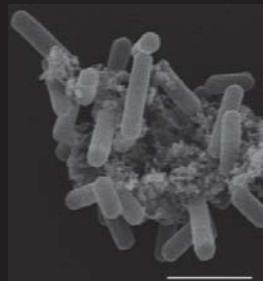




Dimensions of Biodiversity



National Science Foundation Fiscal Year 2010 – 2011 Projects

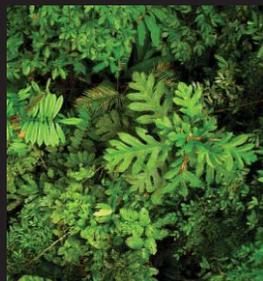
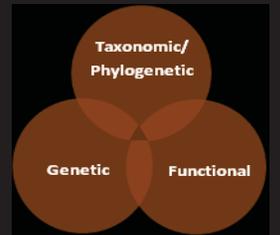


Table of Contents

<i>Introduction</i>	i
<i>Fiscal Year 2011 Projects</i>	1
<i>Fiscal Year 2010 Projects</i> [Abstracts updated: Fall 2011]	27

Acknowledgements

Many NSF staff members, too numerous to mention individually, assisted in the development and implementation of the Dimensions of Biodiversity competitions that resulted in the projects described herein. The Dimensions of Biodiversity investigators are thanked and congratulated for their creativity and achievements in the research and coordination activities that these exciting projects represent. Finally, we are grateful to Dr. Sean M. Watts and Dr. Sara Chun, AAAS Science and Technology Policy Fellows, who were most helpful in strategic planning for Dimensions of Biodiversity, and the production of this abstract book.

Introduction

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

The National Science Foundation (NSF) is now in the third year of the 10-year Dimensions of Biodiversity program to characterize the least-well-known aspects of the diversity of life on Earth. NSF funded 11 new projects in FY 2011 (including a second International Research Coordination Network award), bringing the total number of active projects to 27.

Identifying species is just a first step in the journey of assessing the planet's biological diversity, but for many organisms even this step is far from complete. For example, insects are among the most diverse organisms and the total number of named, living insect species is estimated at 720,000. However, this represents as little as 7% of our 'best guesses' of insect diversity (4-10 million species)¹. Furthermore, all species rely on a vast network of mostly invisible and largely unknown life forms (bacteria, fungi, etc.), that far outnumber the more obvious organisms on the planet in both abundance and diversity.

Beyond taxonomy, the genetic diversity within even a single species can be vast. The tremendous variation among domestic dog breeds illustrates this, and the genetic diversity within crop plants continues to play a critical role in agriculture. Finally, species and genetic diversity are best understood in a phylogenetic context that reflects the interaction networks, past and present, that have shaped the functional dimension, including but not limited to ecological, physiological, behavioral, cellular, and even molecular patterns and processes. Despite centuries of study, we still have much to learn about the origin and maintenance of diversity.

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

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

Addressing the substantial knowledge gaps in our understanding of biodiversity will require new thinking and a coordinated effort among several sub-disciplines of biology. An important distinction of the Dimensions initiative 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 is partnering with NASA to fund projects that use remote sensing

technologies to expand biodiversity investigations across broad spatial and temporal scales. International partnerships with the Chinese National Natural Science Foundation (NSFC) and two Brazilian funding agencies [Federal Agency for Support and Evaluation of Graduate Education of the Federative Republic of Brazil (CAPES) and the São Paulo Research Foundation (FAPESP)] will support the exchange of students and scientists, joint research projects, university partnerships and the digitization of biological collections.

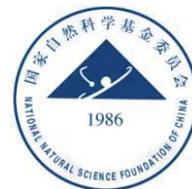
Dimensions is also using a Distributed Graduate Seminar to baseline what is currently known about the genetic, taxonomic/phylogenetic, and functional dimensions of biodiversity. This baseline assessment will be posted on a wiki, crowd-sourced regularly by the broader scientific community, and “frozen” periodically to allow assessment of progress.

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

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

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 will redefine the way we understand the evolutionary and ecological significance of biodiversity in today’s changing environment, and in the geologic past.

¹ Finlay, BJ, JA Thomas, GC McGavin, T Fenchel and RT Clarke. 2006. Self-similar patterns of nature: Insect diversity at local to global scales. *Proceedings of the Royal Society B*. **273**: 1935-1941.



Fiscal Year 2011 Projects

Diversity and symbiosis: Examining the taxonomic, genetic, and functional diversity of amphibian skin microbiota **4**

Lisa K. Belden, Leanna L. House, and Roderick Jensen, Virginia Polytechnic Institute and State University (NSF 1136640); Reid N. Harris, James Madison University (NSF 1136602); Kevin P. Minbiole, Villanova University (NSF 1136662)

This project will investigate 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.

Integrating genetic, taxonomic, and functional diversity of tetrapods across the Americas and through extinction risk **6**

Thomas Brooks, Gabriel C. Costa, and Bruce Young, NatureServe (NSF 1136586); Catherine Graham, State University of New York, Stony Brook (NSF 1136705); Stephen B. Hedges, Pennsylvania State University, University Park (NSF 1136590); Volker C. Radeloff, University of Wisconsin, Madison (NSF 1136592)

Brooks and colleagues will use 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.

Pattern and process in marine bacterial, archaeal, and protistan biodiversity, and effects of human impacts **8**

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

Fuhrman and colleagues will 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.

Coexistence, herbivore host choice, and plant-herbivore evolution in the recently radiated and speciose Neotropical tree genus, Inga **10**

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

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

Lake Baikal responses to global change: The role of genetic, functional and taxonomic diversity in the plankton **12**

Elena G. Litchman and Christopher A. Klausmeier, Michigan State University (NSF 1136710); Stephanie E. Hampton, University of California, Santa Barbara (NSF 1136637); Marianne Moore, Wellesley College (NSF 1136657); Edward C. Theriot, University of Texas, Austin (NSF 1136667); Lev Yampolsky, East Tennessee State University (NSF 1136706)

This project will study 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.

Integrating dimensions of Solanum biodiversity: Leveraging comparative and experimental transcriptomics to understand functional responses to environmental change **14**

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

This research will highlight 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.

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

16

Ann Pearson and Peter Girguis, Harvard University (NSF 1136484); Jennifer Macalady, Pennsylvania State University, University Park (NSF 1136218)

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

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

18

Nathan J. Sanders, University of Tennessee, Knoxville (NSF 1136703); Robert P. Dunn, North Carolina State University (NSF 1136717); Aaron M. Ellison, Harvard University (NSF 1136646); Nicholas J. Gotelli, Bryan A. Ballif, and Sara I. Cahan, University of Vermont and State Agricultural College (NSF 1136644)

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

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

20

Stefan M. Sievert, Jeffrey S. Seewald, and Craig D. Taylor, Woods Hole Oceanographic Institution (NSF 1136727); Dionysios I. Foustoukos, Carnegie Institution of Washington (NSF 1136608); Ramunas Stepanauskas, Bigelow Laboratory for Ocean Sciences (NSF 1136488); Costantino Vetriani, Rutgers University, New Brunswick (NSF 1136451)

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

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

22

Bess B. Ward and Daniel M. Sigman, Princeton University (NSF 1136345); Andrew E. Allen, J. Craig Venter Institute, Inc. (NSF 1136477)

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

INTERNATIONAL RESEARCH COORDINATION NETWORK AWARD

IRCN: A research coordination network for biodiversity of ciliates

24

PI: John Clamp, North Carolina Central University (NSF 1136580)

Steering Committee:

US MEMBERS: John Clamp; Laura Katz, Smith College; Chris Lobban, University of Guam; Micah Dunthorn, University of Kaiserslautern, Germany

CHINA MEMBERS: Weibo Song, Ocean University of China, Qingdao; Xiaofeng Lin, South China Normal University, Guangzhou.

OTHER COUNTRIES: Alan Warren, Natural History Museum, London, United Kingdom; Laura Utz, Pontifícia Universidade Católica do Rio Grande do Sul, Brazil

This project, jointly supported by the National Natural Science Foundation of China, will establish an International Research Coordination Network for Biodiversity of Ciliates. The network will include researchers from the US, China, the UK, and Brazil and will broaden exploration of these important protists.

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

Lisa K. Belden, Leanna L. House, and Roderick Jensen, Virginia Polytechnic Institute and State University (NSF 1136640); Reid N. Harris, James Madison University (NSF 1136602); Kevin P. Minbiole, Villanova University (NSF 1136662)

All animals host internal and external symbiotic microbes; most cause no harm and many are beneficial. This project will investigate 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.

In humans, symbiotic microbes outnumber human cells ten to one. Most of these microbial symbionts are not harmful and many species are beneficial. The composition of these microbial communities can influence the likelihood that pathogens are able to successfully establish themselves in the body, how quickly toxins are metabolized and even whether individuals are lean or obese. Amphibians also possess a diverse symbiotic microbiota. Recent research suggests that the bacterial symbionts on the skin of amphibians may limit infection by pathogens, such as the chytrid fungus *Batrachochytrium dendrobatidis* that has decimated many natural amphibian populations around the globe.

But how do these diverse microbial communities of vertebrates achieve beneficial functions? Can microbial communities of varying species composition perform the same disease resistance function or is the presence of specific mutualists critical in disease resistance? Does the presence of a virulent pathogen like the chytrid fungus drive selection of the bacterial symbiont community based on critical functions, such as the ability to produce anti-fungal metabolites? This research project will address these questions by examining links between three critical diversity components of the symbiotic microbial communities that reside on amphibian skin: taxonomic diversity (number and relative abundance of species), genetic

diversity (which microbial genes are activated), and functional diversity (disease resistance).

Using focused field surveys and manipulative experiments, three objectives will be addressed: (1) establish the range of taxonomic, genetic, and functional diversity within the microbial community on five amphibian host species in Panama, (2) examine how the presence of the fungal pathogen *Batrachochytrium* impacts diversity components, and (3) examine the relationship between microbial diversity and resistance to disease. As all animals host symbiotic microbes, these results will have broad applicability to other systems, including humans. In addition, new statistical methods for these complex datasets will be developed, which will rapidly expand the ability to integrate these diversity components in a wide array of systems. A partnership with the Panama Amphibian Rescue and Conservation Project (PARC) will also be established. A PARC intern will be supported to work with school groups to stress the importance of conservation, beneficial microbes, and biodiversity. The partnership with PARC will extend to working with them on novel probiotic solutions, based on antifungal skin bacteria, that will allow successful reintroductions of threatened frogs, such as the Panamanian golden frog, thereby helping to restore biodiversity to the Neotropics.



Brian Gratwicke, Smithsonian Conservation Biology Institute



Jenifer Walke, Virginia Tech

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

Left: The bacterial species *Lysobacter gummosus* (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.

Below: Panamanian frogs will be studied in rainforest habitats such as this that vary in exposure to *Batrachochytrium dendrobatidis*.



B. Gratwicke

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

Thomas Brooks, Gabriel C. Costa, and Bruce Young, NatureServe (NSF 1136586); Catherine Graham, State University of New York, Stony Brook (NSF 1136705); Stephen B. Hedges, Pennsylvania State University, University Park (NSF 1136590); Volker C. Radeloff, University of Wisconsin, Madison (NSF 1136592)

Most large-scale efforts to assess biodiversity have focused on genetic, taxonomic, and functional dimensions individually; it is currently unknown how these dimensions relate to each other over space. Brooks and colleagues will use 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.

This project will examine continent-wide variation in the dimensions of biodiversity. New data will be collected on the biodiversity and extinction risk of 2,500 Western Hemisphere reptile species. These data will be combined with existing data for mammals, birds, and amphibians to measure and map the diversity of all 13,000 terrestrial vertebrate species of the Americas, in three dimensions. The first is phylo-temporal diversity, measuring the genetic distinctiveness of the species in an area. The second is compositional diversity, measuring which species occur in an area. And the third is trait diversity, measuring how the species in an area vary in place, food, time, and size niches. For each of the three dimensions, measures will reflect differences over space (dissimilarity). All data will be published in open access databases.

The research is important scientifically because it will be a novel, hemisphere-wide analysis of the genetic, taxonomic, and functional diversity of a major species group. This will allow determination of relationships

among the three dimensions of biodiversity, and, by using the extinction risk data, prediction of impending changes in these relationships. Understanding how these dimensions covary will improve the efficiency and effectiveness of conservation actions.

The PI institutions comprise four universities and the non-governmental organization NatureServe. The latter will provide a channel for incorporation of results into conservation decisions, as well as real-world exposure to the two postdoctoral associates, three graduate and approximately 40 undergraduate students, that will be involved in the project.



Geoffrey A. Hammerson



G.A. Hammerson



G.A. Hammerson

Above left: *Gambelia wislizenii*, long-nosed leopard lizard (USA: Colorado)

Above center: *Crotaphytus collaris*, Eastern collared lizard (USA: Colorado)

Above right: *Aspidoscelis sexlineata*, six-lined racerunner (USA: Colorado)

Below left: *Rhinocheilus lecontei*, long-nosed snake (USA: Colorado)

Below right: *Opheodrys vernalis*, smooth greensnake (USA: Colorado)



G.A. Hammerson



G.A. Hammerson

Below left: *Agkistrodon contortrix*, copperhead neonate (USA: Connecticut)

Below center: *Amblyrhynchus cristatus*, marine iguana (Ecuador: Galapagos Islands)

Below right: *Sphaerodactylus copei*, Haitian big-scaled sphaero (Haiti)



G.A. Hammerson



G.A. Hammerson



S. Blair Hedges, Penn State University

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

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

Fuhrman and colleagues will 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.

Bacteria, Archaea, and Protista dominate global elemental cycling and are immensely diverse genetically, taxonomically, and functionally. Yet the extent of marine microbial diversity, its patterns and relationships are very poorly characterized, even though the ocean covers 70% of the planet's surface. Among the least well known variables is the effect of human impacts on native marine microbial systems, although it is recognized that disturbed systems are more prone to events like harmful algal blooms. Knowledge of these relationships and impacts are necessary to anticipate the responses of biota to global changes and feedback mechanisms that may alter the extents, rates, and even pathways of such changes. This project expands upon an existing NSF-funded 10+-year monthly ocean time series (Microbial Observatory) to include quarterly sampling adjacent to the disturbed LA Harbor region and the barely-disturbed Santa Catalina Island coast. The investigators will measure, 1) Genetic diversity: high throughput DNA sequences of "housekeeping" and functional genes; 2) Taxonomic diversity: high throughput tag sequences of small subunit ribosomal RNA genes, flow cytometry, automated image analysis; 3) Functional Diversity: a) Functional measurements (carbon fixation and respiration rates, microbial growth and grazing rates, cell size, morphology, and biomass variations), b) distribution and expression of target functional genes relevant to carbon, nitrogen, and sulfur cycles, c) evaluation of whole-community RNA to explore

unanticipated functionalities; 4) Integration will include: Multivariate statistical and network approaches including newly developed techniques (e.g. Bayesian networks to examine cause-effect relationships), and high speed computational approaches to assess the relationships among the genetic, taxonomic, and functional aspects of biodiversity observed. The researchers will also examine the data for signatures and specific effects (on organism identity and functions) associated with the disturbed site vs. the relatively pristine one.

This project offers an unprecedented and potentially transformative opportunity to combine and integrate measurements of genetic, taxonomic, and functional diversity along with direct measurements of system function in a well-studied marine system that includes a gradient from one of the world's busiest harbors to a largely pristine ocean habitat. Far beyond just describing the distributions of organisms and functions (itself a necessary first step), this project will specifically link spatial and temporal variations in a variety of functions with variations in genetic and taxonomic community composition.

The project will involve doctoral training of participants as well as a direct connection to K-12 education *via* the Centers for Ocean Sciences Education Excellence (COSEE) teacher training program at USC. Outreach will include an interactive website and direct interaction with the public at the Wrigley Marine Science Center.



Jed Fuhrman, University of Southern California



J. Fuhrman

Above left: Sampling for the San Pedro Ocean Time Series and the USC Microbial Observatory

Above right: Sampling from a small boat near Catalina Island

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



Below: Looking out to sea in the general direction of the USC Microbial Observatory from Catalina Island, near the USC Wrigley Marine Science Center

J. Fuhrman



J. Fuhrman

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

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

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

Tropical forests are extremely diverse, yet the factors that generate and maintain such high diversity are poorly understood. Over half of the species in tropical forests are plants and the insects that feed on them (herbivores), so examining these interactions may shed light on this long-standing puzzle. Plants have evolved a battery of defenses to protect their leaves from insects and insects are continually evolving counter-adaptations. Consequently, high rates of defense evolution may contribute in important ways to the origin of new species.

This research will explore how herbivores drive the evolution of plant defenses, how plant defenses influence which plant species herbivores consume, and how plant-herbivore interactions might influence plant community composition and diversity in the world's most species-rich forests. The interdisciplinary study will focus on the genetic, taxonomic, and functional diversity of the tree genus *Inga* (Fabaceae) and its insect herbivores at five sites in Central and South America (the Neotropics). *Inga* is the most locally diverse and abundant tree genus in Neotropical forests. This interdisciplinary study will measure plant defenses, including toxins, physical defenses and the attraction of ants (that may protect plants against herbivores) to sugar-producing nectaries on the leaves. DNA sequencing of herbivores and *Inga* will quantify diversity of

species, test whether closely related *Inga* have similar defenses, and determine whether herbivores choose hosts based on the similarity of their defenses.

It is hypothesized that if plants differ in their defenses, they will be attacked by different herbivores. If this is true then many plant species that differ in defenses can coexist as neighbors despite the fact that they are closely related. This process could help to explain the amazingly high local diversity of plants typical of tropical forests.

This research will be communicated to a variety of audiences to enhance appreciation of nature and science. The team will create a theater of biodiversity for school children and families in Utah, conduct Saturday science days for children from poor communities near the Brazil and Peru field stations, give presentations on tropical diversity for tourists at the Royal Botanic Garden, Edinburgh (UK), and develop the use of *Inga* in agroforestry. Agroforestry refers to the use of trees in plantations of coffee and cacao, for shade and to improve the habitat for wildlife, as well as to reforest, provide firewood, and improve soils in degraded areas. The integrative project will also create an open web-accessible site of results to share data and facilitate research by other scientists.

