSITY OF UTAH

An unidentified caterpillar consuming *Inga marginata* (Nouragues, French Guiana).
CREDIT: TOM KURSAR, UNIVERSITY OF UTAH

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

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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)

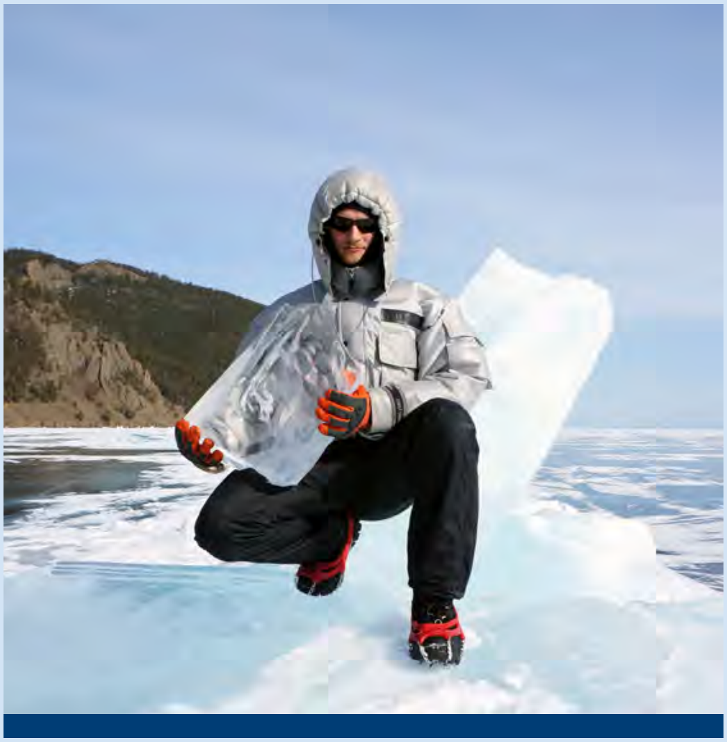
Lev Yampolsky
East Tennessee State University
(NSF 1136706)

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.

HTTPS://BAIKALDIMENSIONS.WORDPRESS.COM

Update

In 2013 Litchman and colleagues embarked on both winter and summer sampling. The summer sampling trip included a circum-Baikal cruise and allowed for successful sampling of the southern, central and north basins of the lake as well as several bays. From these collections, genetic material from 165 single individual cells from four species were isolated and amplified. Temperature and sample depth were the most influential environmental parameters that the team measured in structuring bacterial communities. To communicate their work broadly, the team routinely publishes on their research blog. Through this forum the team offers updates on field surveys, collections and research findings.



^ 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

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Proj. 8 / 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.

< Some populations of *S. habrochaites* have flowers thickly covered in sticky plant hairs (trichomes).
CREDIT: DAVID HAAK

Update

Substantial progress has been made on the comparative transcriptomics analysis portion of this project on 12 species of wild tomatoes (e.g. the study of the RNA and gene expression of these species). Additional achievements have been made in developing and testing bioinformatics tools and platforms to analyze, display and distribute the genomic data. Moyle and colleagues have also been involved in several outreach activities in local schools, using tomato and other Solanaceous species to connect children with the concept of biodiversity and evolution.

Publications

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

< Mahoney Lake, Penticton, BC Canada.
CREDIT: JENNIFER GLASS, ASU

Update

Because less than 1% of known microorganisms can be grown in pure culture, the physiologies and functional relationships of many environmental microbes are poorly understood. Through this Dimensions research, Pearson and colleagues are developing technologies to bridge this gap and they are seeking a more comprehensive understanding of the biological and geochemical dynamics that govern complex microbial communities. In 2014 three new papers were published from their work, and additional manuscripts are in development. Their next steps will be to utilize these new approaches to develop "stable isotope fingerprints" of environmental proteins. These isotope fingerprints can illuminate the trophic structure of microbial communities, while the protein sequences can be used to identify the dominant taxa.

Publications

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

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Robert P. Dunn
North Carolina
State University
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Aaron M. Ellison
Harvard University
(NSF 1136646)

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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

Sanders and colleagues have maintained multi-year ongoing experimental plots at the Harvard and Duke Forests. The team samples the ants monthly to estimate activity density. Additional work on gene expression and comparative physiological trait analysis is underway. Preliminary results suggest a strong variation in temperature response, both within and among species. Overall, this research extends our understanding of how organisms respond to climate, and in particular, has demonstrated links between key physiological traits and the performance and function of keystone species.

