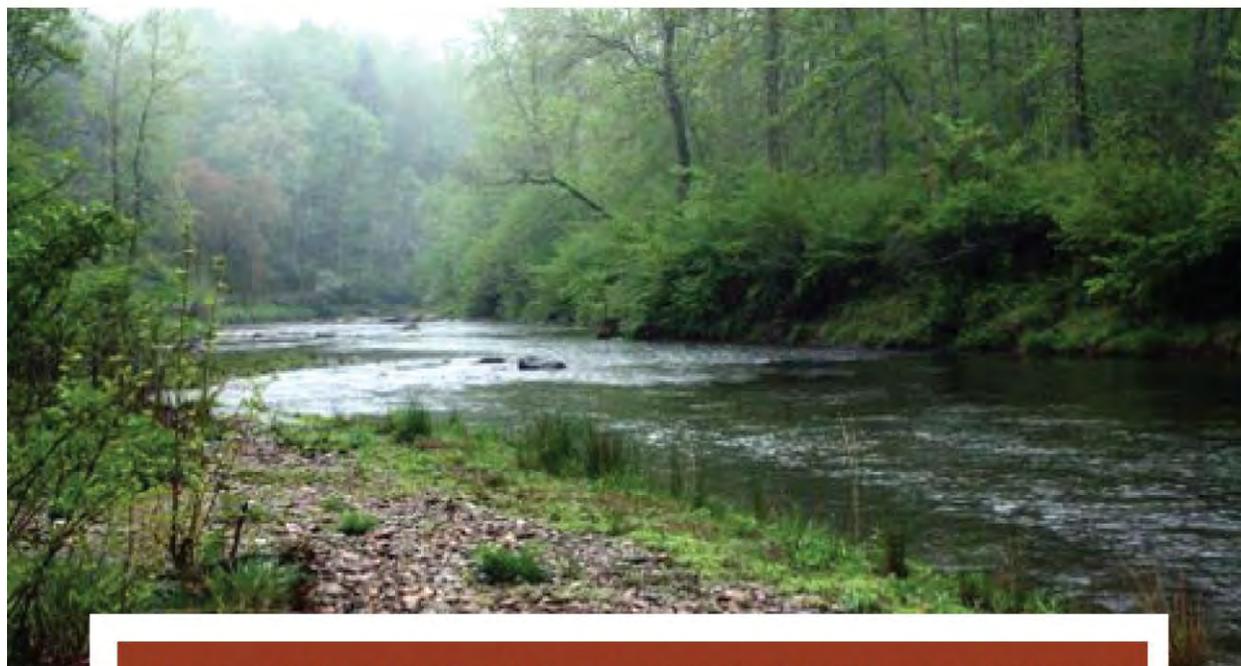
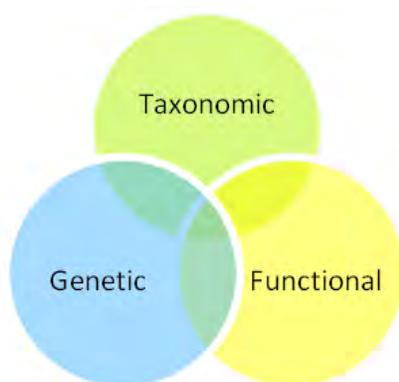




National Science Foundation Fiscal Year 2010 Projects



DIMENSIONS *of* BIODIVERSITY



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INTRODUCTION

Despite centuries of discovery, most of our planet's biodiversity remains unknown. Understanding the scale of that unrecognized biodiversity is vital given its rapid and permanent loss around the globe. To respond to the need for more knowledge and a better understanding of Earth's biodiversity, the National Science Foundation (NSF) has awarded 16 grants in Fiscal Year 2010 --- the first year of the 10-year Dimensions of Biodiversity activity.