Right: Inflorescences of *Inga punctata* (Peru: Los Amigos)

Center right: Herbivores prefer tender, expanding leaves, such as these (*I. suberosa*; Brazil: Manaus, Reserva Ducke).



Tom Kursar, University of Utah

T. Kursar

T. Kursar

Above far right: An unidentified caterpillar in the family Lycaenidae consuming *I. cylindrica* (French Guiana: Nouragues)

Far left: An unidentified caterpillar ("bagworm") consuming *I. bourgonii* (French Guiana: Nouragues)

Near left: An unidentified caterpillar consuming *I. marginata* (French Guiana: Nouragues)



T. Kursar

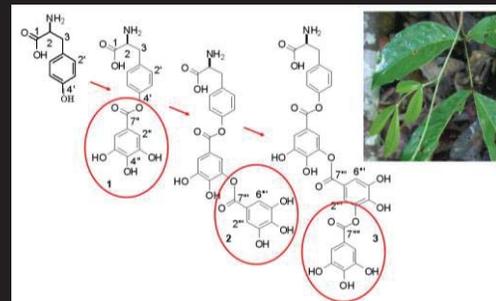
T. Kursar

Left: Ants are attracted to sugary rewards provided by the nectaries of expanding leaves. Nectar provides carbohydrates, but no protein. Therefore, ants also search for and consume high-protein herbivores, defending the plant in the process.



T. Kursar

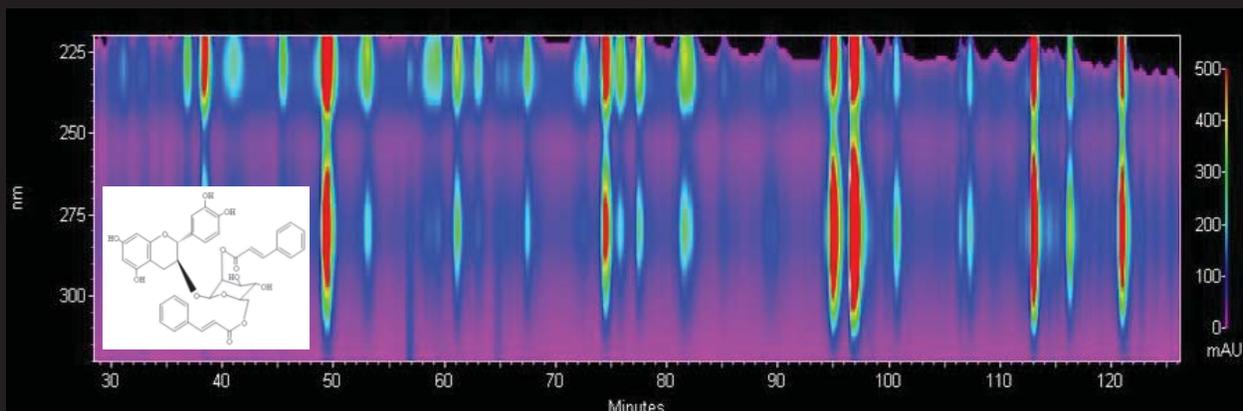
Right: The evolution of toxins in *Inga* begins by over expression of the amino acid, tyrosine (leftmost compound). High concentrations of tyrosine are toxic to herbivores. Tyrosine derivatives, e.g. tyrosine depsides (circles 1 3), are found in other *Inga* species (Inset: *I. laurina*; Panama: Barro Colorado Island).



John Lokvam, University of Utah

Below: Separation of the series using chromatography on a column. The vertical axis shows detection of the toxins by ultraviolet light absorbance. The horizontal axis shows release time from the column for each toxin. The figure indicates approximately seven abundant compounds (red/blue) and roughly 15 less abundant compounds (blue/blue-yellow).

Inset: One example of the structure of an extensive series of newly discovered chemical toxins made by *Inga umbellifera* (flavan 3 ols; Barro Colorado Island, Panama)



J. Lokvam

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

Elena G. Litchman and Christopher A. Klausmeier, Michigan State University (NSF 1136710); Stephanie E. Hampton, University of California, Santa Barbara (NSF 1136637); Marianne Moore, Wellesley College (NSF 1136657); Edward C. Theriot, University of Texas, Austin (NSF 1136667); Lev Yampolsky, East Tennessee State University (NSF 1136706)

Microscopic plant- and animal-like plankton are the first links in aquatic food chains. This project will study 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.

Human-induced global change is altering most ecosystems on Earth. How ecosystems will respond greatly depends on their biodiversity: genetic diversity may allow populations to adapt to change and functional diversity allows different species to carry out many different 'jobs' in the ecosystem, increasing its resilience. The exact mechanisms of how different dimensions of biodiversity determine ecosystem responses to global change are, however, poorly understood. An interdisciplinary team of researchers will use 60 years of unique ecological data, extensive field sampling, genetic analyses, laboratory experiments and novel mathematical models to examine for the first time multiple aspects of biodiversity in the largest, oldest and most biodiverse lake in the world – Lake Baikal in Siberia – and to predict how this ecosystem will respond to accelerating environmental change. Lake Baikal's planktonic food web (microscopic algae and zooplankton) fuels the rest of Baikal's incredibly diverse biota and is dominated by endemic species that are extremely sensitive to rising temperatures and other anthropogenic stressors. The researchers will determine if the genetic and functional diversity in the endemic species will allow them to adapt and persist in the changing climate or whether the lake's unique food web will collapse and be replaced by widely distributed (cosmopolitan) species, which may have dramatic consequences for the

entire ecosystem, including the world's only freshwater seal.

Holding 20% of world's unfrozen fresh water, this UNESCO World Heritage Site is recognized internationally as a globally important freshwater resource, a treasure trove of biodiversity and a unique natural laboratory to study evolution. With an unprecedented diversity of endemic species found nowhere else, Lake Baikal serves as a model for ecosystems with highly unique biota and cold aquatic environments undergoing rapid warming.

Data collected on this project will be publically available so that their uses and value extend beyond this project and the researchers' laboratories. Researchers and students will engage in an interdisciplinary international collaborative research program. Funding will support graduate training in both applied and basic areas of science, including molecular biology, ecology, and informatics. The results will be communicated to environmental organizations in Russia and the US and to a US-based film team planning an IMAX movie about Lake Baikal and freshwater conservation. School teachers from Michigan, Texas and Tennessee will participate in the project and, together with researchers, develop educational activities on aquatic ecology, biological diversity and global change.



Nick Rodenhouse, Wellesley College

Above: Irkutsk State University Research Vessel *Kozhov*



N. Rodenhouse

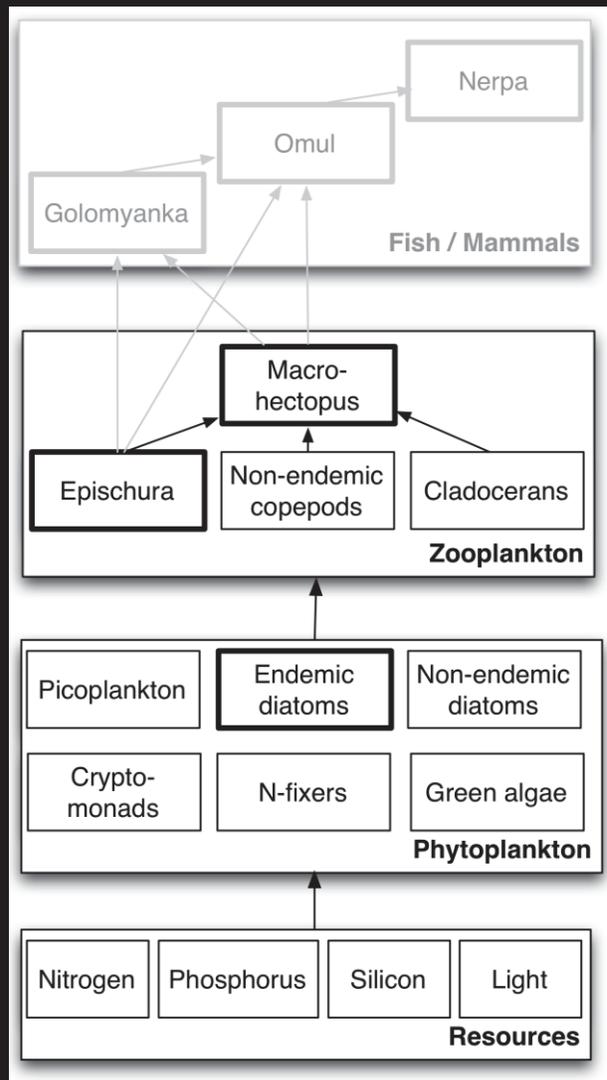
Above: Wellesley College students sampling Lake Baikal



Marianne Moore, Wellesley College

Above: Night sampling for *golomyanka* (*Comephorus* sp), an endemic oil fish

Right: Model food web of Lake Baikal: lower black boxes are modeled, gray boxes are non-modeled higher trophic levels. Thick borders denote endemic species that make up the backbone of the present day food web.



Elena Litchman, Michigan State University

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

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

This research highlights the role of environmental variation and herbivore defense in the remarkable diversity of wild tomato species by integrating analyses of DNA, gene expression, and phenotypes in this clade with data on their ecological and evolutionary history.

Global environmental change is expected to fundamentally alter patterns of biodiversity, but predicting the direction and magnitude of this change is extremely difficult. One factor in long-term responses to environmental change is the genetic basis of traits that mediate organism-environment interactions. The relative complexity of these traits and their interactions can influence how rapidly adaptation can occur and which traits are most responsive to environmental change. This research aims to understand how current biodiversity is shaped by environmental variation, by focusing on two critical plant traits: leaf ecophysiology (which influences plant responses to water, light, and carbon dioxide), and constitutive and induced defense responses (which influence plant responses to herbivores). Understanding the molecular genetics and adaptive history of these key traits will allow assessment of the mechanisms that may regulate future adaptive responses to environmental change.

This research will generate data on biodiversity in DNA sequences, in gene expression in response to abiotic and biotic stress, and in morphological and physiological traits, in 18 diverse ecotypes from 12 species in the plant group *Solanum* section *Lycopersicum* ('wild tomatoes'). This closely related group of Andean species spans a broad range of natural phenotypic and ecological variation, including ecotypes adapted to extremes in drought, salt, altitude, and temperature. Species also differ widely in the kind and magnitude of their defense responses to natural predators. As

such, this group is a potentially powerful model in which to understand the genetics of natural adaptive responses to environmental change over recent ecological and evolutionary timescales.

First, by coupling data on molecular genetic differences with differences in phenotypes and ecological interactions across the wild tomatoes (comparative transcriptomics), the project will identify the genetic changes that have attended adaptive differentiation. Second, examining gene expression responses in different ecotypes to drought and induced defense (experimental transcriptomics) will clarify how molecular responses to these abiotic and biotic stresses are integrated, and whether this changes over short ecological and evolutionary timescales. Finally, combining these findings with existing data, the research will generate a core set of loci underpinning functional responses to abiotic and biotic environmental variation across an entire group of wild species.

The project will contribute to workforce by training researchers in a broad set of skills at the interface of experimental genetics, genomics and bioinformatics. By examining wild relatives of several important crops, including tomato, potato, and pepper, this research may also help identify valuable natural variation that confers plant tolerance to critical environmental stresses. Finally, uncovering the genetics of diversification is crucial in the Andes, where land-use and climate change threaten a cradle of biodiversity with an estimated 12% of global flowering plant diversity.

Right: Diversity of leaf shapes and sizes among wild tomatoes, *Solanum* spp

Top row: *S. peruvianum*, *S. galapagense*, *S. chesemani*, *S. pennellii*, *S. habrochaites*

Middle row: *S. pimpinellifolium*, *S. lycopersicoides*

Bottom row: *S. neorickii*, *S. chilense*, *S. lycopersicum* var. *cerasiforme*, *S. ochranthum*.



Leonie Moyle, Indiana University



David Haak, Indiana University

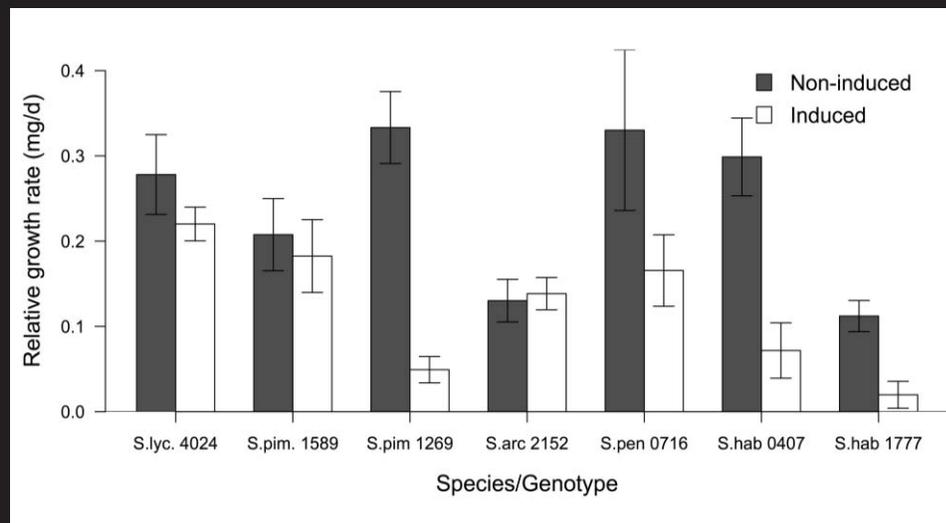
D. Haak

D. Haak

Above left: A tobacco hornworm (larvae of the Carolina sphinx moth, *Manduca sexta*) navigates the dense hairs on leaves and buds of *S. habrochaites*

Above center: Silhouette of *M. sexta* feeding on a leaf of *S. pennellii*

Above right: *M. sexta* tastes and rejects a leaf of *S. pimpinellifolium*



D. Haak

Left: Natural *Solanum* variation in non and induced defense to the specialist herbivore *M. sexta*

X-axis: seven genotypes that span within and among species diversity

Y axis: shows growth rate of *M. sexta* larvae on each genotype. Induction via Jasmonic acid-treatment

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

Ann Pearson and Peter Girguis, Harvard University (NSF 1136484); Jennifer Macalady, Pennsylvania State University, University Park (NSF 1136218)

Studying the ecological interactions among microbes is difficult given their immense diversity and the scale of observation. This project will use isotopic ratios of carbon, nitrogen, hydrogen, and sulfur produced during microbial metabolism to link guilds of microbes to their roles in biogeochemical and ecosystem processes. This novel approach will contribute to our understanding of what maintains functional and genetic diversity in microbes and, by extension, the roles those microbes play in ecosystems.

Recent advances in DNA sequencing technology have accelerated the pace of discovery of species and gene distributions. This contrasts with slower progress in linking environmental genetics and taxonomic diversity to the functions, resource utilization, and ecological niches occupied by species. This work will develop a novel application of isotope geochemistry and will apply it in the field of aquatic biochemistry as a first step toward tackling these challenges. The goal of the project is to combine natural isotope ratio data with proteomics. Different metabolic processes yield different ratios of the stable isotopes of carbon, nitrogen, hydrogen, and sulfur. By measuring these ratios on specific proteins with simultaneous sequencing, these natural isotope signals can attribute biogeochemical processes (functions) to specific microbes (taxonomic and genetic information). The approach will be called P-SIF (protein stable isotope fingerprinting). Because this is a novel methodology, the project first will seek to identify the fundamental principles of natural isotopic sorting that could result from different types of trophic ecosystem structure. This will be implemented using pure cultures and then tested on a model ecosystem from a stratified lake. Example questions include: How does the distribution of P-SIF fingerprints in a mixed community scale with the genetic diversity of a sample's metagenome and expression of its

metaproteome? Does higher diversity predict more trophic levels?

Examining this “how, when, and why” of microbial processes yields insight about environmental conditions on Earth today, in the past, and about potential human impacts on our future. This project will help to develop a concept of trophic guilds and ecosystem dependence for microbes. Such concepts are well developed in macro-ecology, but remain less well understood for microbial diversity. Ecosystem maintenance and conservation is not possible without a better understanding of what maintains microbial functional and genetic diversity. The success of this project could lead to many further applications to understanding the physiological and/or ecological roles of uncultured microbes in the environment. The project has three principal investigators: an isotope geochemist, a microbial physiologist, and a microbial ecologist. This team is ideally suited to achieve the interdisciplinary goal of linking geochemistry with microbial ecology. The proposed activities will educate a post-doctoral investigator, two graduate students, and several undergraduate summer students. Additional activities such as The Cambridge Science Festival and Science by the Pint (<http://cambridgesciencefestival.org/Home.aspx>; <https://sitn.hms.harvard.edu/>), will communicate the research to the public.



Left: Mahoney Lake, (Canada: British Columbia, Penticton)

Jennifer Glass, Arizona State University

Right: Direct sample of the Mahoney chemocline, showing a dense community rich in photosynthetic and chemosynthetic sulfur bacteria



J. Glass



Left: Hotel room “kitchen laboratory” (Canada: British Columbia, Penticton)

J. Glass

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

Nathan J. Sanders, University of Tennessee, Knoxville (NSF 1136703); Robert P. Dunn, North Carolina State University (NSF 1136717); Aaron M. Ellison, Harvard University (NSF 1136646); Nicholas J. Gotelli, Bryan A. Ballif, and Sara I. Cahan, University of Vermont and State Agricultural College (NSF 1136644)

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

Climate is rapidly changing and biodiversity is changing with it: species evolve or disappear locally, regionally, or entirely. However, we know surprisingly little about the mechanisms that lead to these shifts in biodiversity. Why do some species track changes in environmental temperatures while others stay put? What physiological and evolutionary mechanisms allow species to stay put?