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

CREDIT: AARON M. ELLISON

Publications

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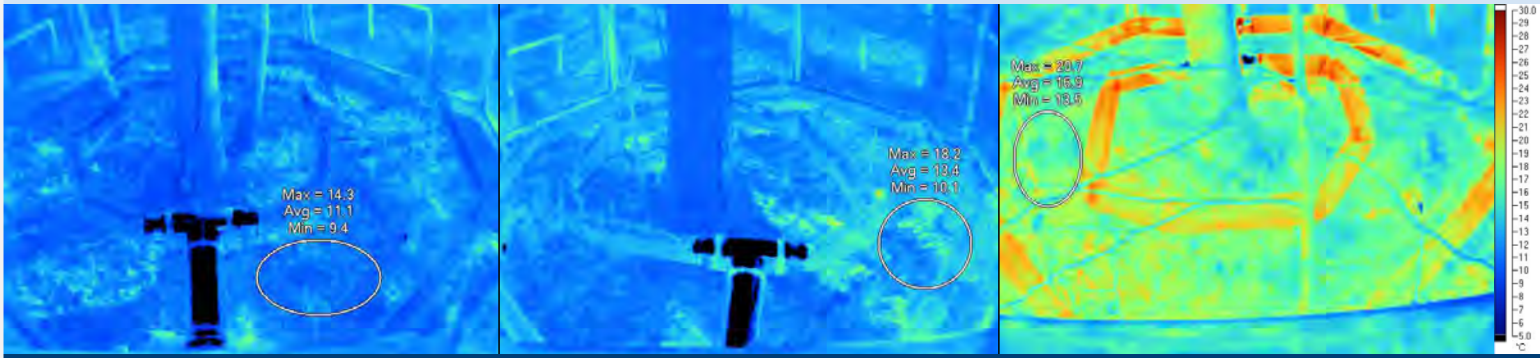

Top: These images illustrate the levels of atmospheric warming achieved in the research chambers.

CREDIT: PAUL J. HANSON

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

CREDIT: AARON M. ELLISON

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

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

Ramunas Stepanauskas
Bigelow Laboratory for Ocean Sciences
(NSF 1136488)

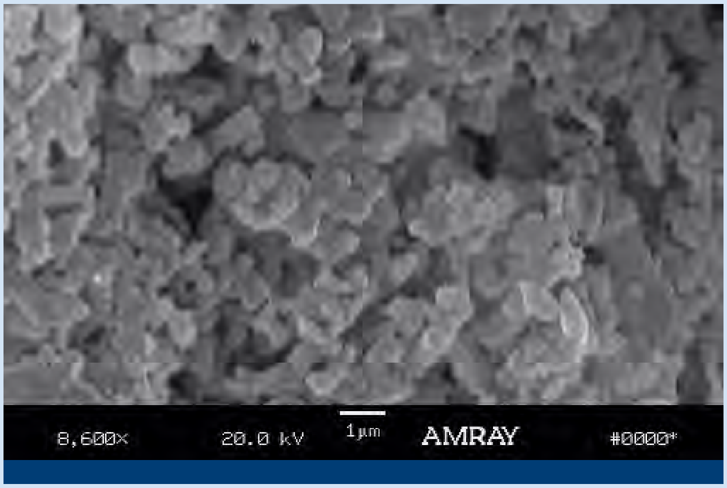
Costantino Vetriani
Rutgers University New Brunswick
(NSF 1136451)

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

HTTP://WWW.DIVEDISCOVER.WHOI.EDU/EXPEDITION15

Update

In January of 2014, several investigators on the research team participated in an oceanographic expedition to the East Pacific Rise on the R/V Atlantis ship. During the expedition, researchers had the opportunity to sample both focused and diffuse flow vents along the submerged thermal vent ridge. Biofilm, fluid and sulfide samples were all collected for further lab work. Among the team's accomplishments, Stepanauskas and colleagues developed a semi-automated computational pipeline for viral sequence detection to help uncover novel viral-host interactions within the new microbial groups being studied. Intriguing preliminary data have resulted from this new computational tool. While the research team investigates a variety of microbial organisms living at these deep sea-vents, several species are of particular interest. By understanding their chemical physiology and metabolism the researchers now have a greater understanding of the link between the carbon and nitrogen cycles at the deep-sea vents. Lastly, through the highly popular "Dive & Discover" website, the research team engages people in their research and in the deep-sea environment. During their cruises, the team provides daily updates and numerous pictures and videos.



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

CREDIT: CONSTANTINO VETRIANI, RUTGERS UNIVERSITY

Publications

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

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This project uses two North Atlantic sites in two seasons to link genetic diversity and species composition of phytoplankton communities to the biogeochemistry of the surface ocean.

Update

Ward and colleagues participated in a second round of ship expeditions in the North Atlantic. The data from the two subarctic North Atlantic cruises will be compared to the data from two 2012 cruises that took place in the Sargasso Sea in the North Atlantic. By developing large-scale phylogenetic analyses of "geogenes," genes that encode enzymes that perform major biogeochemical transformations, the Ward research team will shed light onto which phytoplankton species perform which functions in the ocean environment.

The research team sampling for the Bermuda Atlantic Time-series Study (BATS).

CREDIT: SARAH FAWCETT, PRINCETON UNIVERSITY

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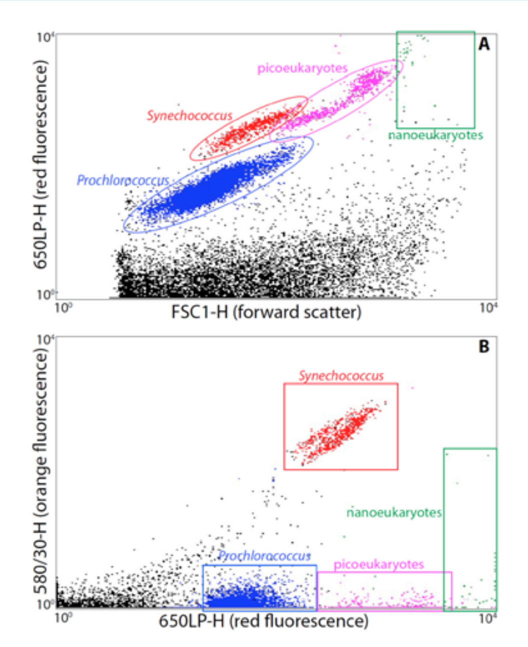
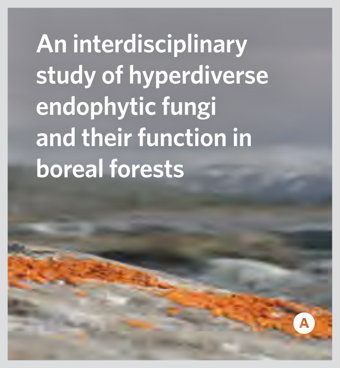


Scattergram of flow cytometry data showing differentiation between different groups of phytoplankton on the basis of size and autofluorescence.