Dimensions of Biodiversity seeks to characterize biodiversity on Earth by using integrative, innovative approaches to fill rapidly the most substantial gaps in our understanding. It will take a broad view of biodiversity, and in its initial phase will focus on the integration of genetic, taxonomic, and functional dimensions of biodiversity. Projects integrate these three dimensions to understand interactions and feedbacks among them. While this focus complements several core NSF programs, it differs by requiring that multiple dimensions of biodiversity be addressed simultaneously, in innovative or novel ways, to understand the roles of biodiversity in critical ecological and evolutionary processes.

Scientists across the globe continue to discover new life forms, unsuspected metabolic pathways, significant symbiotic associations, novel patterns of both vertical (i.e. hereditary) and horizontal (across species) gene transfer, and even major new evolutionary lineages. Growing understanding of the diversity of life on earth has highlighted the connectedness as well as the vulnerability of biological phenomena at every scale of resolution. New tools and approaches are accelerating data acquisition, digitization, visualization, access, analysis and synthesis. With these new capabilities come opportunities for rapid advances in integrated science for biodiversity. Dimensions of Biodiversity is supporting fundamental research, and planning is underway for cyberinfrastructure, workforce, collections, and synthesis elements. It is being "baselined" with a Distributed Graduate Seminar (page 32) so that progress can be assessed on a periodic basis.

Dimensions of Biodiversity is expected to transform how we describe and understand the role and scope of life on Earth. It promotes novel, integrated approaches to identifying and comprehending the evolutionary and ecological significance of biodiversity in today's changing environment, and in the geologic past.

"Dimensions of Biodiversity is a new way of thinking about biodiversity that integrates genetic, taxonomic, and functional questions. Dimensions may accomplish in 10 years what, with a piecemeal approach, would have taken 50 years—a half-century we can no longer wait."

Dr. Joann P. Roskoski, Acting Assistant Director
Directorate for Biological Sciences
National Science Foundation

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.

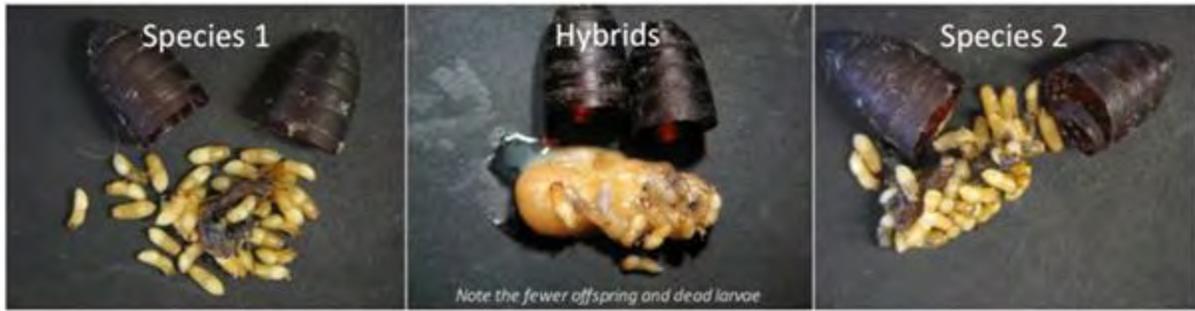
One of the central questions in biology is how do new species arise - that is, how does one species become two and so on to ultimately produce the more than 1.8 million species that now inhabit the planet. Traditionally, animal species are categorized as groups of individuals that can interbreed, and 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, while the other 10% are human. 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. To that end, the investigation will examine 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 species is different than that in hybrids. Alterations of the microbial community in hybrids would suggest an incompetence of the host to regulate a normal consortia 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 undergraduate course at Vanderbilt University that will involve students in the research, the creation of an online repository for taxonomic information on the symbionts discovered in this research, the 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.



Above: Hybrid lethality in *Nasonia* occurs during larval development. This image depicts a normal larva next to a dead, melanized larva from an interspecific cross.



Below: A *Nasonia* parasitoid wasp, the model organism of this Dimensions of Biodiversity project. These wasps are smaller than the size of a fruit fly and parasitize house flies or blow flies.