This project builds off of an ongoing warming experiment carried out by a team of investigators located at four institutions (University of Tennessee, North Carolina State University, University of Vermont, and Harvard Forest). The core of the research focuses on how populations and species of forest ants adapt to climate change and avoid local extinction. Why ants in forests? Ants process soil, cycle nutrients, and disperse seeds of perhaps more than 50% of "spring ephemerals" - understory herbs such as trillium, bloodroot, and winged polygala - which flower on the forest floor in early spring before tree canopies close. Ants also respond, often quickly, to changes in air temperature, so climate change could have dramatic implications for the structure and function of eastern US forests.

Samples of the most common ant species will be collected from forests throughout the eastern US, and gene sequencing will be used to reconstruct the evolutionary history of these ants to reveal genes that may have evolved in response to past climate change. Genes will also

be sequenced from ants collected from the ongoing experimental warming chambers at Harvard Forest and Duke Forest that have been continuously heated (from ambient temperatures up to +5 °C) for the past three years. In controlled laboratory experiments, ants will be briefly exposed to a range of high temperatures predicted by climate change models, and the production of heat shock proteins will be measured. Heat-shock proteins are molecules that are produced in greater quantities when organisms are exposed to high temperatures, and they represent important adaptations to heat stress. Heat shock proteins from different ant species will be analyzed to determine their biochemical structure, which can provide clues to how well species can adapt physiologically to high temperatures. Taken together, the results of this research will help to understand the many ways that key species are likely to respond to climate change. Additionally, it will provide information about the interplay among evolutionary history, behavior, and ecological interactions in response to climate change.

This research will train undergraduate and graduate students, and provide public outreach and education on the effects of climate change on biodiversity. Summer high school outreach programs for both teachers and students will be enhanced, and citizen-scientists will be engaged in documenting the effects of climate change on biodiversity.



© Aaron M. Ellison



© A.M. Ellison



© A.M. Ellison

Above left: A member of the *Aphaenogaster rudis* complex tending a brood of larvae and pupae

Above right: Species in the *A. rudis* complex nest in and around damp, fungus laden soil

Left: This photograph shows a 22 m³ atmospheric warming chamber *in situ* at Harvard Forest

Below: These images illustrate the levels of atmospheric warming achieved in the chambers. False color infra red shows that the hottest chambers (*right*) are 5–6 °C warmer than the control chambers (*left*).



Paul J. Hanson

Below: The Climate Cascade team: PI N. Sanders (far left), co-PIs A. Ellison (far right), R. Dunn (back row, right of Sanders), N Gotelli (center, with black vest), with graduate students and post-docs from the University of Tennessee, Harvard University, North Carolina State University, and the University of Vermont



© A.M. Ellison

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

Stefan M. Sievert, Jeffrey S. Seewald, and Craig D. Taylor, Woods Hole Oceanographic Institution (NSF 1136727); Dionysios I. Foustoukos, Carnegie Institution of Washington (NSF 1136608); Ramunas Stepanauskas, Bigelow Laboratory for Ocean Sciences (NSF 1136488); Costantino Vetriani, Rutgers University, New Brunswick (NSF 1136451)

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

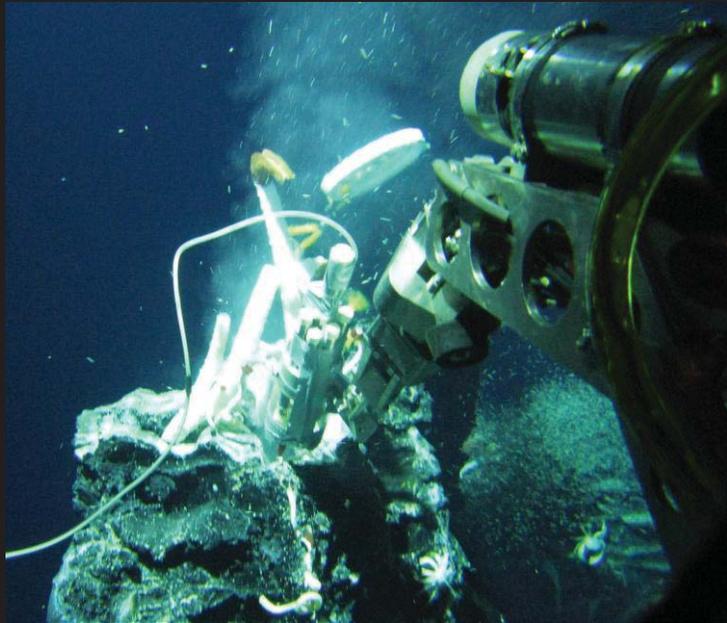
First discovered in 1977, deep-sea hydrothermal vents, are 'poster child' ecosystems where chemosynthesis rather than photosynthesis, is the primary source of organic carbon, fueling complex and productive ecosystems. Chemosynthesis is the production of organic matter from CO₂ coupled to inorganic chemical reactions to obtain energy. While biological productivity at vents is generally well-described, significant gaps remain in our understanding of the microbiology and biogeochemistry of these fascinating ecosystems. In particular, we do not have a good understanding of the metabolic pathways used by the microbes, the rates of the catalyzed reactions, the specific microorganisms mediating these reactions, the amounts of organic carbon being produced, and the larger role of these ecosystems in global biogeochemical cycles.

To fill these gaps and better understand the fluxes of energy and matter at deep-sea vents the researchers will pursue an *interdisciplinary, international* program. This project will couple an assessment of taxonomic diversity using cultivation-dependent and -independent approaches with methodologies that address genetic diversity, including a) metagenomics (genetic potential and community diversity), b) single cell genomics (genetic potential and diversity of uncultured single cells), c) meta-transcriptomics and -proteomics (identification and function of active community members;

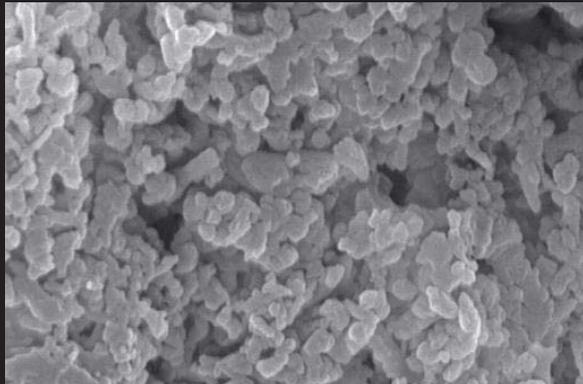
realized potential of the community). To assess function and response to the environment, these approaches will be combined with 1) *in situ* rate measurement of chemoautotrophic production, 2) geochemical characterization of microbial habitats, and 3) shipboard incubations under simulated *in situ* conditions (hypothesis testing under controlled physicochemical conditions). Network approaches and mathematical simulation will further be used to reconstruct the metabolic network of the natural communities. The integration of laboratory and field experiments in combination with a suite of cutting edge analytical techniques will create unprecedented opportunities that will lead to unique insights into the functioning and environmental interactions of deep-sea vent microbial communities, ultimately enabling us to place these systems into a quantitative framework and thus a global context.

This is an interdisciplinary and collaborative effort between 4 US and 4 foreign institutions, creating unique opportunities for networking that benefit also the involved students and postdoctoral associate. A variety of educational and public outreach activities aiming at a diverse audience ranging from grades 4 – 12, community colleges, and undergraduate universities to the general public are an integral part of this project. The research cruise will also be featured on the highly successful WHOI Dive & Discover program.

Right: At “Crab Spa,” a diffuse flow hydrothermal vent site (East Pacific Rise at 9°N 50', 104°W 17'), the manipulator arm of the submersible *Alvin* holds a sensor developed by collaborator Nadine Le Bris, that measures temperature, pH and sulfide *in situ*. Chemosynthetic microbial communities manifest themselves as white biofilms attached to the basalt, are released from the sub-seafloor and suspended in the fluid or live in symbioses with invertebrates such as the giant tube-worm *Riftia pachyptila* (left of center). An integration of *in situ* and laboratory-based studies to assess the function and diversity of these microbial communities is at the core of this project.



Stefan Sievert, Woods Hole Oceanographic Inst.

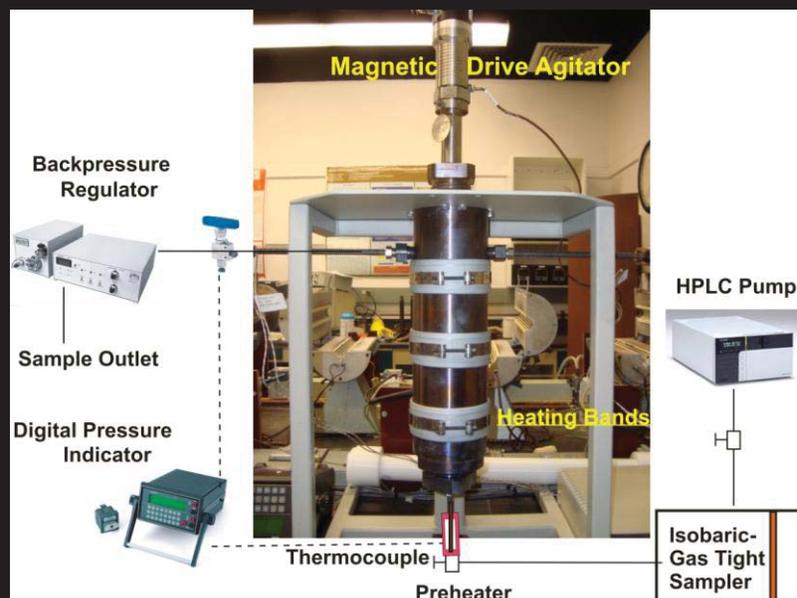


8,600x 20.0 kV 1µm AMRAY #0000*

Costantino Vetriani, Rutgers University

Left: Scanning electron micrograph of chemosynthetic biofilm collected from a deep-sea hydrothermal vent

Right: Dual-flow titanium reactor to investigate metabolic rates and growth efficiency of chemo autotrophs across redox gradients. This experimental setup facilitates continuous culturing experiments to be performed in laboratory under seafloor temperature and pressure conditions.



Dionysis I. Foustoukos, Carnegie Inst. of Washington

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

Bess B. Ward and Daniel M. Sigman, Princeton University (NSF 1136345); Andrew E. Allen, J. Craig Venter Institute, Inc. (NSF 1136477)

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

Phytoplankton form the basis of the marine food web and thus are a crucial element in the biological pump whereby atmospheric CO₂ is sequestered in the deep ocean. For decades, biological oceanography focused on eukaryotic phytoplankton. In the 1970-80's, it was found that single celled picocyanobacteria are numerically dominant in oceans and responsible for a large fraction of ocean photosynthesis. What resulted was a new paradigm in which the picocyanobacteria dominate upper ocean biology and biogeochemistry. In fact, new data support the classic view that the eukaryotic phytoplankton are disproportionately important in both N and C cycling, even in regions where very small cells dominate and where the eukaryotes themselves are in the "pico" size fraction. In oligotrophic environments, where very small cells dominate, *in situ* recycling appears to supply most of the nitrogen (i.e., ammonium) required for primary production. On the basis of still quite limited molecular surveys, it is recognized that the diversity of both large and small eukaryotic phytoplankton is greater than previously thought and that the most abundant and widespread eukaryotes are probably not in culture and may not be closely related to known cultivated organisms.

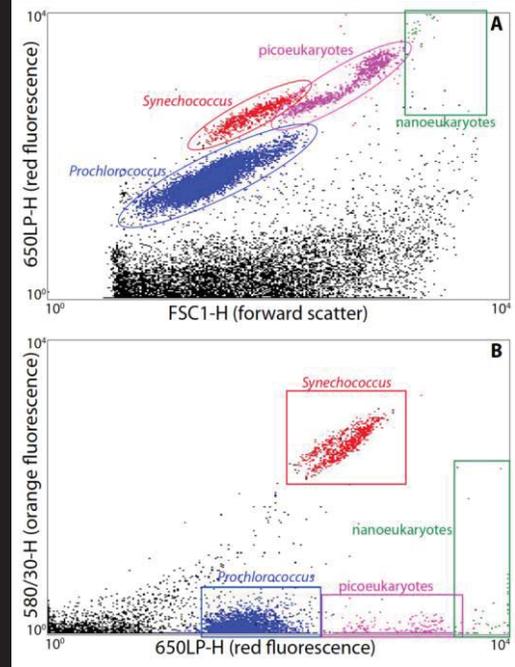
Ward and colleagues will investigate the taxonomic, genetic and functional diversity of eukaryotic phytoplankton and link this diversity

and assemblage composition to the carbon and nitrogen biogeochemistry of the surface ocean at two North Atlantic sites (subarctic and subtropical) in two seasons. They are investigating taxonomic diversity by identifying the components of phytoplankton assemblages using molecular, chemical and microscope methods. Genetic diversity will be explored at several levels, including direct sequencing of clone libraries of key functional genes and metatranscriptomic sequencing and microarray analysis of size fractionated/sorted phytoplankton assemblages. Finally, genetic and taxonomic diversity will be linked to functional diversity in C and N assimilation in size-fractionated and taxon-sorted populations using natural abundance and tracer stable isotope methods.

This project will contribute to fundamental research and education through development of methods of isotope analysis in environmental samples; undergraduate teaching and research experiences; and training the next generation of microbial ecology/ biogeochemistry researchers through classroom and research experiences at the graduate level. In addition, the researchers will provide a new module, *The Forests and Deserts of the Ocean*, to the Princeton outreach program for middle school teachers (QUEST, Questioning Underlies Effective Science Teaching).



Sarah Fawcett, Princeton University

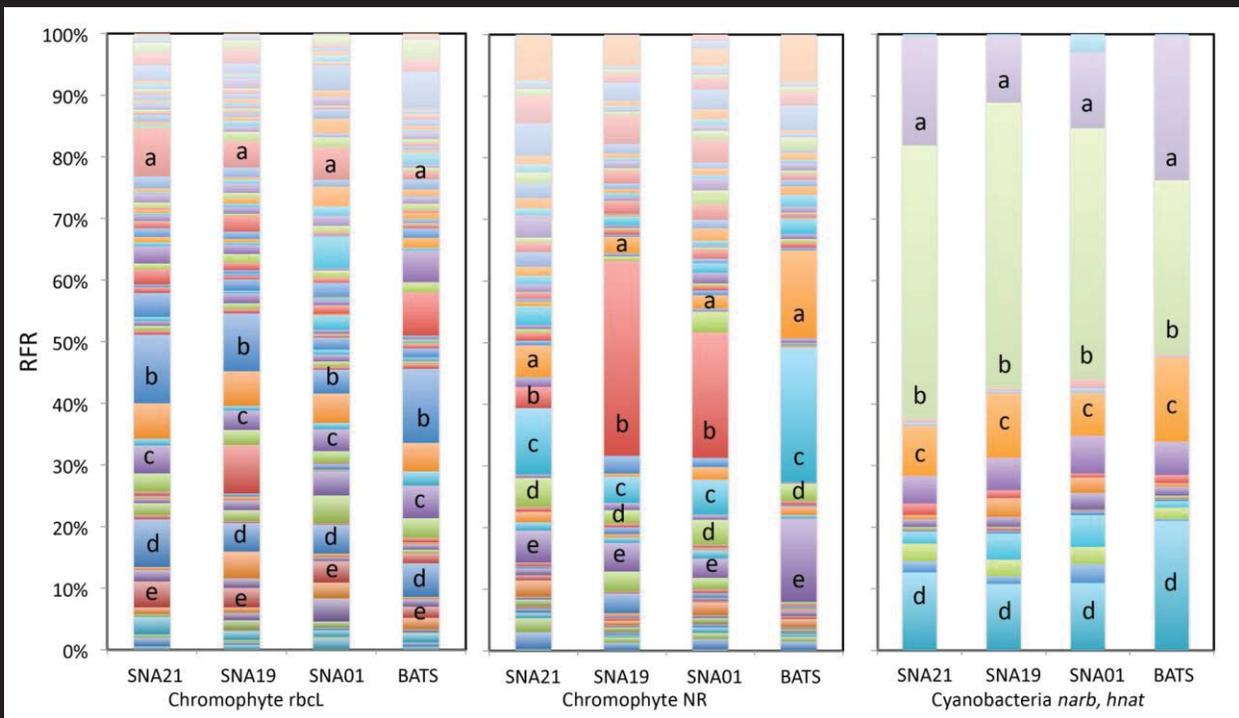


S. Fawcett

Above left: Post doc Katy Altieri and graduate student Sarah Fawcett deploying a CTD rosette (used to measure sea water conductivity, temperature and density) for the Bermuda Atlantic Time series Study (BATS)

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

Below: Relative contribution of diverse archetypes to the phytoplankton community in the Subarctic North Atlantic (SNA; May 2009) and at BATS (March 2009) analyzed on Phytoarray 2. The colors represent Relative Fluorescence Ratio, the fraction of total fluorescence due to each probe (average of two replicate arrays for each sample)



Bess Ward, Princeton University

INTERNATIONAL RESEARCH COORDINATION NETWORK: A research coordination network for biodiversity of ciliates

PI: John Clamp, North Carolina Central University (NSF 1136580)

US MEMBERS: John Clamp; Laura Katz, Smith College; Chris Lobban, University of Guam; Micah Dunthorn, University of Kaiserslautern, Germany

CHINA MEMBERS: Weibo Song, Ocean University of China, Qingdao; Xiaofeng Lin, South China Normal University, Guangzhou.

OTHER COUNTRIES: Alan Warren, Natural History Museum, London, United Kingdom; Laura Utz, Pontificia Universidade Católica do Rio Grande do Sul, Brazil

This project, jointly supported by the National Natural Science Foundation of China, will establish an International Research Coordination Network for Biodiversity of Ciliates. The network will include researchers from the US, China, the UK, and Brazil and will broaden exploration of these important protists.

Ciliates are a major group of unicellular, eukaryotic organisms that play important roles in nearly all ecosystems and serve as model organisms for basic research in genetics and cell function. Approximately 7,500 species are known, but three times that many may be undiscovered, especially in poorly explored places like tropical forests or the deep ocean.