CREDIT: SARAH FAWCETT, PRINCETON UNIVERSITY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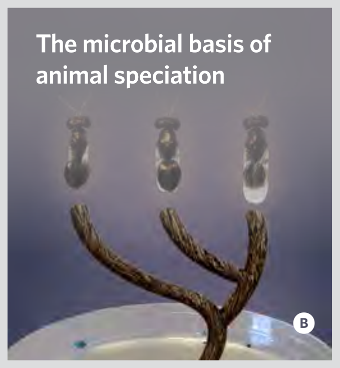
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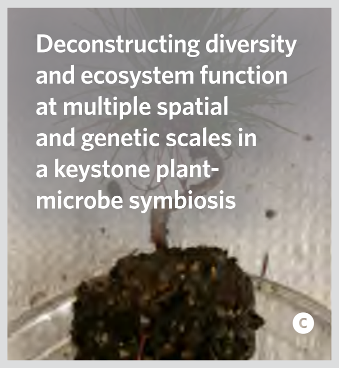
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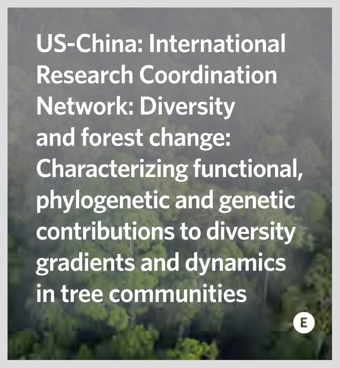
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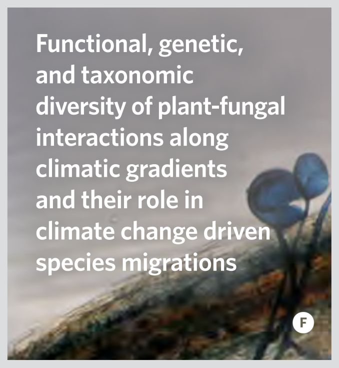
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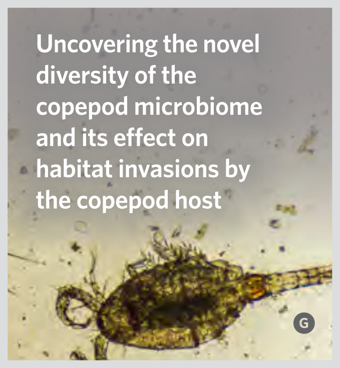
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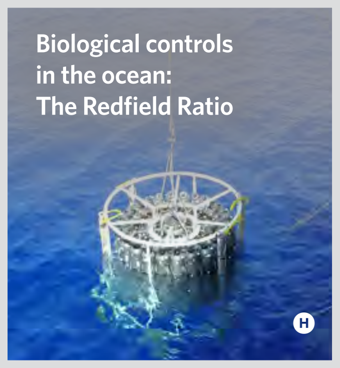
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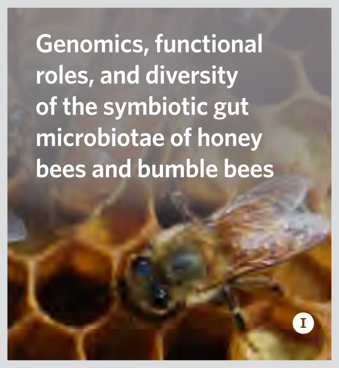
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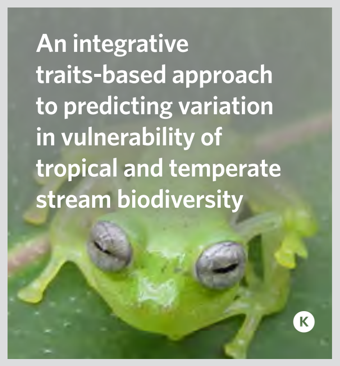
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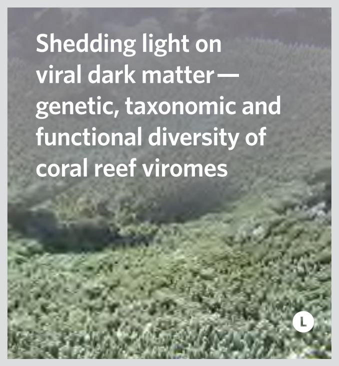
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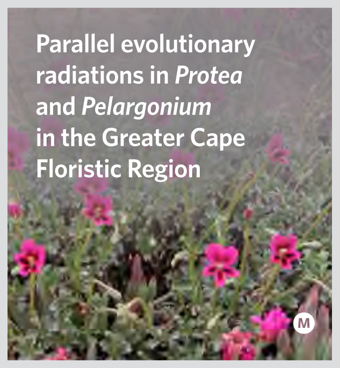