Above: A *Nasonia* female wasp uses her ovipositor to pierce through the fly host casing to deposit her eggs inside. The host provides a protective environment in which wasp offspring develop.

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

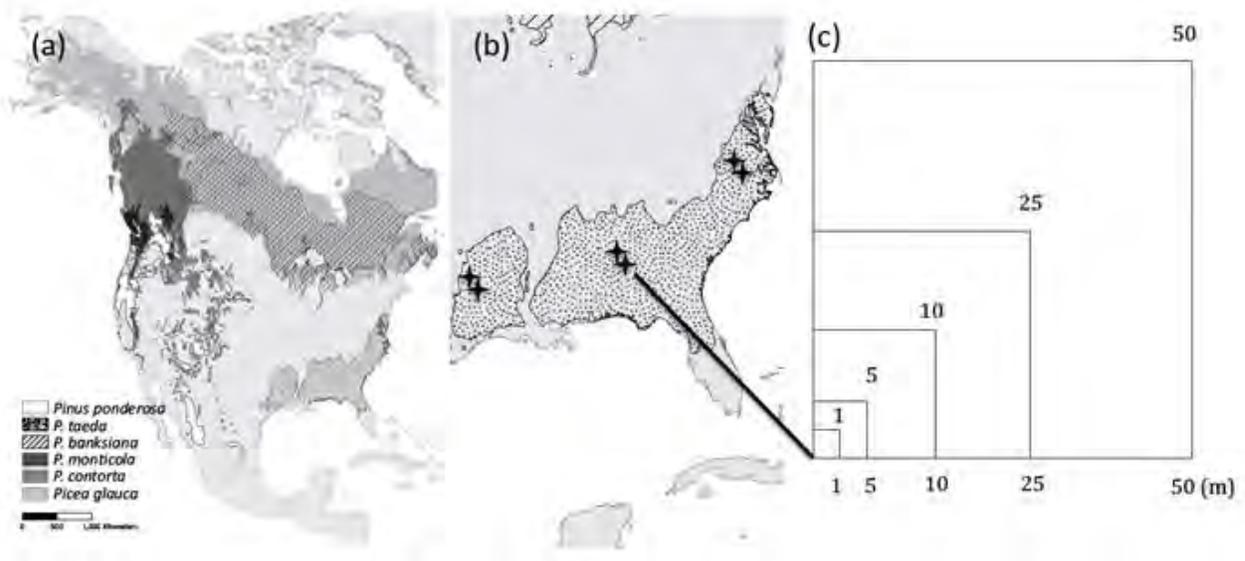
Thomas Bruns and John W. Taylor, University of California, Berkeley (NSF 1046115); Kabir G. Peay, University of Minnesota – Twin Cities (NSF 1045658); Rytas Vilgalys, Duke University (NSF 1046052).

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.

Like many other soil microbial communities, fungal communities are hyper-diverse and poorly known in even the best-studied ecosystems. Next generation DNA sequencing technologies 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 work will provide the first continental-scale sample of taxonomic, genetic and functional diversity of ectomycorrhizal fungi from pine ecosystems. These 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 selection for multiple ectomycorrhizal fungi across North America, use a hierarchical phylogenetic sampling design to measure variation in functional enzyme production across individuals, populations and species, and use RNA based metagenomics to measure functional trait expression on mycorrhizal root tips.

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.



Sampling design for assessing spatial, historical, and environmental drivers of EMF diversity across multiple spatial scales. (a) North American distribution maps for selected host species, (b) potential regional arrangement of six plots for sampling of *Pinus taeda* EMF, and (c) nested sampling design for each plot. Soil samples will be taken at the vertices of each rectangle. 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.



To answer their research questions, the investigators will use three approaches: (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.

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

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 U.S., 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 networks maintain 24 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 functional traits and phylogenetic relatedness of communities link to forest function; how functional traits and environmental tolerances vary among individuals within species; and how gene flow contributes 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 100 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.



25-ha forest research plot at Changbaishan National Nature Reserve, China. Photo by Stuart Davies.