Better knowledge of the biodiversity of ciliates could translate into more effective management of ecosystems or new model research organisms, but achieving these objectives has been slower and more difficult than with multicellular organisms. Modern studies of biodiversity often rely on DNA from preserved specimens in museums, but there is no such archive for ciliates. Also, sequencing most genes of ciliates is more challenging than in animals or plants. Lastly, researchers who study biodiversity of ciliates are scattered thinly and unevenly across the world, and many are younger investigators who have little money for travel to professional meetings or other laboratories to build collaborations, which are the best way to make rapid progress.

The Research Coordination Network for Biodiversity of Ciliates (RCN-BC) is a project begun by Chinese and US laboratories that will address these problems. It will be a worldwide

network of researchers designed to lower the barriers to research on ciliate biodiversity, an ‘engine’ for generating new collaborations, new procedures for archiving material, and—most significantly— new research projects that unite the three dimensions of biodiversity. The RCN-BC will create the means to advance research in biodiversity of ciliates more quickly by (1) sponsoring workshops and symposia to build strategies and develop techniques; (2) creating archives for preserved samples of cells and DNA; (3) maintaining a website to report activities, attract new members, promote collaborations, and share data; and (4) funding travel for researchers.

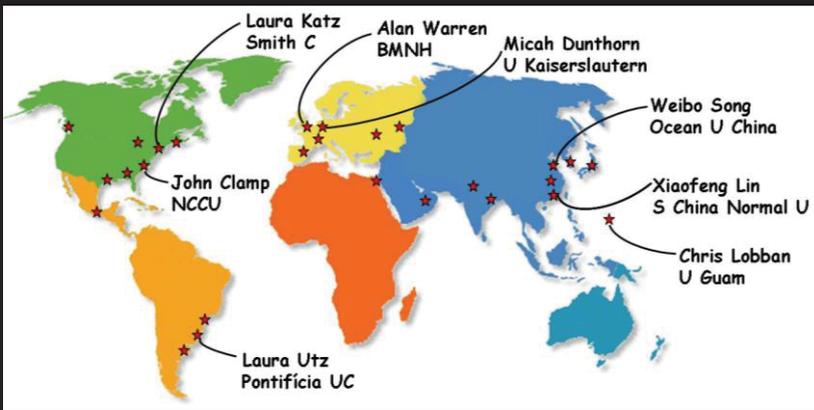
The RCN-BC will be a model for accelerating multidimensional investigation of biodiversity in other protistan groups. Also, students at Minority Serving Institutions (MSIs) traditionally get scant exposure to areas of biology outside biomedicine. The RCN-BC will create an email listserv of contacts at MSIs to inform faculty and students about the RCN-BC, especially connections between biodiversity and biomedicine. Students from underrepresented minority groups (African-American, Pacific Islander) will be included in two workshops.



Examples of two of the many species of ciliated protists that occur in environments world wide:

Left: *Diophrys* sp., a hypotrich; these ciliates form one of the largest groups in the phylum and are significant components of food webs in marine, freshwater, ephemeral, and terrestrial habitats.

Right: *Acineta tuberosa*, a suctorian; these ciliates attach to many sorts of substrates, including a wide array of animals, and prey on other ciliates.



Left: Distribution of members in the Research Coordination Network for Biodiversity of Ciliates. The RCN has grown out of active research collaborations between the Laboratory of Protozoology at the Ocean University of China and other major laboratories (steering committee members are labeled)

Below: Students and faculty of the Laboratory of Protozoology, Ocean University of China, Qingdao (Spring 2007). Dr. W. Song, principal Chinese RCN partner (fourth from right in standing row); Dr. A. Warren, Museum of Natural History, UK, is a long time Qingdao lab collaborator (left of Dr. Song); Dr. J. Clamp, N.C. Central University, is the principal US RCN partner, project PI, and long time collaborator with Dr. Song and others in the Qingdao lab.



All images: John C. Clamp, North Carolina Central

Fiscal Year 2010 Projects

The microbial basis of animal speciation

30

Seth Bordenstein, Vanderbilt University (NSF 1046149)

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

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

32

Thomas Bruns and John W. Taylor, University of California, Berkeley (NSF 1046115); Kabir G. Peay, University of Minnesota – Twin Cities (NSF 1045658); Rytas Vilgalys, Duke University (NSF 1046052)

This project will consider 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.

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

34

Bradley Cardinale, University of Michigan Ann Arbor (NSF 1046121); Charles F. Delwiche, University of Maryland College Park (NSF 1046075); Todd H. Oakley, University of California Santa Barbara (NSF 1046307)

Cardinale and colleagues will examine how evolutionary processes among algae generate and maintain diversity at levels from genes to ecosystems in freshwater lakes.

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

36

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.

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

38

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 will test how the diversity and functions (metabolic and ecological) change when the saline copepod invades a novel habitat (fresh water).

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

40

Francois Lutzoni, Duke University (NSF 1046065); Anne Arnold, University of Arizona (NSF 1045766); Ignazio Carbone, North Carolina State University (NSF 1046167); Georgiana May, University of Minnesota, Twin Cities (NSF 1045608)

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

Biological controls in the ocean: the Redfield Ratio **42**

Adam Martiny and Steven Allison, University of California Irvine (NSF 1046297); Simon Levin, Princeton University (NSF 1046001); Michael Lomas and Benjamin Van Mooy, Bermuda Institute of Ocean Sciences (NSF 1045966); and 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.

Genomics, functional roles, and diversity of the symbiotic gut microbiotae of honey bees and bumble bees **44**

Nancy Moran, Yale University; and Jay Evans, USDA ARS (NSF 1046153)

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

An integrative traits-based approach to predicting variation in vulnerability of tropical and temperate stream biodiversity **46**

N. Leroy Poff, William C. Funk, Cameron Ghalambor, and Boris Kondratieff, Colorado State University (NSF 1046408); Alexander Flecker, Joseph Bernardo, and Kelly Zamudio, Cornell University (NSF 1045960); and 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 will examine the influence of climate change on stream biodiversity in a tropical stream system in the Andes of Ecuador and a temperate alpine stream system in the Colorado Rockies.

Shedding light on viral dark matter--genetic, taxonomic, and functional diversity of coral reef viromes **48**

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

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

Parallel evolutionary radiations in Protea and Pelargonium in the Greater Cape Floristic Region **50**

Carl Schlichting, Kent Holsinger, Cynthia Jones, and John Silander, University of Connecticut (NSF 1046328); Andrew Latimer, University of California Davis (NSF 1045985); Justin Borevitz, University of Chicago (NSF 1046251)

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

Significance of nitrification in shaping planktonic biodiversity in the ocean **52**

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

Stahl and others will examine the diversity and function of ammonia oxidizing Archaea (AOA) in the ocean and determine the role of these newly discovered organisms in structuring the diversity of phytoplankton.

The role of viruses in structuring biodiversity in methanotrophic marine ecosystems **54**

David Valentine, University of California, Santa Barbara (NSF 1046144)

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

Roles of functional, phylogenetic, and genetic diversity in structuring and sustaining plant communities through environmental change **56**

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

Waller and colleagues will examine the functional traits, phylogenetic relationships, geographic distributions, and patterns of genetic variation in native and introduced plants in Wisconsin forests and grasslands.

DISTRIBUTED GRADUATE SEMINAR AWARD

Dimensions of Biodiversity Distributed Graduate Seminar **58**

Julia Parrish, University of Washington (NSF 1050680)

A distributed graduate seminar will provide a baseline for the planned 10-year program. A synthesis of current understanding of the dimensions of biodiversity will be posted on a wiki, crowd-sourced regularly, and “frozen” periodically to allow assessment of progress.

INTERNATIONAL RESEARCH COORDINATION NETWORK AWARD

IRCN: Diversity and forest change: Characterizing functional, phylogenetic and genetic contributions to diversity gradients and dynamics in tree communities **60**

US TEAM: Stuart Davies, Harvard University; Nathan G. Swenson, Michigan State University; W. John Kress, Smithsonian National Museum of Natural History; Rick Condit, Center for Tropical Forest Science, Smithsonian Tropical Research Institute (STRI); and Helene Muller-Landau, STRI (NSF 1046113)

CHINA TEAM: Zhanqing Hao, Institute of Applied Ecology, Chinese Academy of Sciences (CAS); Keping Ma, Institute of Botany, CAS; Wanhui Ye, South China Botanical Garden, CAS; Jie Li, Xishuangbanna Tropical Botanical Garden, CAS; Xiangcheng Mi, Institute of Botany, CAS; Xugao Wang, Institute of Applied Ecology, CAS.

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

The microbial basis of animal speciation

Seth Bordenstein, Vanderbilt University (NSF 1046149)

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

One of the central questions in biology is how do new species arise- that is, how does one species become two and so on to ultimately produce the more than 1.8 million species that now inhabit the planet. Traditionally, animal species are categorized as groups of individuals that can interbreed, and new species thus arise by the accumulation of genetic mutations that ultimately cause the inability for two populations to interbreed. Once these barriers to interbreeding evolve, speciation is underway.

However, animal species may also change by acquiring differences in the millions of bacteria that typically inhabit them in symbiotic relationships. For instance, in humans 90% of the cells in the body are microorganisms, not human cells. This research will address a major gap in our knowledge about how biodiversity arises in animals: whether or not the symbiotic community of bacteria within a host can contribute to hybrid lethality between host species. The investigation has three aims using several species of interfertile parasitoid wasps in the genus *Nasonia* that vary in their level of hybrid lethality. First, the investigators will test if the normal, resident bacteria within a species are different than those in hybrids. Alterations of the microbial community in hybrids would suggest an incompetence of the host to regulate a normal consortium of bacteria. Second, they will test the prediction that the host's genes that are used to regulate its immune system and defend against pathogens are not turned on properly in hybrids, and these changes in hybrid genes will be associated with changes in the hybrid's bacterial community. Third and finally, the researchers will test if hybrid mortality between the species is due to either a reduction in beneficial bacteria or an

increase in pathogenic bacteria. To do this they will investigate whether hybrids free of their bacteria or transplanted with specific infections die prematurely or not.

The studies will integrate genetic, taxonomic, and functional dimensions of animal-microbe symbioses to comprehensively determine the consequences of bacterial symbionts on speciation in a model system. The research will characterize new species of bacteria and existing species of bacteria in novel functions. Genetic aspects of the studies will include the effects that hybridization can have on animal gene expression and the genetic diversity of their bacterial symbionts. Functionally, this work will unravel the host's dependence on bacterial symbionts throughout development and test if bacterial symbionts are as important as genes in the generation of new animal species.

Broader impacts of this project include the development of a new course at Vanderbilt University that will involve undergraduates in the research, creation of an online repository for taxonomic information on the symbionts discovered in this research, dissemination of data through publically accessible databases, and extensions to understanding speciation and symbiosis in new ways across all animals, including humans. Finally, the proposed research will provide training to one graduate student, one research assistant, and several undergraduates involved in volunteerships, internships, and research for credit.

Recent news:

Brucker, RM & SR Bordenstein. 2011. The roles of host evolutionary relationships (Genus *Nasonia*) and development in structuring microbial communities. *Evolution*. DOI: 10.1111/j.1558-5646.2011.01454.x



Left: A *Nasonia* parasitoid wasp, model organism of this Dimensions of Biodiversity project. *Nasonia* are smaller than fruit flies and parasitize house flies or blow flies.



Right: A *Nasonia* female uses her ovipositor to pierce the fly host casing and deposit her eggs inside. The wasp offspring develop in this protective environment.

Below: The four species of the genus *Nasonia* are interfertile, but hybrids display varying levels of lethality during the larval pupal transition. These three images demonstrate the reduced success of hybrid larvae.



Left: A conceptual framework showing that the general microbiota (bacterial colonies represented on the culture plate by different colors) may diverge in parallel with the host's evolutionary relationships. The trunk and three branches of the tree depict the relationships of both the bacterial symbiont communities and the host's genes.

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

Below Right: Seth Bordenstein, right, and Robert Brucker examining a bottle filled with *Nasonia* wasps.



All images: Robert Brucker & Seth Bordenstein, Vanderbilt University

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

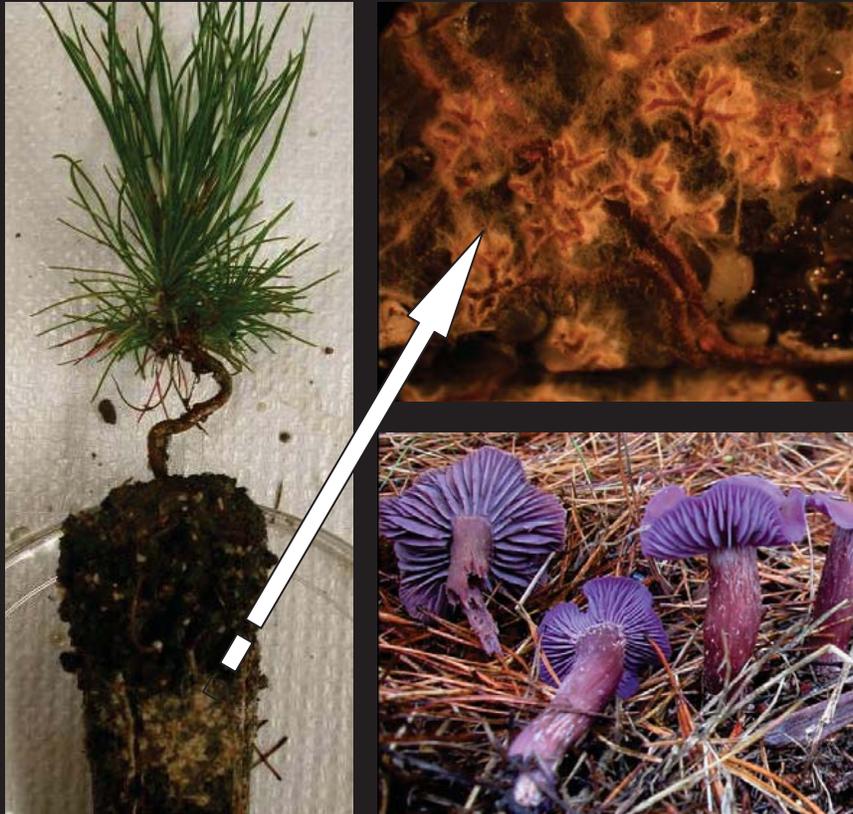
Thomas Bruns and John W. Taylor, University of California, Berkeley (NSF 1046115); Kabir G. Peay, University of Minnesota – Twin Cities (NSF 1045658); Rytas Vilgalys, Duke University (NSF 1046052)

This project will consider 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.

Fungi are a critical component of the biodiversity and functioning of terrestrial ecosystems. They play many roles in the environment – fungi are the primary degraders of dead plant material, they are major pathogens of living plants and soil animals, and they also form mutually beneficial symbioses with the roots of most plant species. Like other groups of cryptic, soil dwelling organisms, fungal communities are hyper-diverse and poorly known in even the best-studied ecosystems. Major advances in molecular biology techniques, such as Next Generation high-throughput DNA sequencing, are just beginning to allow robust exploration of taxonomic diversity in soil communities. However, simple enumeration of species diversity reveals little about the ecological processes structuring communities, or how community structure affects key ecosystem processes. This research project will provide the first continental-scale sample linking taxonomic, genetic and functional diversity of a key guild of plant root symbionts –the ectomycorrhizal fungi - from pine ecosystems across North America. Ectomycorrhizal fungi form symbiotic

relationships with the roots of dominant forest plants and provide them with nutrients and water in exchange for photosynthetically-fixed carbon. Despite the importance of ectomycorrhizal fungi in global nutrient cycles, little is known about large-scale patterns of fungal community structure relative to plants, animals, or even bacteria. This project will establish patterns of gene flow and adaptation for multiple ectomycorrhizal fungi across North America and measure variation in key biochemical characteristics of individuals, populations and species.

The project will result in a large, open access database of taxonomic barcode and functional genes that can be used by researchers to generate predictive models of fungal ecosystems. It will include training of graduate students and postdoctoral scholars in cutting-edge techniques in an understudied field, will result in outreach activities targeted toward the general public, and will include activities for K-12 students and educators designed to foster early student interests in fungi.



Kabir G. Peay

Left: Mycorrhizal symbiosis is an integral component of forest ecosystems.

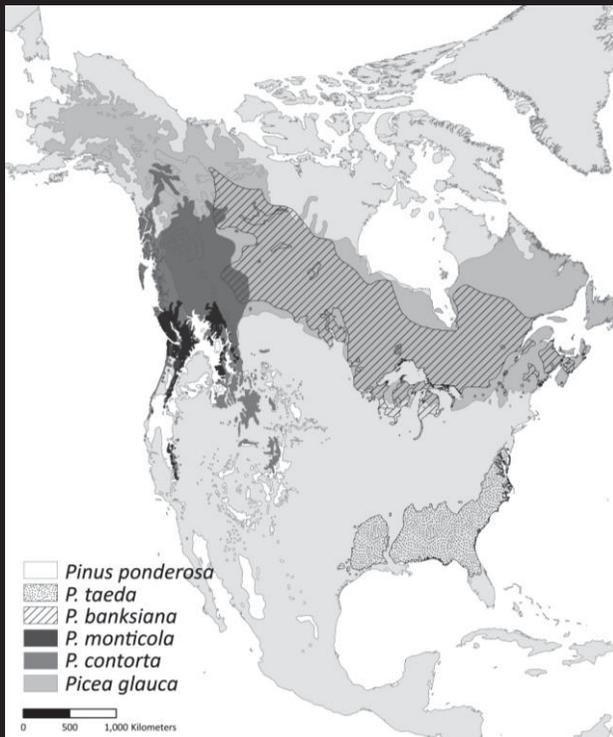
Far left: Most dominant tree species in temperate forests, such as pines, depend on fungi for the acquisition of soil nutrients necessary for their growth and reproduction

Left above: 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

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

The diversity of these symbiotic fungi is poorly known, but may have important implications for ecosystem health.

Below: Sampling design for assessing spatial, historical & environmental drivers of ectomycorrhizal fungi (EMF) diversity across multiple spatial scales:



Thomas D. Bruns

Left: N. American distribution for selected host species

Below left: Potential regional arrangement of six plots for sampling of *Pinus taeda* EMF

Below right: Nested sampling design for each plot. Soil samples will be taken at the vertices of each rectangle (n=16 samples per plot). Six plots will be sampled for each host species for a total of 36 plots in the study.