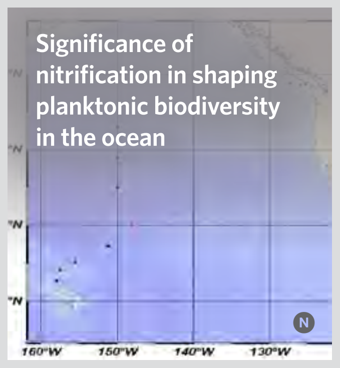

IMAGE CREDIT

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

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

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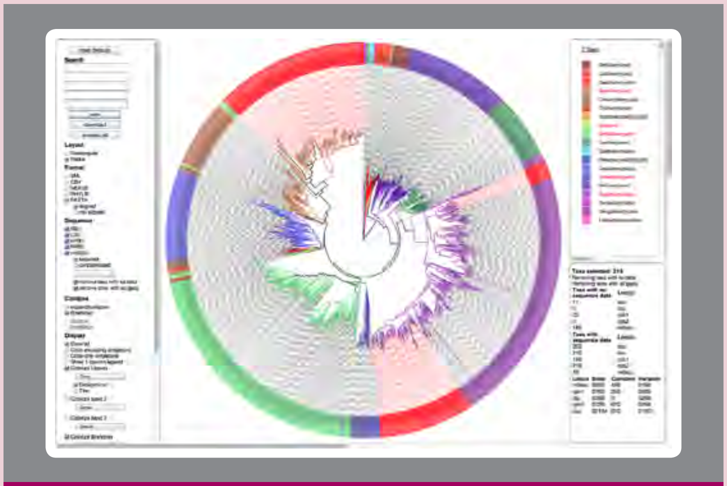
The EnDoBiodiversity project aims to understand the diversity of endophytic fungal symbionts of plants and lichens in threatened boreal systems, and to identify the fundamental processes that generate and maintain that diversity.

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

Update

The EnDoBiodiversity project spans the circumboreal belt, and includes sites in eastern and central Russia, eastern and western Canada, north-central Sweden, central Alaska, and northern Michigan. The team has collected and sequenced more than 15,000 cultures of endophytic and endolichenic fungi and more than 23,000 host tissue segments have been processed for high-throughput metagenomic analyses. A novel tool developed through this project, the Tree-Based Alignment Selector (T-BAS), is now enabling the synthesis of ecological, genomic, phenotypic, and phylogenetic information. In addition, through this Dimensions award, the research team has hosted semester-long workshops on fungal biology and involved over 200 high school students in research. Some of these students have even received state and national recognition for high school research activities.



Top: Tree-Based Alignment Selector (T-BAS): the online tool for selecting single and multi-locus DNA sequence alignments within a phylogenetic tree.

CREDIT: JAMES B. WHITE AND IGNAZIO CARBONE, DEPARTMENT OF PLANT PATHOLOGY, NORTH CAROLINA STATE UNIVERSITY

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

CREDIT: A. ELIZABETH ARNOLD, UNIVERSITY OF ARIZONA

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The microbial basis of animal speciation

Seth Bordenstein
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(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.

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

CREDIT: ROBERT BRUCKER AND SETH BORDENSTEIN, VANDERBILT UNIVERSITY

Update

Animals and their microbial communities can either coassemble in a random fashion without consistent relationships or they can coassemble according to "phylosymbiosis." In phylosymbiotic assemblages, the relationships of the microbiota correspond with the ancestry of the animal host species. The research team this year expanded their discovery of phylosymbiosis in *Nasonia* to include diverse animal-microbe systems spanning invertebrates to vertebrates. Bordenstein and colleagues also continued their microbial diversity analyses to support the hologenome theory of evolution. This theory proposes that the object of natural selection is not only the host organism, but also includes the host's organelles and associated microbiota. The research team has established RNAi technology in the lab and has evaluated the fitness effects of interspecific gut microbiota transplants within and between related species. The 2013 Funkhouser et al. publication in *PLoS Biology* has contributed significantly to the understanding of maternal microbial transmission in animals and has even had implications for the previously accepted "sterile womb" theory in humans. The results of this research have been highlighted in several international media outlets, including the *New York Times*, *Discover Magazine*, PBS.org, BBC Radio and NPR's "Living on Earth."

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

CREDIT: ROBERT BRUCKER AND SETH BORDENSTEIN, VANDERBILT UNIVERSITY

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

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Kabir G. Peay
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(NSF 1249341)

Rytas Vilgalys
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(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.

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

Update

Bruns and colleagues have made a great deal of progress towards their goals. Last summer the team completed their field sampling and is in the process of completing sample processing and analysis. The team has also begun to develop protocols for high throughput metagenomics that can be used as an additional method for examining the functional diversity of the microbial communities. Research findings are indicating that fungal communities in pine forests across North America are highly diverse: > 10,000 species total and >2,000 species of ectomycorrhizal fungi. Additionally, findings suggest that these communities largely mirror the structure of the North American continent and that few taxa are shared between regions. The functional role of fungi in these forests, however, appears to be driven by environmental conditions and there is strong convergence across geographic regions.