Seeds from the 50-ha plot at Huai Kha Khaeng Wildlife Sanctuary, Thailand. Photo by Christian Ziegler.



Researchers from the Center for Tropical Forest Science and the Chinese Forest Biodiversity Monitoring Network in China. Photo by Stuart Davies.



Understory of the 52-ha plot at Lambir Hills National Park, Malaysia. Photo by Sabrina Russo.



50-ha forest research plot at Yasuni National Park, Ecuador. Photo by Stuart Davies.



Canopy of the 52-ha plot at Lambir Hills National Park, Malaysia. Photo by Christian Ziegler.



25-ha forest research plot at Yosemite National Park, USA. Photo by James Lutz.



Understory in the 25-ha plot at Wabikon Lake Forest in the Chequamegon-Nicolet National Forest, USA. Photo by Robert Howe.

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 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?

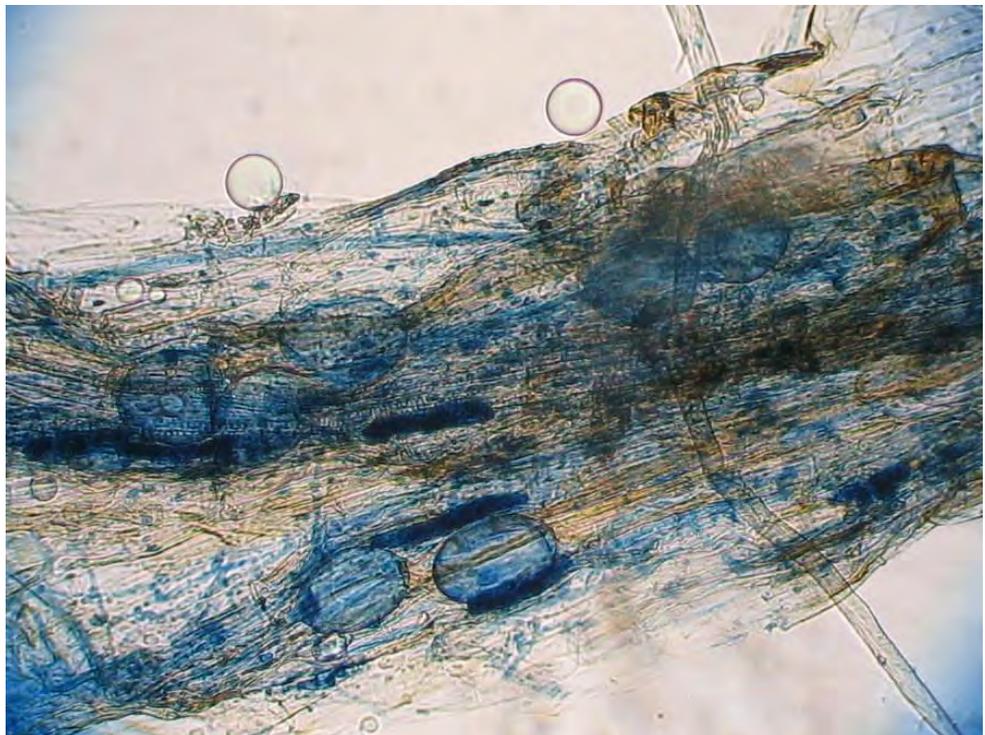
In this project soil microbial sampling will provide basic information on how these microbes are distributed as well as how their distribution relates to current climates and genetic structure of the tree species. Trees and soil microbes will likely not move at equal speeds as climates change. For instance, 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.