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

Bradley Cardinale, University of Michigan Ann Arbor (NSF 1046121); Charles F. Delwiche, University of Maryland College Park (NSF 1046075); Todd H. Oakley, University of California Santa Barbara (NSF 1046307)

Cardinale and colleagues will examine how evolutionary processes among algae generate and maintain diversity at levels from genes to ecosystems in freshwater lakes.

Understanding how biodiversity loss will impact the productivity and sustainability of Earth's natural ecosystems is a primary goal of modern science. The goal of this project is to identify and predict which extinction events are likely to have the greatest impacts on *primary production*, the process by which plants capture sunlight and use atmospheric CO₂ to produce energy at the base of the food web.

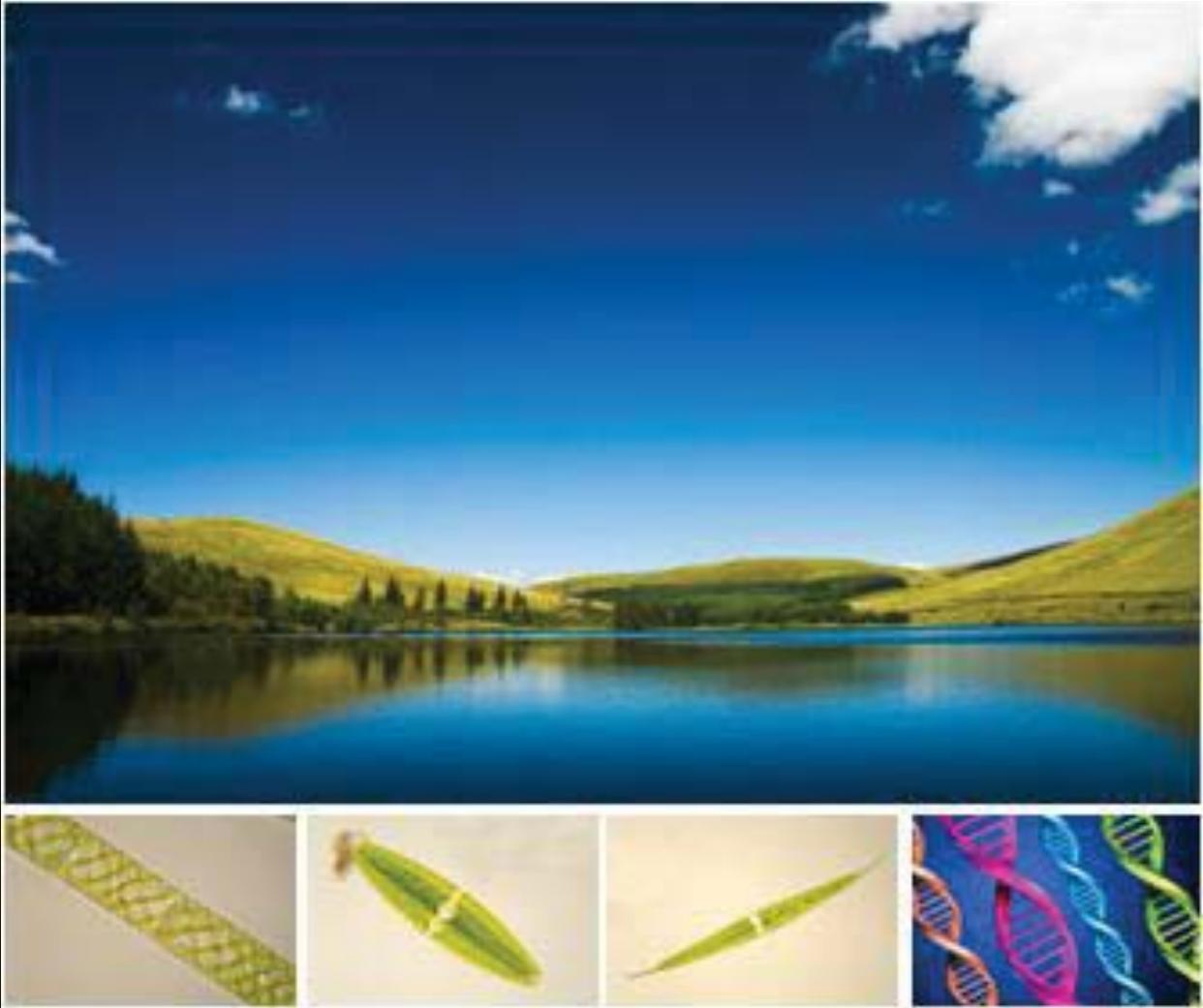
These researchers hypothesize that the impacts of species extinction on primary production can be predicted if one knows the evolutionary relationships among species. They propose that evolution has led to a functional 'division of labor' that determines how efficiently groups of plants capture essential resources like nutrients or light. If evolution leads to species that are genetically unique, and ecologically irreplaceable, then we should be able to use our understanding of evolution to predict which species losses will have the greatest impacts on processes like primary production.

This project includes experts in genomics, phylogenetics, and ecology integrating research efforts to understand how one of the most widespread and ecologically important groups of algae controls the productivity of lakes throughout North America. The investigators will use molecular data to determine whether communities of algae that live together are more genetically diverse than one would expect by random chance. Then they will artificially create lakes of algae where the species differ in

their evolutionary history, and therefore, their levels of genetic divergence. This will allow them to directly measure how evolutionary and genetic differences control the functional differences among species and, in turn, how these functional differences influence primary production. Finally, they will identify genes that allow species to use biologically essential resources in different ways and determine which genes are turned 'on' and 'off' as species try to survive when in competition with each another.

The findings of this work will help prioritize conservation efforts by identifying species that have the largest impacts on important ecological processes. This research will also provide an underpinning for conservation prioritization in ecosystems that are too large (rain forests), too remote (the ocean floor), or too endangered (threatened species) to perform biodiversity experiments.

This project will include participation by a variety of students, ranging from high school interns, to Ph.D. students, to postdoctoral fellows. These individuals will be trained in an exciting new area of research that merges genetics and evolution to understand modern environmental problems. The project also will develop a new college-level course that integrates genomics, phylogenetics and ecology. This course will provide our next generation of researchers with the ability to address environmental problems with tools from the level of genes to whole ecosystems.



The investigators will use three approaches to identify and predict which extinction events are likely to have the greatest impacts on primary production in lake communities: (1) an evolutionary approach that determines whether genes are phylogenetically conserved for natural species assemblages, (2) a genomic approach that determines whether conservation of genes translates to unique ecological niches among species, and (3) an ecological approach that determines whether niche differences impact the productivity of entire communities.

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 will support research to understand how the taxonomic diversity of soil fungi interacts with the genetic diversity of two tree species.

Climates are currently warming at unprecedented rates. In order to avoid extinction, species must move to track the changing climate, or evolve to tolerate warmer conditions. Researchers have predicted that many eastern forest tree species will shift their ranges considerably as climates warm, by expanding to the north or up in elevation, and contracting from the south or down to lower elevations. Long-term data from the eastern US has already shown the beginning stages of this range movement for some species. However, these predictions are based on very simplified models that do not consider how interactions among species may constrain or promote a given tree species' ability to expand its range. Most plant species, especially forest trees, rely on intimate associations with microbial species living in soil in order capture the resources they need for proper growth. Little is known about how these invisible, but very important, soil microbes are distributed across the continent, and how they will respond to climate change. This basic knowledge on the geographic distribution of these soil microbes will be important to predict how well tree species will be able to track their moving climates. For instance, if a tree species shifts north 100 kilometers to maintain its current climate conditions, will it be encountering a completely different soil microbial community? Or will some of its preferred microbial partners already be present in that new area? Additionally, there is currently very little known about the climatic

tolerances of important soil microbial groups. As climates warm, will they also shift their ranges? Or are they so broadly distributed already that the predicted rates of climate warming will exert little pressure on them?

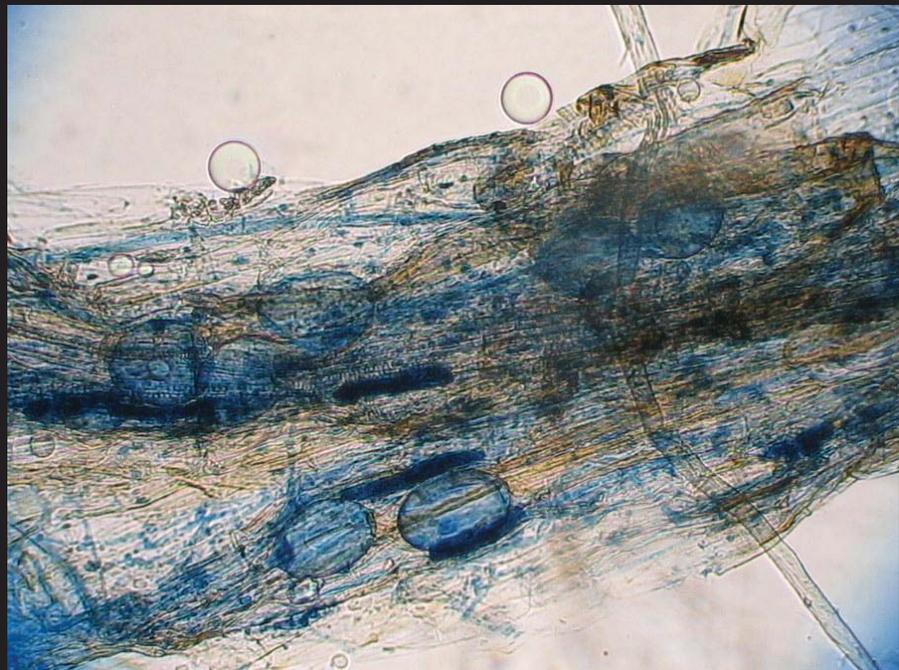
In this project soil microbial sampling will provide basic information on how these microbes are distributed as well as how their distribution relates to current climates and genetic structure of the tree species. Trees and soil microbes will likely not move at equal speeds as climates change. For instance, if these microbes are not able to disperse as quickly as their host tree species, then this may constrain the tree's ability to migrate north (as it will have to wait for its microbial associates to catch up). Therefore, experiments will test the functional consequences for tree growth for situations where microbial species migrate faster than trees, or vice versa. This research will allow for more precise predictions about how forests will change as climates warm.

This research will involve citizen scientists from across the eastern US in collecting samples for the soil survey. Several undergraduate students will also be involved in performing the research. Finally, by helping to improve our ability to predict ecological changes in response to climate change, this research will increase our ability to mitigate and adapt to the undesirable consequences of a rapidly warming world.



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

Below: Arbuscular mycorrhizal fungi colonizing a sycamore (*Platanus occidentalis*) root. Thin blue lines are hyphae, blue ovals are vesicles (storage structures), and dark blue rectangles are arbuscles, the site of nutrient exchange between the plant and fungus. Plants and mycorrhizal fungi have a mutualistic relationship, in which the plant provides sugars to the fungus in exchange for soil nutrients (especially phosphorous).



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 at Baltimore (NSF 1046371)

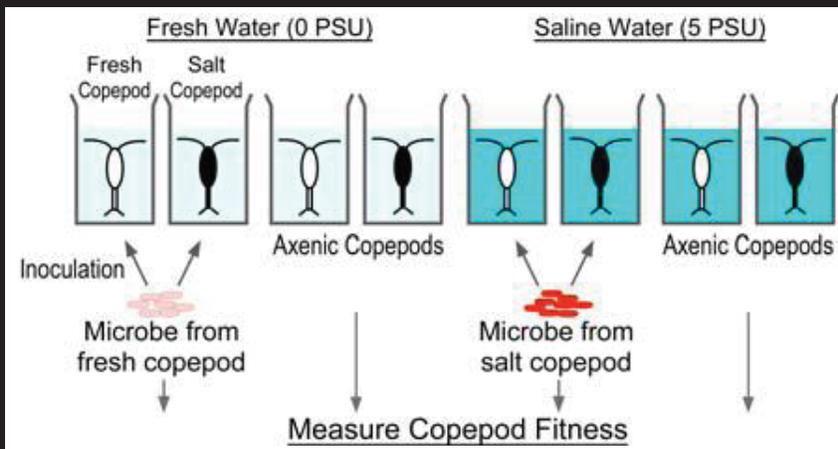
This project characterizes diversity and metabolic functions of the microbiome of a copepod, and will test how the diversity and functions (metabolic and ecological) change when the saline copepod invades a novel habitat (fresh water).

Copepods form the largest biomass of metazoans on the planet, yet their microbiota remain largely unexplored. The microbial community associated with copepods might perform key metabolic processes that affect host fitness and ecosystem functioning. The copepod *Eurytemora affinis* is dominant in coastal habitats throughout the world, and recently has invaded inland freshwater habitats. Associated with *E. affinis*, preliminary sequencing revealed high diversity of microbial taxa, including many undescribed genera and families. There also were parallel shifts in microbial composition during independent invasions from saline to freshwater habitats. Yet, a core set of microbial taxa remained present in all copepod populations across all locations. The copepod microbiome is likely to play fundamental roles in biogeochemical processes in many aquatic ecosystems. Microbial-host interactions could influence invasive success, and exotic microbes in the invading consortia could have vital impacts on the invaded community. This study will address the taxonomic composition of the copepod microbiome, and how it shifts during habitat invasions; the metabolic functions performed by the copepod microbiome; and the nature of copepod host-microbial interactions, and how these interactions shift during invasions. Preliminary sequencing of the *E. affinis*

microbiome uncovered a wide variety of potentially pathogenic taxa, including *Salmonella*, *Shigella*, *Campylobacter*, *Corynebacterium diphtheriae*, *Yersinia*, and *Vibrio cholerae*. Thus, *E. affinis* might play an important role as a reservoir and vector of waterborne disease. This collaborative research will be promoted through workshops that integrate diverse perspectives across fields, such as microbial ecology, disease ecology, ecosystem ecology, and evolutionary biology. The project will also involve an internship program for underrepresented students to partake in genomic data analysis and an annual public symposium on applied evolution, including a teacher-training workshop at the high school level. This project will support one postdoc, and up to two graduate and three undergraduate students per year, including those from underrepresented backgrounds.

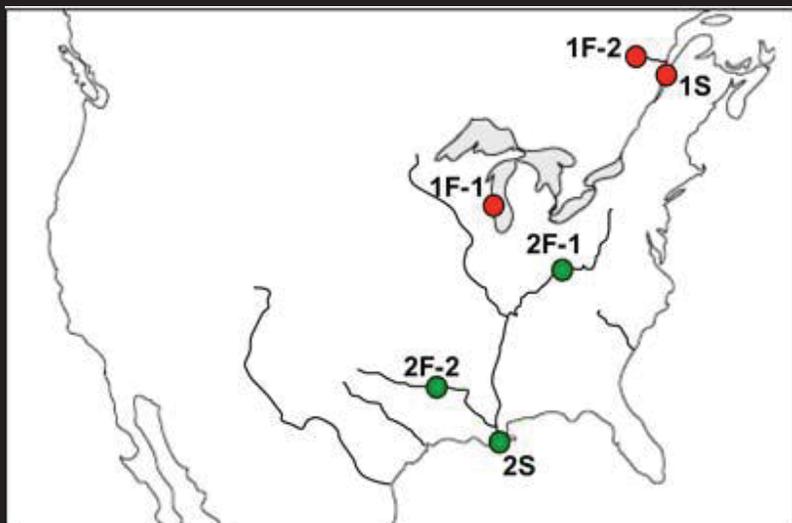
This study will provide integrated insights into the taxonomic, genetic, and functional diversity of the copepod microbiome. The assembled sequences will link specific metabolic functions with particular microbial taxa, illuminating functional diversity across deeply divergent lineages. Sequence data also will reveal genetic diversity of metabolic functions within microbial taxa, and the potential sharing of functions across taxa (e.g. via horizontal gene transfer).

Right: The coastal copepod *Eurytemora affinis*. This copepod is a dominant grazer of algae and a major food source for some of the world's most important fisheries, such as herring, anchovy, salmon, and flounder.



Left: A factorial test of copepod response to microbes. The scientists will measure copepod host fitness (e.g. egg production, development time, survival) in response to the microbes relative to axenic conditions.

Right: Population sampling of *Eurytemora affinis* for the preliminary study and proposed research. Sampling includes saline and freshwater populations, from two genetically distinct clades (red, green). Sampling captures independent invasions from saline into freshwater habitats.



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

Francois Lutzoni, Duke University (NSF 1046065); Anne Arnold, University of Arizona (NSF 1045766); Ignazio Carbone, North Carolina State University (NSF 1046167); Georgiana May, University of Minnesota, Twin Cities (NSF 1045608)

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

Although the global diversity of fungi is estimated to far exceed 1,500,000 species, mycologists have described only about 100,000 species so far. The disparity largely reflects an immense but invisible richness that is hidden within other organisms through symbiosis. Symbioses drive genome evolution, ecological diversification, and speciation, thereby shaping all dimensions of the diversity of life. The goal of this project is to study one of the planet's most prevalent but least-understood symbioses: that of *endophytic fungi* (*endophytes*), which occur within healthy above-ground tissues of all plants in biomes ranging from tropical rainforests to Arctic tundra.

Endophytes comprise as many as 1 million species, less than 1% of which have been described to date. They have been found in every plant and lichen species, including wild-, crop- and forage plants, and their communities often change markedly across hosts' geographic ranges. Endophytes produce metabolites of use in agriculture, medicine, and industry, and can provide defense against pests and pathogens, and tolerance to heat and drought. Endophytes peak in phylogenetic diversity in boreal forests, an ecosystem of immense global importance and one in which their ecological associations, genetic diversity, and functional roles are largely unknown.

The goal of this project is to develop a

biodiversity-informatics pipeline to describe the taxonomic, functional, and genetic diversity of endophytes at multiple scales. As a result, the scale of endophyte biodiversity will be unveiled for the world's largest biome, transformative taxonomic practices to capture unknown diversity will be established, new and useful model systems for functional and genetic studies will be developed, biological functions of endophytes will be tested systematically through experimental work, and the mechanisms underlying the genetic and functional diversity of these hyperdiverse symbionts will be elucidated.