Top: Plant and fungal tissue intermingle in roots to form a new absorptive organ — the mycorrhiza. In ectomycorrhizas, fungal tissue encases the plant roots and nutrients are absorbed by hyphal filaments that forage the soil. *Bottom:* Many of the fungi involved in ectomycorrhizal symbiosis produce conspicuous fruiting bodies, commonly known as mushrooms.

CREDIT: KABIR G. PEAY

Publications

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

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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 influences species coexistence and primary production in freshwater.

Update

Through the research funded by this Dimensions of Biodiversity award, Cardinale and colleagues have found evidence that debunks a common myth in biology. Darwin argued that closely related species are more ecologically similar than distant relatives and, as such, they should be more strongly influenced by competition than distantly related species that are more ecologically unique. Research from this team has illustrated that this hypothesis does not hold generally true across organisms, and therefore challenges a highly influential hypothesis in biology. This work not only has impacts across the disciplines of ecology, phylogenetics and genomics, but may also influence conservation decision makers in developing priorities for species conservation.

Top: Water droplets suspended on chemostat lids.
Bottom: Undergraduate research assistants sampling algae from lab experiment.
CREDIT: BRADLEY CARDINALE

Publications

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Undergraduate research assistant maintains chemostats.
CREDIT: BRADLEY CARDINALE

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Proj. 5 / 16

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

(CO-FUNDED WITH NSFC)

US TEAM	**Stuart Davies** Smithsonian Institution (NSF 1354741) **W. John Kress** Smithsonian National Museum of Natural History (NSF 1354741)	**Rick Condit** Center for Tropical Forest Science, Smithsonian Research Institute (STRI) (NSF 1354741)	**Nathan G. Swenson** Michigan State University (NSF 1354741) **Helene Muller-Landau** STRI (NSF 1354741)
CHINA TEAM	**Zhanqing Hao** Institute of Applied Ecology, Chinese Academy of Sciences (CAS) **Kaping Ma** Institute of Botany, CAS	**Wanhui Ye** South China Botanical Garden, CAS **Min Cao** **Jie Li** Xishuangbanna Tropical Botanical Garden, CAS	**Xiangcheng Mi** Institute of Botany, CAS **Xugao Wang** Institute of Applied Ecology, CAS

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

Research plot at Yasuni, Ecuador.
CREDIT: STUART DAVIES

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

Update

In the summer of 2014 the IRCN hosted its fourth workshop. This year it took place in Xishuangbanna Tropical Botanic Garden in Yunnan China. Over 55 scientists, representing 17 countries, participated in the workshop. The workshop was extremely successful in bringing together the research teams and facilitating data analysis from the species level to global scale evaluations. Furthermore, this research team has been extremely prolific in the last year, producing dozens of publications in biodiversity science. The team is preparing for its fifth workshop, slated to take place at the Smithsonian Tropical Research Institute in Panama.

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^ Research plot at Changbaishan, China.

CREDIT: STUART DAVIES

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Canopy of the plot at Lambir, Malaysia.

CREDIT: CHRISTIAN ZIEGLER

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^ *Top:* Temperate Forest at CTFS plot in Changbaishan, China.

CREDIT: STUART DAVIES

Bottom: Understory in the plot at Wabikon Lake Forest, USA.

CREDIT: ROBERT HOWE AND AMY WOLF

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

In 2014, Lankau and colleagues completed two major greenhouse experiments. They made significant strides in understanding patterns of fungal community composition as well as uncovering relationships between plant growth with microbial communities and soils. In addition, they have nearly finalized the sampling and storage protocols for a new citizen science endeavor.

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

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: freshwater.

Update

Major sequencing efforts are underway by the research team. Analysis of copepod genomes from numerous freshwater and saline populations as well as genetic analysis of their associated microbes has already yielded interesting preliminary results. The team has found that the copepod gut harbors high concentrations of bacteria. Furthermore, these bacteria are highly distinct from the surrounding water, suggesting these microbes may have a specialized metabolic function in the copepod gut. These same species of microbes, in insect guts, produce antibiotics or nutrients for their hosts. Their specific functional role in the copepod gut is still unknown. Within the next year, the research team plans to complete sample collections. Considering that copepods constitute the largest animal biomass in the world's oceans, understanding the function of their microbiome could significantly impact our understanding of global biogeochemical cycles.

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

CREDIT: ISTOCK

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Biological controls in the ocean: The Redfield Ratio

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(NSF 1046297)

Michael Lomas
Bigelow Laboratory for
Ocean Sciences
(NSF 1303287)

Benjamin Van Mooy
Woods Hole
Oceanographic
Institution
(NSF 1045966)