Left: External hyphae of arbuscular mycorrhizal fungi with spores growing around sycamore (*Platanus occidentalis*) roots.
Photo by Richard Lankau

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 arbuscules, 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).
Photo by Richard Lankau



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

Carol Lee, University of Wisconsin Madison (NSF 1046372); Joana Carneiro da Silva, University of Maryland at Baltimore (NSF 1046371)

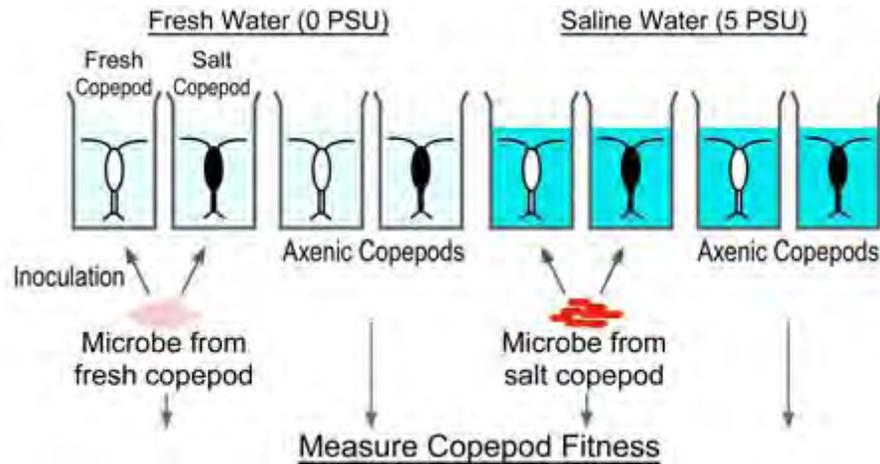
This project will characterize diversity and metabolic functions of the microbiome of a copepod, and will experimentally test how the diversity and functions change when the copepod invades a novel habitat (freshwater). The investigators seek to understand how the dimensions of biodiversity between an organism and its microbiome are changed when the organism moves from one distinct ecosystem to another, and how that affects the ecosystem.

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*

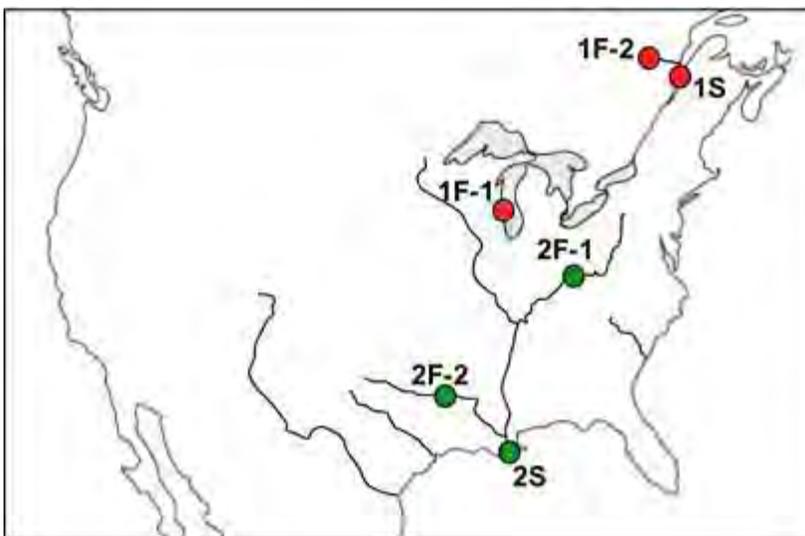
microbiome uncovered a wide variety of potentially pathogenic taxa, including *Salmonella*, *Shigella*, *Campylobacter*, *Corynebacterium diphtheriae*, *Yersinia*, and *Vibrio cholerae*. Thus, *E. affinis* might play an important role as a reservoir and vector of waterborne disease. This collaborative 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).



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



Left: 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.



Lichens (here, *Peltigera leucophlebia*) growing in close association with plants (*Empetrum nigrum*, *Pleurozium schreberi*, *Polytrichum* sp., and *Hylocomium splendens*) in a boreal forest community harbor a rich array of symbiotrophic fungi, including the axenic cultures of endophytes (from asymptomatic plant tissue) and endolichenic fungi (which grow in association with lichen photobionts inside healthy lichen thalli) shown at left. 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. Photo by A. Elizabeth Arnold

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.