Every component of this proposal, including the core hypotheses driving it, resulted from fusion of the complementary strengths of the PI team and an international network of collaborators in taxonomic, genetic, and functional biology. The result is an exquisite opportunity to address ecological, evolutionary, and mechanistic questions in a synthetic manner far exceeding the scope of any individual lab. Innovative training of STEM teachers, high school, undergraduate, and graduate students, and postdoctoral fellows both locally and abroad will contribute to a broader understanding and appreciation of the boreal biome, the roles of cryptic fungal symbionts, and the scope and importance of Earth's undiscovered biodiversity.



A. Elizabeth Arnold

Above right: Lichens (here, *Peltigera leucophlebia*) growing in close association with plants (*Empetrum nigrum*, *Pleurozium schreberi*, *Polytrichum* sp., and *Hylocomium splendens*) in a boreal forest community.

Above left: Axenic cultures of a rich array of symbiotrophic fungi from these lichens and plants, including endophytes (from asymptomatic plant tissue) and endolichenic fungi (associated with lichen photobionts inside healthy lichen thalli)

Together these highly diverse fungal communities provide clues to the evolution of major trophic modes in the Ascomycota, the most species rich phylum of Fungi.

Biological controls in the ocean: The Redfield Ratio

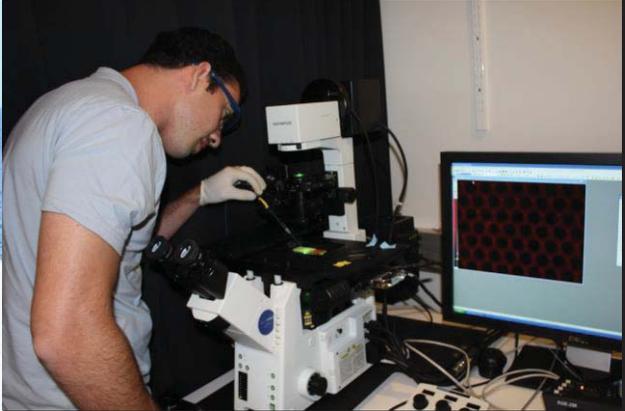
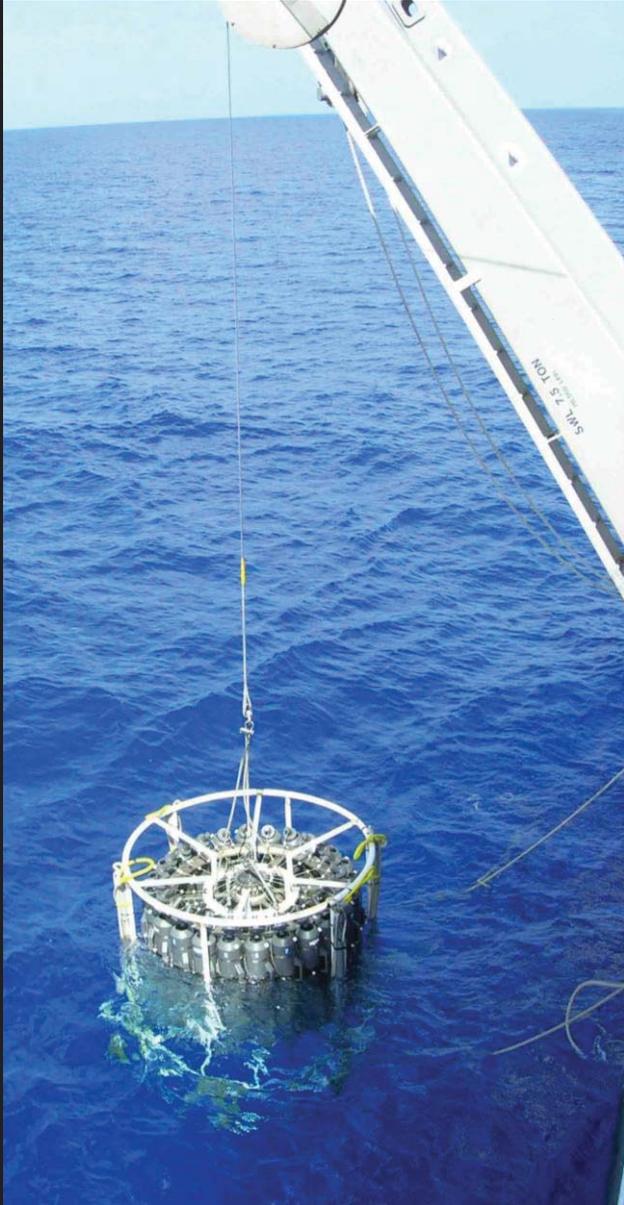
Adam Martiny and Steven Allison, University of California Irvine (NSF 1046297); Simon Levin, Princeton University (NSF 1046001); Michael Lomas and Benjamin Van Mooy, Bermuda Institute of Ocean Sciences (NSF 1045966); and Kun Zhang, University of California San Diego (NSF 1046368)

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.

Decades ago, Alfred Redfield observed that the ratio of nitrogen-to-phosphorous in ocean surface plankton matched the ratio of dissolved nitrogen-to-phosphorous in the deep ocean. Furthermore, this ratio was constant all over the ocean. Redfield proposed that the hydrolysis of sinking surface particles controlled the deep ocean chemistry and this hypothesis remains a central tenet for our understanding of ocean biogeochemistry. There is, however, substantial elemental variation among plankton species as well as communities in different ocean regions. This led the investigators to propose that the biodiversity of ocean plankton regulates the elemental composition of the ocean and differences in biodiversity can lead to substantial deviations in the nitrogen-to-phosphorous ratio.

This project will measure the *in situ* elemental composition of abundant plankton lineages in different ocean regions. The investigators will apply a novel technique combining fluorescence activated cell sorting

with high-sensitivity elemental analysis to achieve this. Simultaneously, they will identify variations in biodiversity using next-generation high-throughput sequencing technologies and single-cell genome sequencing. Finally, a series of controlled laboratory experiments will be used to delineate specific effects of environmental variation versus changes in biodiversity on the elemental composition of a plankton community. The researchers aim to understand how ocean taxonomic (i.e. different lineages), genetic (difference in genome content within a lineage), and functional (i.e. ability to use particular food sources) biodiversity integrate to control chemical composition of the ocean. Beyond significantly advancing our basic understanding of biodiversity, the study will also provide important new information of how ocean plankton can control major nutrient cycles.



Above: A student from co PI K. Zhang's laboratory using a microfluidic chip to amplify and pick single cell genomes

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

Below left: Members of PI A. Martiny and co-PI S. Allison laboratories at the sampling site at Newport Pier, California

Below right: Co-PI Lomas participates in the outreach program "crush-a cup" aboard the R/V *Atlantic Explorer*



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

Nancy Moran, Yale University; and Jay Evans, USDA ARS (NSF 1046153)

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

All animals live in close association with microbes, primarily bacteria, and the large majority of these bacteria are not associated with disease. The gut is especially rich in diverse lineages and species of bacteria. These have been studied in only a few host species, in which they have been shown to benefit particular hosts by assisting with digestion of food, provisioning essential nutrients, and enhancing defenses against pathogens. The diversity and functional roles of gut microbiota are almost entirely unknown for most species. Also, little is known of how environmental change impacts gut bacteria and consequently the hosts themselves.

The focus of this project is the diversity, functional roles, and genetic diversity of bacteria living in the guts of honey bees and bumble bees. As dominant pollinators, these insects are critical players in terrestrial ecosystems, including agricultural systems. Furthermore both honey bees and bumble bees have experienced population declines in recent years, and better understanding of their basic biology and of the impact of environmental change is essential to addressing these declines.

The honey bee is a single species introduced nearly world-wide for the production of honey and for pollination of crops. Worldwide, honey bee adults contain a distinctive set of bacterial types in their guts, and bumble bees contain some related bacterial

species. Using the latest technology, the genome sequences of these bacteria will be obtained and analyzed to characterize their metabolic capabilities and their potential functions in hosts. Further experiments will measure the impact of bacterial presence on the health of honey bees. The impact of environmental variation on the diversity and composition of the microbiota will be assessed by using high throughput DNA sequencing to compare microbiota from honey bees worldwide, and from selected species of bumble bees in North America and in China, the regions with the highest bumble bee diversity globally. In particular, the impact of different human-mediated changes will be assessed by comparing the gut microbiota of bees from agricultural and other sites with different management practices.

By analyzing these impacts in the context of knowledge of the functional roles of these bacteria, possible linkages between anthropogenic environmental changes and the health of bee populations will be assessed. Because the work combines methods from genomics, experimental biology and ecology, the research team is interdisciplinary and includes scientists from both academic institutions and government agencies. This research will be integrated into a high school science education program, organized by the Yale Peabody Museum for New Haven students.



Jay Evans, USDA



Waldan Kwong, Yale University

Far left: Honeybee workers on the hive (*Apis mellifera*)

Left: Honey bee queen being tended by her workers on the comb



N. Moran



Nancy Moran, Yale University

Right: Common eastern bumblebee, *Bombus impatiens*, on aster

Far right: Sonoran bumblebee, *Bombus sonorus*, on hibiscus



Kim Hammond, Yale University

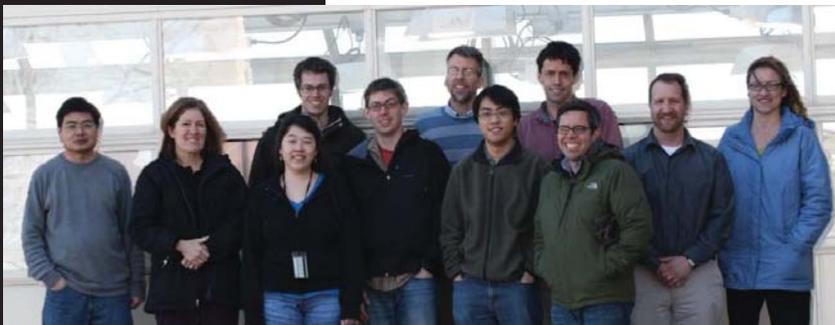
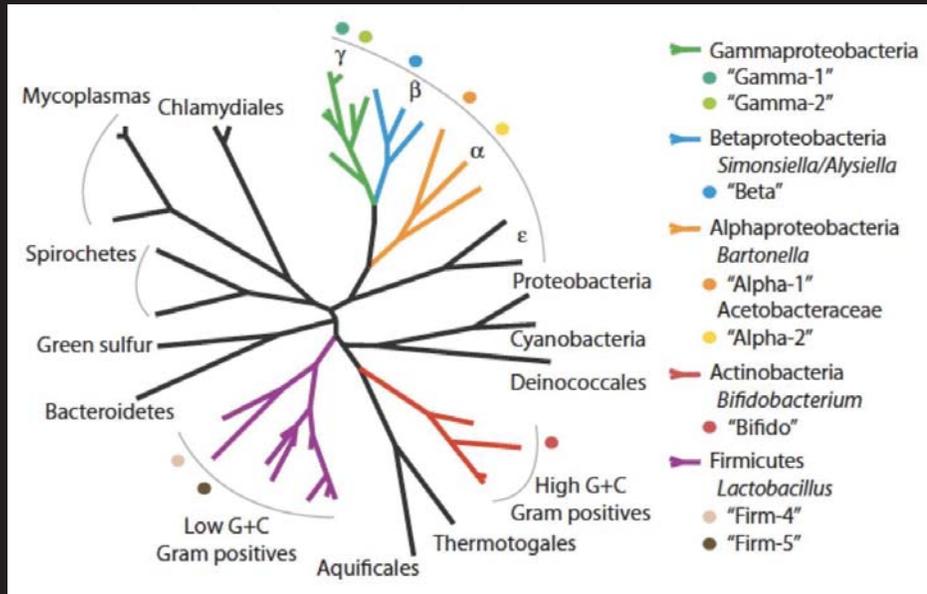
Left: Graduate students netting honey bees in order to sample the bee gut microbiota



K. Hammond

Right: Researchers removing bee pupae from comb in the laboratory

Right: Relationships of bacteria known to live in honey bees



N. Moran

Vince Martinson, University of Arizona

Left: Bee microbiota researchers at planning meeting in New Haven Connecticut

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

N. Leroy Poff, William C. Funk, Cameron Ghalambor, and Boris Kondratieff, Colorado State University (NSF 1046408); Alexander Flecker, Joseph Bernardo, and Kelly Zamudio, Cornell University (NSF 1045960); and 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 will examine the influence of climate change on stream biodiversity in a tropical stream system in the Andes of Ecuador and a temperate alpine stream system in the Colorado Rockies.

Predicting the consequences of rapid climate change on biodiversity loss and ecosystem function is an urgent scientific challenge. Species responses will reflect both the magnitude of environmental change and their relative sensitivity to that change. In this project the investigators will develop a new conceptual framework that integrates evolutionary, ecological, and physiological perspectives, unifies disconnected themes of biodiversity theory, and experimentally quantifies mechanisms of species vulnerability and ecosystem sensitivity to warming and increased variation in precipitation. The research will take place in small streams that occur along a broad elevational gradient in the Colorado Rockies and the Ecuadorian Andes.

Theory predicts tropical stream species (aquatic insects, frogs, and fish) should be more sensitive to a unit increase in warming than temperate species because tropical species have evolved in thermally stable habitats. As climate warms, species will either need to move to higher elevations, and/or exhibit physiological adjustments to tolerate changing environmental conditions. Species vulnerability to rapid climate change will reflect a complex interplay of physiological response to warming, capacity to disperse to favorable habitats and ecological sensitivity to modified disturbance

and ecosystem processes. To test predictions arising from these interactions, the investigators will use genetic techniques to discover new species and assess their ability to move between streams as climate changes; physiological techniques to experimentally measure tolerance of species to warming and reduced oxygen; and ecological experiments that conduct whole system manipulations of disturbance regimes and oxygen levels in sensitive alpine streams.

This study will provide a novel, integrative model for predicting species and stream ecosystem responses to climate shifts. It will advance fundamental knowledge of tropical stream diversity required to understand vulnerability of these systems to rapid climate change relative to mid-latitude temperate streams. By combining results from field surveys and experiments with projected future scenarios of temperature and precipitation change, this study will be the first to map spatial variation in stream species and ecosystem vulnerability across latitude and elevation gradients in multiple taxonomic groups (aquatic insects, frogs, and fish) and thus will be highly relevant to policy makers concerned with freshwater biodiversity conservation and sustainable water management.



Left: A waterfall and stream located near the Mindo Biological Station at about 1700 m (Pacific versant of the Ecuadorian Andes)



Right: Investigators Ghalambor and Poff investigate the contents of a Hess sample while scouting creeks in Ecuador

Below right: *Nymphargus wileyi*, a holotype of a new species of centrolenid (glass frogs) that PIs discovered & described at Yanayacu Biological Station at ~2000 m (Amazonian versant of the Ecuadorian Andes)

Below left: A transect is laid along a creek at one of the Colorado Bioblitz sites

Below center: PhD student, Brian Gill searches his aerial net for adult aquatic insects at a high elevation site in the Colorado Rockies

Right: A vial of stoneflies collected at 3400m in the Colorado Rockies



Below: US investigators and Ecuadorian collaborators in Ecuador, March 2011



All Images: W. Chris Funk, Colorado State University

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

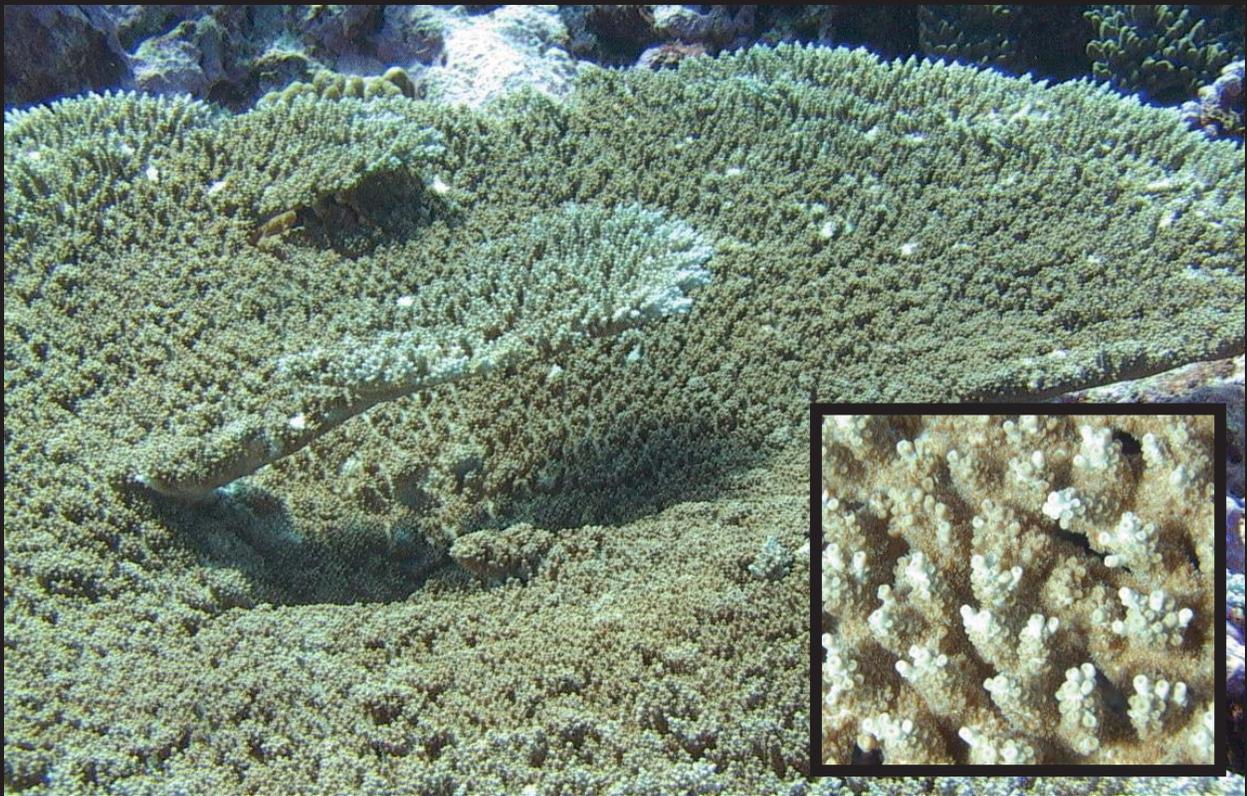
Forest Rohwer, Robert A. Edwards, and Anca Segall, San Diego State University (NSF 1046413)

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

Viruses are the most abundant, most diverse, and least understood biological entities on Earth. It is very likely that the most common organism on the planet is a virus that is currently unknown to science. Because viruses reproduce within a host cell, they can have enormous impacts on the well being of the host and possess genes that are integral to the host's ability to carry out important biological functions, such as photosynthesis in marine environments. A major goal of this research project is to develop novel high-throughput methods to rapidly reveal and characterize the diversity of this biological "dark matter". First, the size of the global viral gene pool will be determined by analyzing viral DNAs from the world's major biomes. The work will then focus on the viruses of coral reefs by examining the

most abundant viral proteins and determining their functions using genetics and protein structures. Combined and integrated, these approaches will address the genetic, functional, and taxonomic dimensions of viral biodiversity.