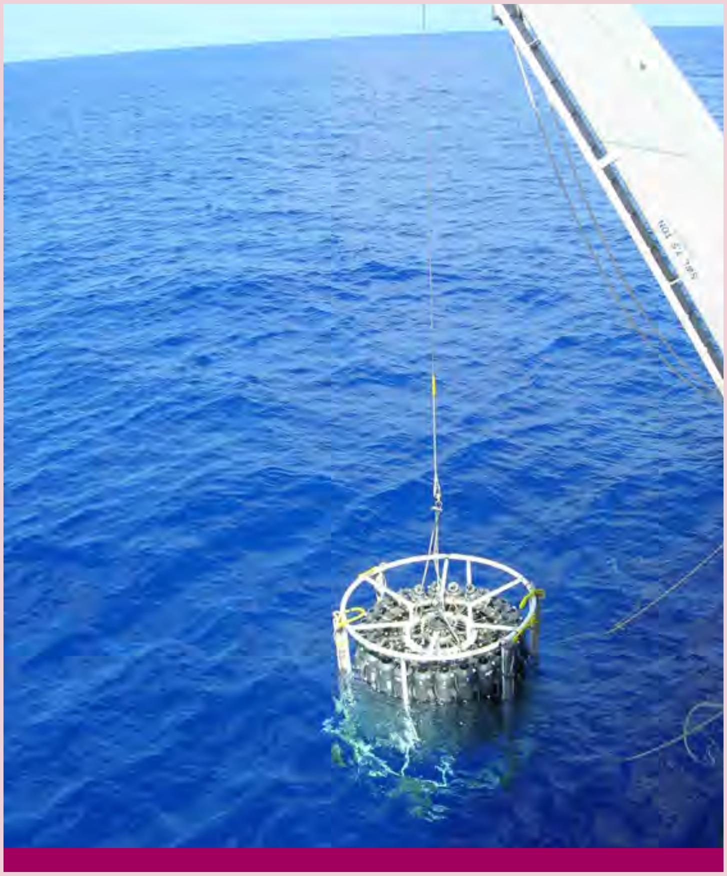
Simon Levin
Princeton University
(NSF 1046001)

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.

Update

This research team has achieved major accomplishments in the last year. Several members of the research team participated in a fruitful sampling cruise from Maine to Bermuda, the Levin lab made significant advancements in their ocean nutrient modeling endeavors, and several of the team's research articles were published. On the genetics side of the project, the Zhang lab received noteworthy accolades upon the completion of their novel single cell genome sequencing technique. This technology was featured on the cover of the journal Nature Methods and was identified as the 2013 "Method of the Year."



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

CREDIT: ADAM MARTINY, UNIVERSITY OF CALIFORNIA, IRVINE

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

CREDIT: CELINE MOUGINOT, UNIVERSITY OF CALIFORNIA, IRVINE

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

Nancy Moran
University of Texas
Austin
(NSF 1415604)

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

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

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

Update

The Moran and Evans research team have had a productive year of research. Through their Dimensions award, this team has identified three novel species of bacteria, two of which are in an entirely new taxonomic order of Gammaproteobacteria. The genomes of these newly described species have been fully sequenced and deposited into GenBank. During this year, the team has also investigated the functional role of these microbes. They have found associations between species composition of bacteria in the gut and the presence or absence of a trypanosome parasite, suggesting that these bacteria may act in defense against harmful pathogens. Many of the technological methods that have been developed by this research team, have been compiled and submitted as a chapter in an open access "Bee Book" soon to be available by the International Bee Research Association. Furthermore, this team's important work has been featured in Livescience.com and *Science Magazine*. By describing the diversity, metabolic and functional roles of the bee microbiome, these findings are not only impacting the understanding of microbial-host symbiosis, but they will likely have practical applications in the management of bee health.

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

CREDIT: WALDAN KWONG, YALE UNIVERSITY

^ *Bombus impatiens* individual foraging on flowers.

CREDIT: NANCY MORAN, UNIVERSITY OF TEXAS, AUSTIN

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

CREDIT: JAY EVANS, USDA

Dimensions of Biodiversity Distributed Graduate Seminar

Julia Parrish
University of Washington
(NSF 1050680)

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

HTTP://WWW.BIODIVERSEPERSPECTIVES.COM

Update

While the Distributed Graduate Seminar (DGS) course has come to an end, the catalytic activities initiated through the Dimensions DGS have continued on fervently. Students from the Dimensions DGS have continued their analysis and synthesis of large datasets and they continue to spearhead the publication of peer-reviewed articles. The student initiated *BioDiverse Perspectives* blog has maintained a strong following and readership. Media outlets have even highlighted popular posts from the blog. The blog has served as an important platform of student networking both within and beyond the original DGS student body, and in fact, the current editorial board is composed of several students who were not originally in the DGS. With contributions from over 53 authors, representing 23 Universities on 5 continents, this blog is facilitating a gathering place and communication forum for the next generation of biodiversity scientists.

Publications

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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

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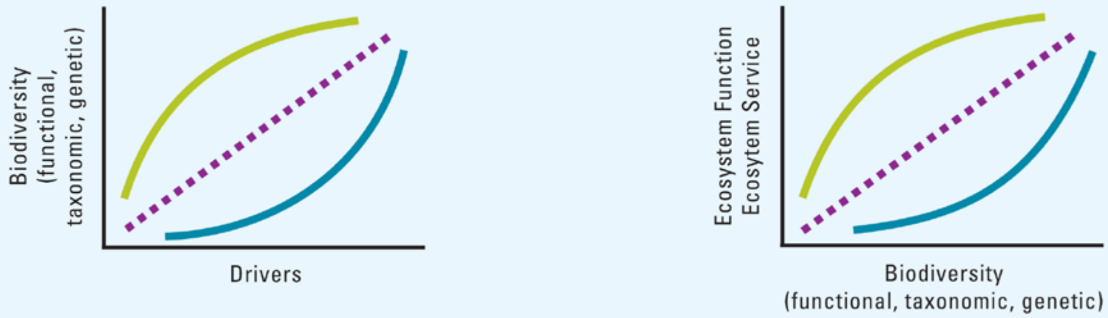

Top: DBDGS participating university teams.
Bottom: DBDGS teams addressed one of two broad framing questions: 1) What forces create/maintain biodiversity pattern, and 2) What patterns of system function, service, or even associated human well-being does biodiversity drive?
CREDIT: CATHY SCHWARTZ

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

LeRoy N. 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.