Discoveries stemming from the study of viruses have been at the forefront of many breakthroughs in biological research. Values to society from this specific work will include more comprehensive knowledge of global viral biodiversity and of the role of viruses in the health of coral reefs—valuable ecosystems that are under considerable stress due to climate change and other human activities. It is expected that this research will improve our fundamental understanding of the interactions of viruses, human activities, and the biodiversity of the planet.



Coral reefs are among the most complex and diverse biological systems on Earth. Dr. Rohwer's lab uses metagenomics to study the microbial and viral communities inhabiting coral reefs.

Above: *Acropora* sp. with closeup of polyps (inset)

Below: Dr. Rohwer sampling corals



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

Carl Schlichting, Kent Holsinger, Cynthia Jones, and John Silander, University of Connecticut (NSF 1046328); Andrew Latimer, University of California Davis (NSF 1045985); Justin Borevitz, University of Chicago (NSF 1046251)

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

Rapidly changing climate will drive dynamic responses at all levels of biodiversity, from the traits of individuals to distributions of species and biomes. Current approaches to predicting such responses are based on static assessments, e.g., what is a species' current ecological envelope and where will that range of conditions occur in the future? This project will expand the information used for evaluating such responses to include: a) relationships between species' attributes that affect their function in a given environment (functional traits), b) genetic variation underlying those functional traits, and c) the dynamics of the communities of which they are part. The investigators also suggest that studies of clades that have evolved and flourished through dramatic historical climate change may be able to provide significant information about the evolution of functional traits and the potential for further adaptive evolution.

Southern Africa possesses higher plant diversity than most tropical regions, yet much of this diversity stems from radiations in just 30 major lineages. This research will focus on two highly successful plant genera, *Protea* (112 spp) and *Pelargonium* (280 spp), that have diversified over the past 15 MY in response to, or in spite of, radical (and at times rapid) changes in the climate of southern Africa. These genera span two biodiversity hot spots, the

fynbos and succulent karoo biomes in the Greater Cape Floristic Region (GCFR). Over 65% of GCFR plant species are endemic, an extraordinary level for a continental region.

The goal is to develop an understanding of variation of functional traits (e.g. leaf size and shape, leaf longevity, photosynthesis, and water use) in both genetic and evolutionary contexts in *Protea* and *Pelargonium* at intraspecific and community levels. This will allow the investigators to predict the characteristics of communities in which they occur and the resilience of those communities to climate change.

This integrated team has expertise in a wide range of ecological and botanical disciplines and the project will expose post docs, grad students, undergrads and high school students to international research, including students actively recruited from underserved populations both in the US and South Africa. The project will host annual methods workshops and actively enhance conservation infrastructure by working closely in all aspects of the project with the South African National Botanical Institute (SANBI) which has one of the best track records in the world in promoting biodiversity science, policy and conservation action.

Proteas, the national flower of South Africa, are key inhabitants of the Fynbos biome, a Mediterranean shrubland of southwestern South Africa. Fynbos is critically threatened by climate change.



Jane E. Carlson, University of Connecticut



J.E. Carlson



J.E. Carlson

Left: *Protea aurea*, Blesberg, Western Cape Province, South Africa

Above center: *Protea cyanaroides*

Above right: *Protea venusta*

Pelargoniums are the ancestors of cultivated 'geraniums'. These plants are marked by their diversity in growth form, leaf shape and flower types



Carl D. Schlichting, U.of Connecticut



Cynthia S Jones, U.of Connecticut



C.D. Schlichting

Far left: *Pelargonium crithmifolium*

Center left: *Pelargonium exhibens*

Left: *Pelargonium peltatum*



C.D. Schlichting

Left: *Pelargonium sericifolium*

Right: Fieldwork in South Africa with bontebok (*Damaliscus pygargus pygargus*)



C.S. Jones

Significance of nitrification in shaping planktonic biodiversity in the ocean

David Stahl, E. Virginia Armbrust, Allan Devol, and Anitra Ingalls, University of Washington (NSF 1046017); James Moffett, University of Southern California (NSF 1046098)

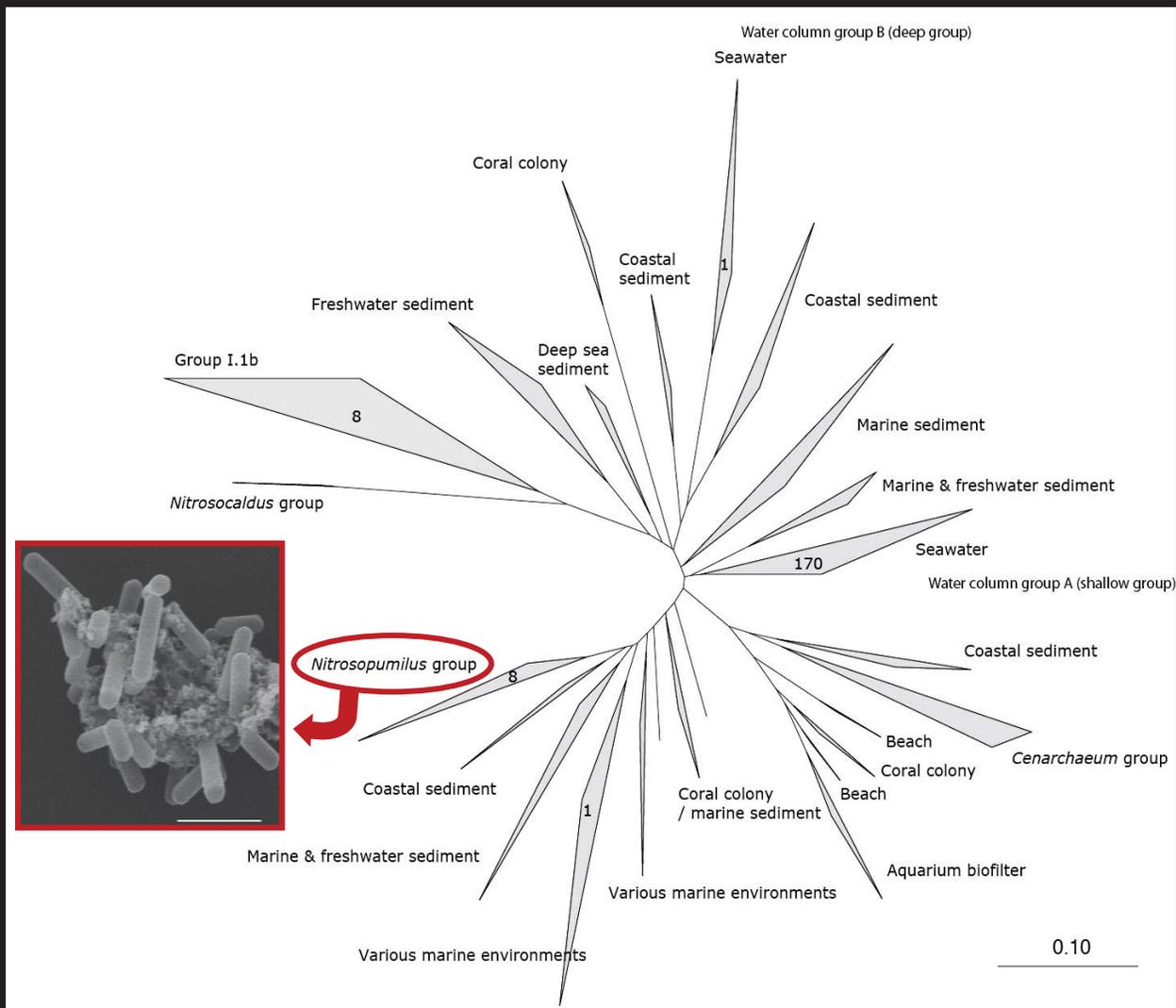
This project examines the diversity and function of ammonia oxidizing Archaea in the ocean and the role of these newly discovered organisms in structuring the diversity of phytoplankton.

Microorganisms sustain the biogeochemical cycling of nitrogen, one of the most important nutrient cycles on earth. This nutrient cycle has been profoundly altered by agriculture and industry, together greatly increasing biologically available nitrogen with uncertain impacts on terrestrial and marine systems. A key step in the nitrogen cycle, the microbial oxidation of ammonia to nitrite, was for a century thought mediated by a few genera of bacteria. It is now known that much, if not most, ammonia oxidation is due to the activities of a group of microorganisms affiliated with the *Archaea*.

The single-celled *Archaea* are one of three primary evolutionary lineages on earth—bacteria and eukaryotes comprising the other two lineages. Although *Archaea* are highly abundant in the oceans, they have only recently been directly associated with a fundamental biogeochemical process: nitrification, the oxidation of ammonia (released primarily through decay of other organisms) to nitrite and nitrate. Prior analyses of marine ammonia-oxidizing *Archaea* (AOA) has shown that AOA are active within the marine photic zone and that their high abundance is in part attributable to an extremely high affinity for ammonia. The AOA can sustain near maximum growth rates at a concentration of ammonia equivalent to 1 teaspoon of ammonia diluted into 50,000 gallons of water. The compelling inference is that AOA may control the forms of nitrogen available to other microbes within the photic zone by converting ammonia, a nearly universally available form of nitrogen, into nitrite, a form only available to nitrite oxidizing

bacteria and some phytoplankton. In addition to their ability to deprive other marine organisms of ammonia, genetic analyses point to an unusual copper-based system of respiration that may render them more competitive in iron limited environments. The implication is that AOA have a significant impact on marine biodiversity, primary production, and the release of atmospherically active gasses such as nitrous oxide.

The project encompasses and integrates the three dimensions (functional, genetic, and taxonomic) of biodiversity. The project is framed by function: microbial control of the nitrogen-cycle. It is motivated by recent genetic analyses that associate activities of a novel clade of *Archaea* with control of ammonia oxidation in the ocean. It is built upon a compelling synthesis of physiological and environmental data that lead to its central hypothesis—that by altering and possibly controlling the form of nitrogen, the AOA also alter biodiversity and ecological function in one of the most productive environments on earth. It addresses a specific taxonomic imperative. The tremendous genetic diversity among the globally abundant AOA—catalogued almost exclusively by gene sequencing surveys and therefore lacking formal description—makes it essential to resolve membership into ecologically relevant groups or clades as a prelude to developing a formal taxonomy. Outreach programs will enhance understanding among students and teachers of the role of microorganisms in global elemental cycles such as the N cycle.



Above: Diversity of ammonia oxidizing archaea inferred by sequencing a gene (*amoA*) required for the oxidation of ammonia

Inset above: Scanning electron micrograph of *Nitrosopumilus maritimus*, the first marine ammonia oxidizing archaeon isolated in pure culture; Scale bar = 1 μ m

Right: Deployment of instrumentation for analysis of the microbial and chemical structure of Hood Canal (Washington State), one of the field sites for the research project



All images: David A. Stahl, University of Washington

The role of viruses in structuring biodiversity in methanotrophic marine ecosystems

David Valentine, University of California, Santa Barbara (NSF 1046144)

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

Methane (CH₄) is a potent greenhouse gas. Ounce for ounce, over a hundred years, atmospheric methane will cause about 25 times as much global warming as carbon dioxide. About 550 teragrams (Tg) of methane enters the atmosphere each year—but without microbes, that number could be much higher. Some 85–310 Tg of methane is naturally produced beneath the world's oceans each year, and communities of methane-eating (“methanotrophic”) microbes on the ocean floor consume all but about 10 Tg of it. By keeping so much methane from entering the atmosphere, these communities play an essential role in regulating global climate. And we know almost nothing about them.

What little we do know about these microbes explains why it has been so difficult to learn more. We know that they live on and in seafloor sediments, which complicates long-term observations. We know that they live an energy-starved life and this makes them grow very slowly, so they are particularly hard to culture for study onshore. We know that, while the oxygen-using (aerobic) methanotrophs from the shallow sediments are self-sufficient bacteria, the deeper, anaerobic methanotrophs are archaea that live in such close partnership with other microbes that they cannot be isolated and studied alone.

We also know that both the aerobic and the anaerobic microbial communities host huge viral communities—some ten times more viruses than hosts. The prediction that this project will test is that these viruses, as agents

of mortality and genetic transformation, fundamentally shape the biodiversity of the microbial methanotrophic communities. The research will address which microbes are merely present, and which actively consume methane; how diverse the active consumers are; whether the latent methanotrophs were once active; which viruses infect the active methanotrophs; whether viruses carry pirated microbial gene sequences, and whether these sequences have gotten shuffled back into the genomes of active methanotrophs; and how many viruses attack the active and latent methanotrophs. The investigators will use stable isotope probing (SIP) to acquire four separate pools of DNA fragments—from active methanotrophs, other microbes, viruses of active methanotrophs, and other viruses—and new sequencing technologies will be applied to these pools to learn which organisms and which genes are represented in each pool, whether host genes turn up in the viral pools, and how the pools differ in biodiversity. The researchers can also pick out intriguing individual cells and sequence their entire genomes. Comparing these individuals to the microbial communities they come from and the viral communities that preyed on them will provide an additional window into the community's history of genetic transfer and viral predation. Analyzing these data across different methanotrophic communities will tell us whether and how viruses influence the biodiversity of these essential microbes.

Below: Immense communities of methanotrophic microbes carpet the seafloor sediment at sites of natural methane seepage. Orange and white microbial mats grow at the Southwest Mounds, 900 m deep in the Santa Monica Basin off Los Angeles. Scale bar = ~1m



Oscar Pizarro, University of Sydney



Blair Paul, Univ. of Cal., Santa Barbara

Left: Epifluorescence microscopy shows viruses (green pinpoints) greatly outnumber bacteria (large spots) in a methanotrophic mat off Santa Barbara.

Right: ROV Jason 2 is lowered with a payload of incubators and instruments to sample local biogeochemistry at the experiment's beginning.



David Valentine, UC, Santa Barbara

Right: Side, bottom, and top views of aerobic methanotroph incubators. Incubators contain grids that support the growth of microbial mats (see below).



D. Valentine

Below: An incubator is deployed at the Southwest Mounds site, on the SEEPS September 2011 cruise (AT18-11). The top cap of the incubator will be left wide during initial deployment, allowing a natural community to develop. After two years the cap will be dropped, sealed in place, and injected with labeled methane for the *in situ* stable isotope probing (SIP) phase of the experiment. Several days later, the incubators will be brought to the surface for analysis.



D. Valentine

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

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

Waller and colleagues will examine the functional traits, phylogenetic relationships, geographic distributions, and patterns of genetic variation in native and introduced plants in Wisconsin forests and grasslands.

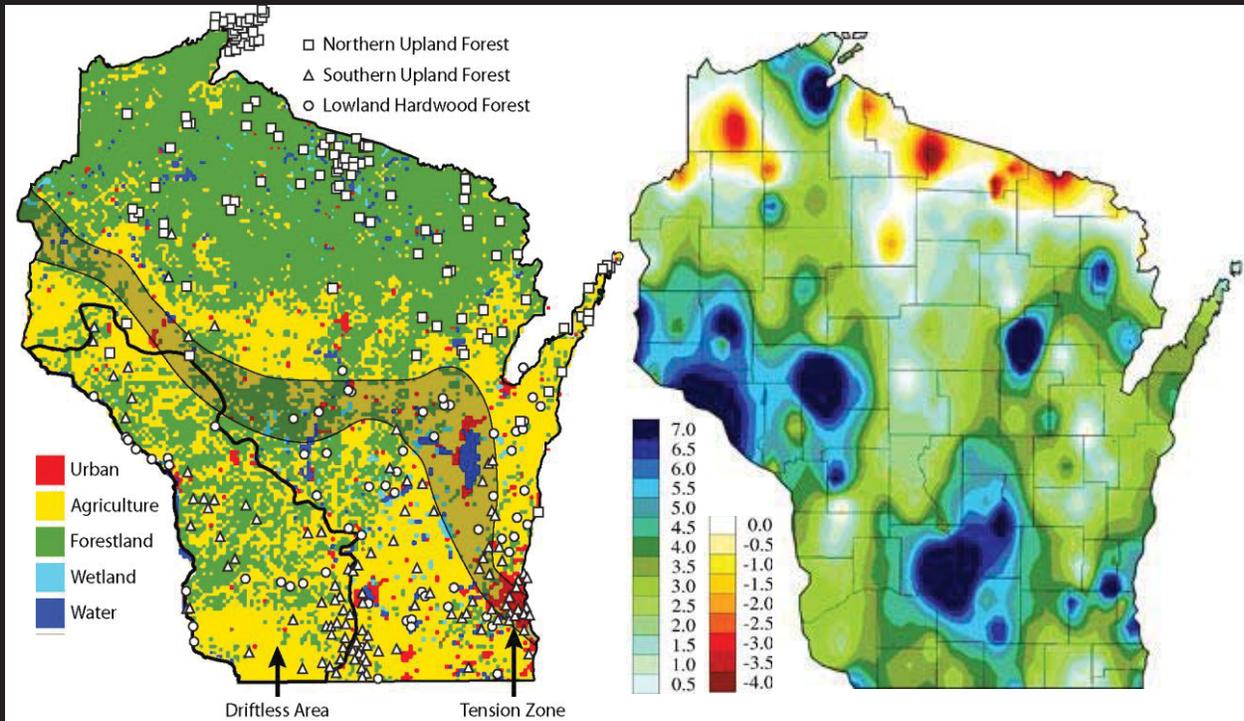
Shifts in the biodiversity of forests and prairies can often be tagged to changes like expanded numbers of browsing animals, invasions of exotic species, the loss and fragmentation of habitat, and accelerating climate change.

In this project, the researchers will examine the functional traits, phylogenetic relationships, geographic distributions, and patterns of genetic variation in native and introduced plants occupying Wisconsin forests and grasslands. The project team seeks to determine trait evolution and community assembly in Wisconsin forests and grasslands; loss of native species and invasions by exotics over the past 50 years; and expected shifts in species distributions and community composition over the next 50 years related to climate and habitat change.

The research emphasizes how phylogeny influences the distribution of functional traits; how traits interact with sites to sort species among habitats; how traits interact with climate to influence present and future geographic ranges; and the extent to which population persistence reflects genetic variation, gene flow, dispersal, genome size, functional traits, and landscape conditions.

Key to this project is the work UW-Madison ecologist John Curtis and his students began in the 1940s, surveying sites throughout Wisconsin. This team has re-surveyed more than 350 forest and prairie plots, providing an exceptionally detailed picture of ecological change and ensuring that both spatial and temporal components are included in the project. The researchers are using genetic bar-coding — sequencing several key genes — to construct a phylogenetic ('family') tree for all 2,500 native and introduced plant species growing in Wisconsin. The tree will contribute to a wider "tree of life" for all North American plants and give the Wisconsin team a tool to analyze how phylogeny and diverging physical characteristics affect the distributions of plant species over sites. Several hundred species are being scored on up to 50 significant traits, allowing the researchers to judge their relative importance in determining plant distributions and changes in abundance.

Better understanding of patterns of genetic variation will help ecologists judge population vulnerability to further changes in landscapes and climate. Three of the world's major biomes will be included in the research: deciduous forests, prairies, and coniferous forests.



Driftless Area Tension Zone
Donald Waller, Univ. of Wisconsin, Madison

From public domain via data visualization

Above: Map of the Wisconsin J.T. Curtis forest sites that have already been re surveyed by the team

Above: Change in precipitation (inches) in Wisconsin - 1950 to 2006



Grégory Sonnier, Univ. of Wisconsin, Madison

Left: A highly diverse prairie dominated by three plant families (Inset): Fabaceae (i.e. *Baptisia alba*), Asteraceae (i.e. *Rudbeckia hirta*), and Poaceae (i.e. *Andropogon gerardii*) (Dane County, Wisconsin, Summer 2011)

Right: A typical example of wind-dispersed species (*Tragopogon* sp., Asteraceae)



G. Sonnier

† Adapted from:
Kucharik, CJ *et al.* 2010. Patterns of climate change across Wisconsin from 1950 to 2006. *Physical Geography* 31: 1-28.
Wisconsin Initiative on Climate Change Impacts (WICCI). 2010. Maps from Climate Working Group. State of Wisconsin

Below left: Dr. Dave Rogers re-surveying an upland forest site in southern Wisconsin

Below right: Principal Investigators Ken Cameron, Don Waller, Ken Sytsma, and Tom Givnish (left to right)



D. Waller



D. Waller

DISTRIBUTED GRADUATE SEMINAR AWARD:

Dimensions of Biodiversity Distributed Graduate Seminar

Julia Parrish, University of Washington (NSF 1050680)

Building on an innovative educational model, this Distributed Graduate Seminar will provide a baseline for the 10-year Dimensions of Biodiversity program while preparing a networked cohort of biodiversity researchers to support the program in the future. Open-access databases will be crowd-sourced to assess the progress of the Dimensions program.

Distributed Graduate Seminars are an innovative approach to advancing science through an integration of research and education. The Dimensions of Biodiversity Distributed Graduate Seminar (DBDGS) focuses on increasing knowledge about biodiversity. The DBDGS will include 13 university teams, with international partners on three continents, and more than 100 students chosen from a wide range of disciplines needed to address biodiversity science (e.g., biology, geophysics, economics, computer science). The scientific goals of the DBDGS include production of an on-line database of the state of knowledge about the taxonomic, genetic, and functional dimensions of biodiversity at the global level and a synthetic review on the integration of these and other dimensions of biodiversity to create a framework for future research and discovery. The project has 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? Each team is committed to using a meta-analytic approach with existing datasets from the literature and elsewhere, creating one or more academic products, and cross-fostering their ideas with other teams via web interactions and in-person synthesis meetings.

DBDGS will have a fundamental impact on this emerging field through its synthesis of the state of knowledge and its focus on the graduate student community, both nationally and internationally. Distributed seminars

provide an intense team-driven, multi-disciplinary research experience that is likely to be important in future biodiversity research. Because Core Team members represent both academic and non-governmental organization institutions, graduate students will be exposed to a range of scientific career paths. The DBDGS will foster international collaboration among young scientists. Products of the seminar will be of interest to a broad range of researchers and will include open-access databases, student-led publications, and a symposium highlighting DBDGS findings at the Ecological Society of America annual meeting.

For more information: <http://www.dbdgs.org/>

Currently participating institutions (faculty leads):

United States:

Oregon State University (Selina Heppell)
University of California, Berkeley (Mary Firestone, Matt Potts)
University of California, Los Angeles (Sassan Saatchi)
University of California, Santa Barbara (Sandy Andelman, Jorge Ahumada, Sarah Lester)
University of Connecticut (Michael Willig)
Univ. of Michigan (Brad Cardinale, Ivette Perfecto)
University of North Carolina (Allen Hurlbert, Charles Mitchell, Robert Peet)
Univ. of Washington (Julia Parrish, Josh Tewksbury)
Virginia Institute of Marine Science (Emmett Duffy)

South America:

Pontificia Universidad Católica de Chile (Juan Armesto, Aurora Gaxiola, Pablo Marquet)
Univ. Federal do Rio Grande do Sul (Valerio Pillar)

Asia:

Fudan University (Bo Li)

Africa:

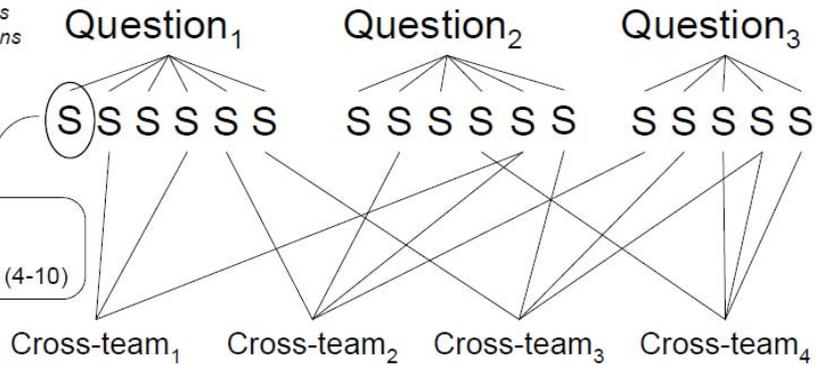
East African Universities TBD (Alex Awiti)

Distributed Seminar Structure:

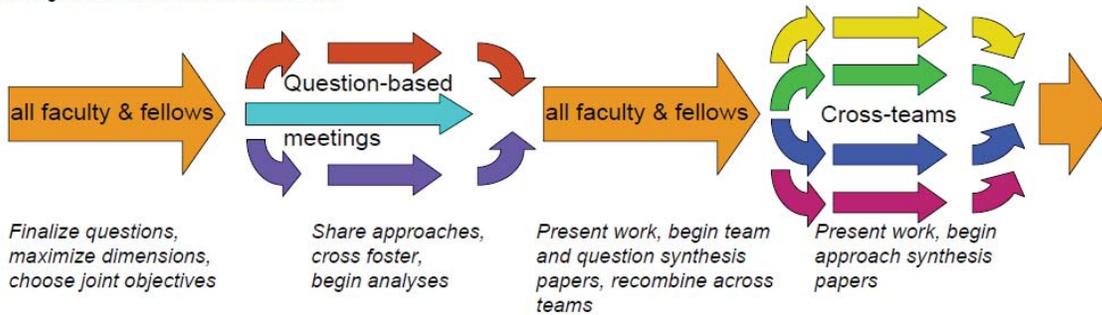
3 sub-groups of ~6 seminar teams each, focused on framing questions

17 seminar teams, 12 national and 5 international, collectively maximizing the dimensions of biodiversity examined

Faculty Leads
Graduate Fellow
Graduate Participants (4-10)



4 invited cross-teams, composed of 15 graduate students self-selected from among the seminar teams, including both national and international



Julia K. Parrish, University of Washington

Above: The structure and schedule for the Dimensions of biodiversity Distributed Graduate Seminar (DBDGS)

Right: The DBDGS team from the University of Michigan is studying drivers of biodiversity in agroecosystems, such as this shade coffee plantation in Chiapas, Mexico



David Gonthier

Below Left: DBDGS Team members at the August 2011 meeting hosted by the University of Washington



David Morgan

INTERNATIONAL RESEARCH COORDINATION NETWORK: Diversity and forest change: Characterizing functional, phylogenetic and genetic contributions to diversity gradients and dynamics in tree communities

US TEAM: Stuart Davies, Harvard University; Nathan G. Swenson, Michigan State University; W. John Kress, Smithsonian National Museum of Natural History; Rick Condit, Center for Tropical Forest Science, Smithsonian Tropical Research Institute (STRI); and Helene Muller-Landau, STRI (NSF 1046113)

CHINA TEAM: Zhanqing Hao, Institute of Applied Ecology, Chinese Academy of Sciences (CAS); Keping Ma, Institute of Botany, CAS; Wanhui Ye, South China Botanical Garden, CAS; Jie Li, Xishuangbanna Tropical Botanical Garden, CAS; Xiangcheng Mi, Institute of Botany, CAS; Xugao Wang, Institute of Applied Ecology, CAS

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

This project will bring together two existing forest research networks in the US and China to advance understanding of how taxonomic, functional, and genetic dimensions of diversity structure tree communities and affect their resilience to global change. Together these teams maintain 42 large-scale forest plots in tropical and temperate forests in Asia and the Americas, providing data on the demography, functional traits, phylogenetic relatedness, and environmental preferences of thousands of species. Through a series of workshops and international scientific exchanges, these data will be used to ask: what functional traits underlie species demographics and distributions across environmental gradients; how do functional traits and phylogenetic relatedness of communities link to forest function; how do functional traits and environmental tolerances vary among individuals within species; and how does gene flow contribute to genetic diversity at local and regional scales. By combining long-term temperate and tropical forest studies across entire tree communities, the investigators will be able to parameterize models that incorporate functional and genetic variation among species to test predictions

about current and future changes in forests.

The project will be implemented through a series of capacity-building initiatives that will expand science and enhance collaboration between the US and China. The strengthening of the network will have long-term benefits for American and Chinese researchers examining the role of forests in a changing global environment. The investigators will engage approximately 200 students and early-career scientists over five years. An international scientific exchange program will enable 10 US students and early-career researchers to spend 3 months in collaborating institutions in China. Chinese scientists will have similar opportunities in the US through a parallel proposal to NSF-China. These scientists will be drawn from the US, China, and other developing countries in Asia and the Americas. In addition, the scientific workshops will result in the development of new analytical tools and data compilations that will be made openly available through the web.

Recent news:

<http://news.harvard.edu/gazette/story/2011/07/gauging-forest-changes/>



Stuart Davies



Robert Howe

Above left: 25-ha deciduous forest plot at Changbaishan National Nature Reserve, China

Above right: 25 ha deciduous forest plot at Wabikon Lake Forest in Chequamegon-Nicolet National Forest, USA



James Lutz

Left: 25-ha mixed conifer forest plot at Yosemite National Park, USA



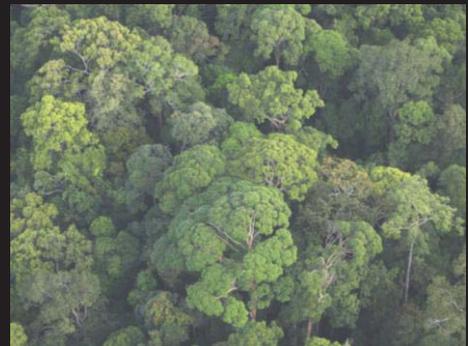
S. Davies

Right: Epiphytic growth in 50-ha plot at Yasuni National Park, Ecuador



Sabrina Russo

Right: Understory of the 52-ha lowland dipterocarp forest plot at Lambir Hills National Park, Malaysia



Christian Ziegler

Right: Canopy of the plot at Lambir Hills National Park, Malaysia

Below left: Seeds and fruits from the 50-ha plot at Huai Kha Khaeng Wildlife Sanctuary, Thailand

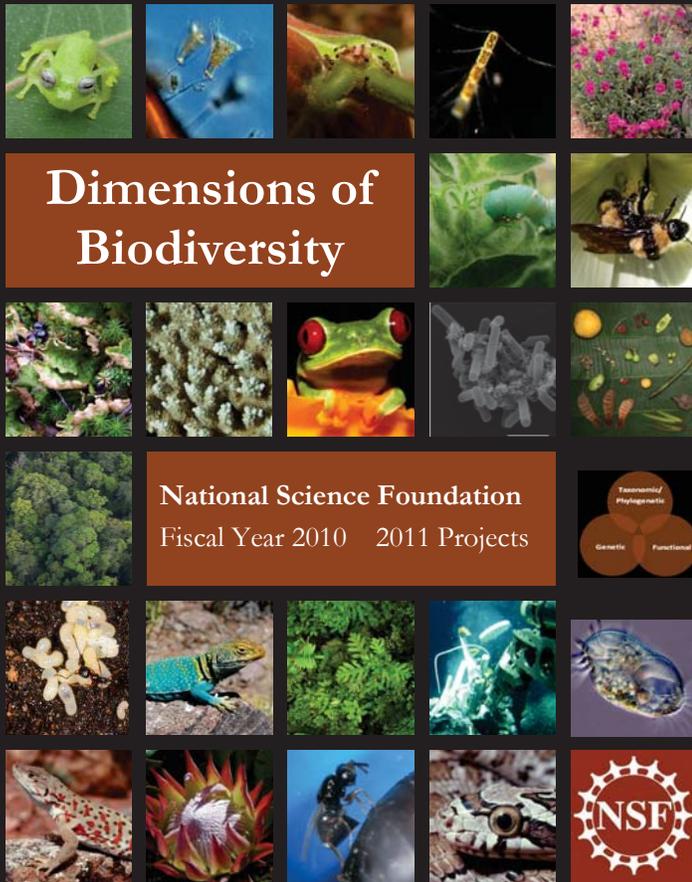
Below right: Researchers from the Center for Tropical Forest Science and the Chinese Forest Biodiversity Monitoring Network in China



C. Ziegler



S. Davies



Row 1 (left to right):

1. Poff, NL (FY10): *Nymphargus wileyi*, a holotype of a new Ecuadorian species of centrolenid (glass frogs)
2. Clamp, J (FY11): *Acineta tuberosa*, a suctorian ciliate
3. Kursar, T (FY11): Ants at nectaries on expanding leaves of a Brazilian species of *Inga*
4. Stahl, DA (FY10): *Chaetoceros convolutus*, a marine planktonic diatom
5. Schlichting, CD (FY10): *Pelargonium sericifolium*, a South African geranium

Row 2:

1. Moyle, LC (FY11): Tobacco hornworm (*Manduca sexta*) on an Andean wild tomato, *Solanum habrochaites*
2. Moran, NA (FY10): Sonoran bumblebee, *Bombus sonorus*, on an hibiscus flower

Row 3:

1. Lutzoni, FM (FY10): Lichens (*Peltigera leucophlebia*) in close association with plants in a boreal forest
2. Rohwer, F (FY10): Close up of coral polyps, *Acropora* sp
3. Belden, LK (FY11): A Panamanian red-eyed treefrog, *Agalychnis callidryas*
4. Stahl, DA (FY10): *Nitrosopumilus maritimus*, the first pure cultured marine ammonia oxidizing archaeon
5. Davies, SJ (FY10): Seeds and fruits from the 50 ha plot at Huai Kha Khaeng Wildlife Sanctuary, Thailand

Row 4:

1. Davies, SJ (FY10): Canopy of a 52-ha lowland dipterocarp forest plot at Lambir Hills National Park, Malaysia
2. Venn diagram depicting the **genetic, taxonomic/phylogenetic, and functional dimensions of biodiversity**. The current phase of the Dimensions program focuses on the simultaneous investigation of all three dimensions.

Row 5:

1. Sanders, NJ (FY11): A foraging ant of the *Aphaenogaster rudis* complex tending a brood of larvae and pupae
2. Brooks, T (FY11): *Crotaphytus collaris*, Eastern collared lizard (Colorado, USA)
3. Davies, SJ (FY10): Understory of a 52-ha lowland dipterocarp forest plot at Lambir Hills National Park, Malaysia
4. Sievert, SM (FY11): The submersible *Alvin* measures temperature, pH, and sulfide at "Crab Spa," a diffuse-flow hydrothermal vent site on the East Pacific Rise
5. Clamp, J (FY11): *Diophrys* sp., a hypotrich ciliate

Row 6:

1. Brooks, T (FY11): *Gambelia wislizenii*, long-nosed leopard lizard (USA: Colorado)
2. Schlichting, CD (FY10): The king protea, *Protea cyanaroides*, national flower of South Africa
3. Bordenstein, S (FY10): A *Nasonia* parasitoid wasp using her ovipositor to deposit eggs inside a fly pupae
4. Brooks, T (FY11): *Pantherophis emoryi*, Great Plains ratsnake (Colorado, USA)