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

Update

In the last year, the EVOTRAC research team (Evolutionary and Ecological Variability in Organismal Trait Response with Altitude and Climate) has achieved significant milestones for the project. Collection efforts in Ecuador and Colorado have been completed and the morphologic and genetic identification of the samples is well underway. The team has finished the DNA bar coding for insect samples and within the upcoming year, aims to finish genetic analysis of the fish and frog samples as well. Substantial progress has been made to advance the experimental physiology and ecosystem characterization studies and the teams have completed optimizing the genomic lab protocols and the bioinformatics analysis. Both genetic data and physical collections from this study are being deposited in freely accessible repositories. This substantial research effort will serve as an important reference for future studies of anthropogenic change.

Publications

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Top: The Papallacta drainage on the eastern flank of the Ecuadorian Andes. *Bottom:* Two students sample aquatic insects in a Colorado stream.
CREDIT: KELLY ZAMUDIO, CORNELL UNIVERSITY

Rio Santa Maria, in the Oyacachi Basin, Ecuador, is one of the streams sampled by EVOTRAC.
CREDIT: KELLY ZAMUDIO, CORNELL UNIVERSITY

Students on their way to sample aquatic insects in streams in the Colorado Front Range for the ECOTRAC project.
CREDIT: KELLY ZAMUDIO, CORNELL UNIVERSITY

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> Aquatic insects sampled from one of the focal EVOTRAC streams in Colorado.
CREDIT: KELLY ZAMUDIO, CORNELL UNIVERSITY

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 human impacts gradient at both regional and global scales.

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

Update

"Life in Our Phage World", a book describing viral genetic, taxonomical and function diversity has been completed as part of this project. It is anticipated that the book will be published in January of 2015. This is a first of its kind publication and includes a number of innovations resulting from this Dimensions project. The Viral Dark Matter research team has also developed multiple laboratory and computational tools that will be used by the scientific community far beyond the lifetime of this project. It is anticipated that the methods being developed by Rowher and colleagues will impact computational, ecological, and biomedical related disciplines.

^ *Acropora* corals.
CREDIT: FOREST ROHWER, SAN DIEGO STATE UNIVERSITY

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

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

Update

In 2013 the research team completed nearly all of their field sampling for both *Protea* and *Pelargonium* species. Many of the samples collected from the *Pelargonium* populations are likely species that have not yet been described and the research team is in collaboration with South Africa's premier *Pelargonium* specialist to complete their species identification. This team continues to develop a database of *Pelargonium* field collections that will incorporate their own extensive field records with herbarium data from across South Africa. The team currently has over 19,000 records, and aims to make the database available online for herbaria and other research teams.

Top: *Pelargonium peltatum.*
Bottom: *Pelargonium sericifolium.*

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

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Significance of nitrification in shaping planktonic biodiversity in the ocean

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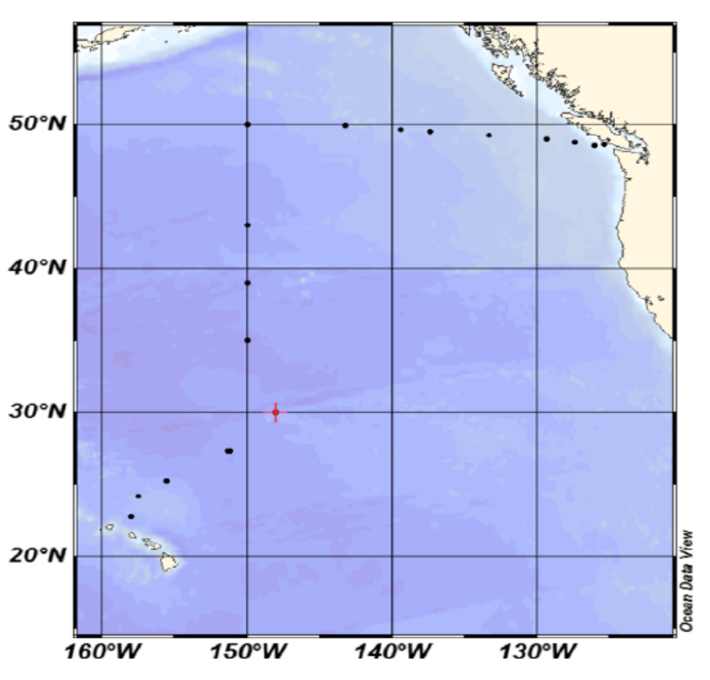
The Stahl research team examines the diversity and function of ammonia oxidizing Archaea (AOA) in the ocean and they are determining the role of these newly discovered organisms in structuring the diversity of phytoplankton.

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

Amin, S.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.

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Scanning electron micrograph of *Nitrosopumilus maritimus*, the first marine ammonia oxidizing archaeon isolated in pure culture. Scale bar = 1 µm.

CREDIT: DAVID A. STAHL, UNIVERSITY OF WASHINGTON

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The role of viruses in structuring biodiversity in methanotrophic marine ecosystems

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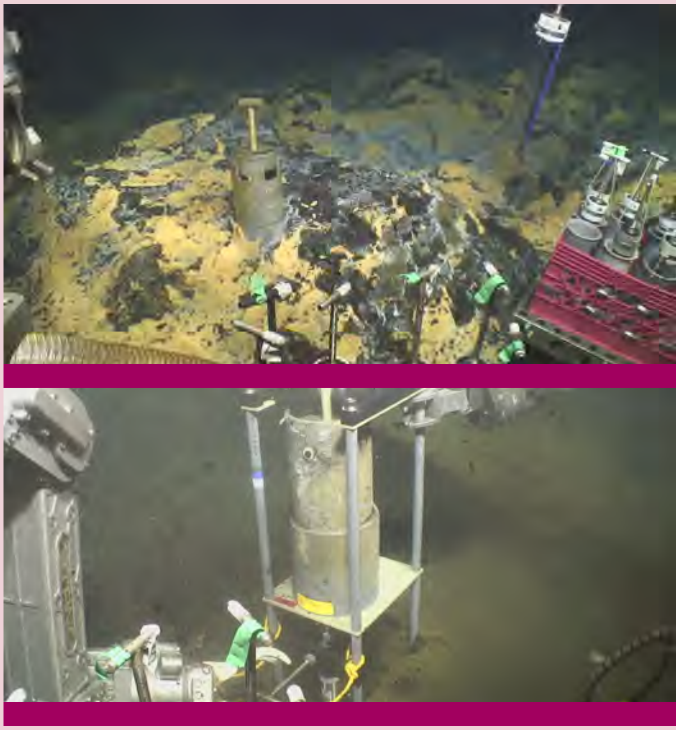
Microbes in ocean sediments form a unique ecosystem. There, methane is consumed, preventing large amounts of this potent greenhouse gas from entering the atmosphere. This research is shedding light on a dark corner of the biosphere, and could identify new and novel genes that support life in these environments.

Update

Valentine and colleagues have already made strides in enabling new techniques to visualize sea floor methane seep environments in three dimensions. Major efforts have been 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. The team has 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.

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

CREDIT: DAVID VALENTINE, UCSB



Top: An incubator as first seen on the return to a second study site in 2013, showing substantial growth of microbial mats on the outer surfaces.
Bottom: Preparing to inject tracer into a sealed incubator after the two-year colonization period.

CREDIT: DAVID VALENTINE, UCSB

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

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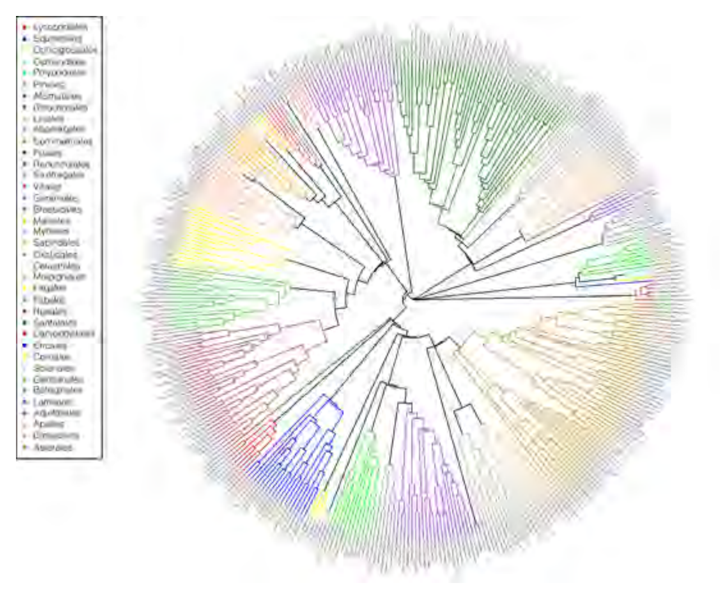
Waller and colleagues are examining the functional traits, phylogenetic relationships, geographic distributions, and patterns of genetic variation in native and introduced plants in Wisconsin forests and grasslands. Their goal is to identify how climate change, habitat fragmentation, invasive species,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

Tragopogon sp, a typical example of a wind-dispersed species.
CREDIT: GREGORY SONNIER, BOTANY DEPARTMENT, UNIVERSITY OF WISCONSIN-MADISON

HTTP://BOTANY.WISC.EDU/DOB

Update

The Wisconsin Dimensions team has made significant strides in the past year and the datasets that they are assembling are expected to have a major impact on the fields of plant ecology and evolutionary biology. The team's comprehensive longitudinal data spans nearly 5 decades. It will serve as a historical perspective on the ecology of plant communities in the U.S. and will be used as a platform for predicting how these relationships will change and shift in the coming years. Furthermore, in conjunction with engineers from the biotechnology company, Promega, the research team has developed a new protocol and kit for extracting large fragment genomic DNA from a wide diversity of plant species.



Evolutionary relationships among all species in the Wisconsin flora have been reconstructed using genetic data. This community phylogeny, here color coded by orders of flowering plants, will be used to study patterns of functional trait evolution, phylogenetic diversity across the landscape, and other dimensions of biodiversity.
CREDIT: KEN CAMERON, KENNETH SYTSMA AND RICARDO KRIEBEL, DEPARTMENT OF BOTANY, UW-MADISON

Publications

Amatangelo, K.L., et al. "Trait-environment relationships remain strong despite 50 years of trait compositional change in temperate forests." *Ecology* 95.7 (2014): 1780-1791.

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Dimensions of Biodiversity

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