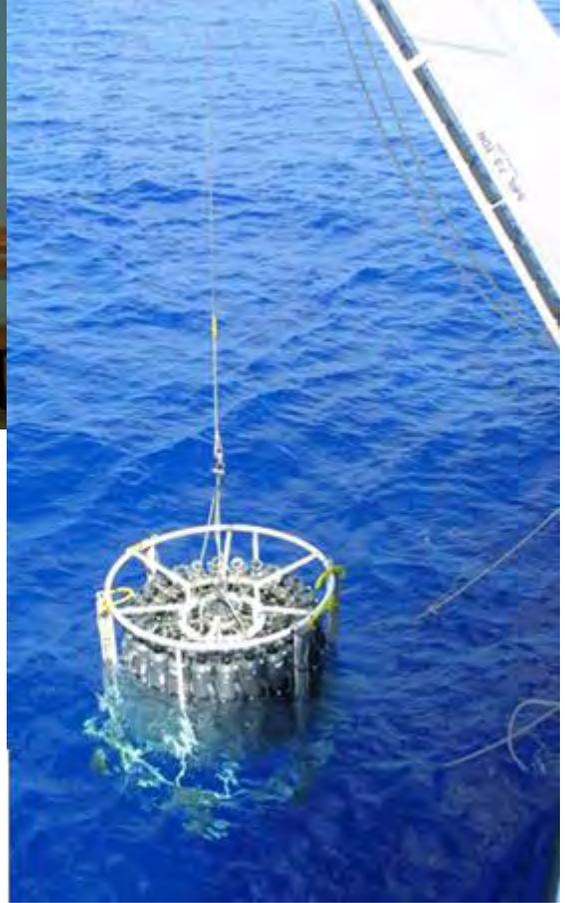
Decades ago, Alfred Redfield observed that the ratio of nitrogen-to-phosphorous in ocean surface plankton matched the ratio of dissolved nitrogen-to-phosphorous in the deep ocean. Furthermore, this ratio was constant all over the ocean. Redfield proposed that the hydrolysis of sinking surface particles 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 leads us 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.

Over the next 5 years, 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: Members of PI Adam Martiny and co-PI Steven Allison laboratories at the sampling site at Newport Pier, California

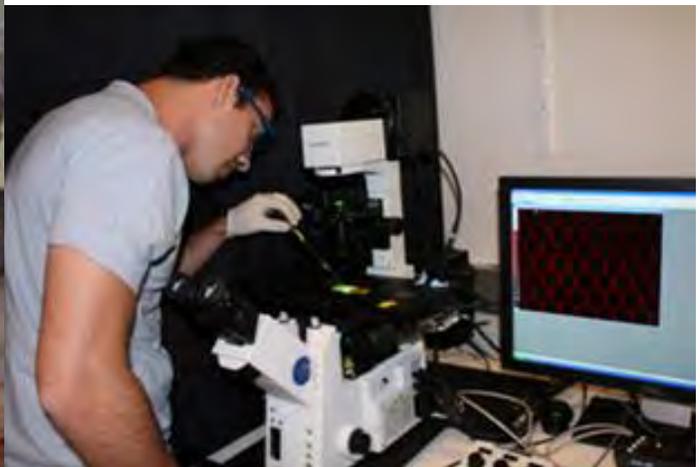


Right: A sampling rosette from R/V Atlantic Explorer

Below: Co-PI Mike Lomas participating in the outreach program “crush-a-cup” aboard the R/V Atlantic Explorer



Below: A student from co-PI Kun Zhang’s laboratory is using a microfluidic chip to amplify and pick single-cell genomes.



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 region 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.



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

Below: The bumblebee, *Bombus sonorus*, at a flower.



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 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 Ecuadoran 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: A holotype of a new species of centrolenid (stream frogs) that the PIs discovered and described from Yanayacu Biological Station at about 2000 m (Amazonian versant of the Ecuadorian Andes) called *Nymphargus wileyi*.



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

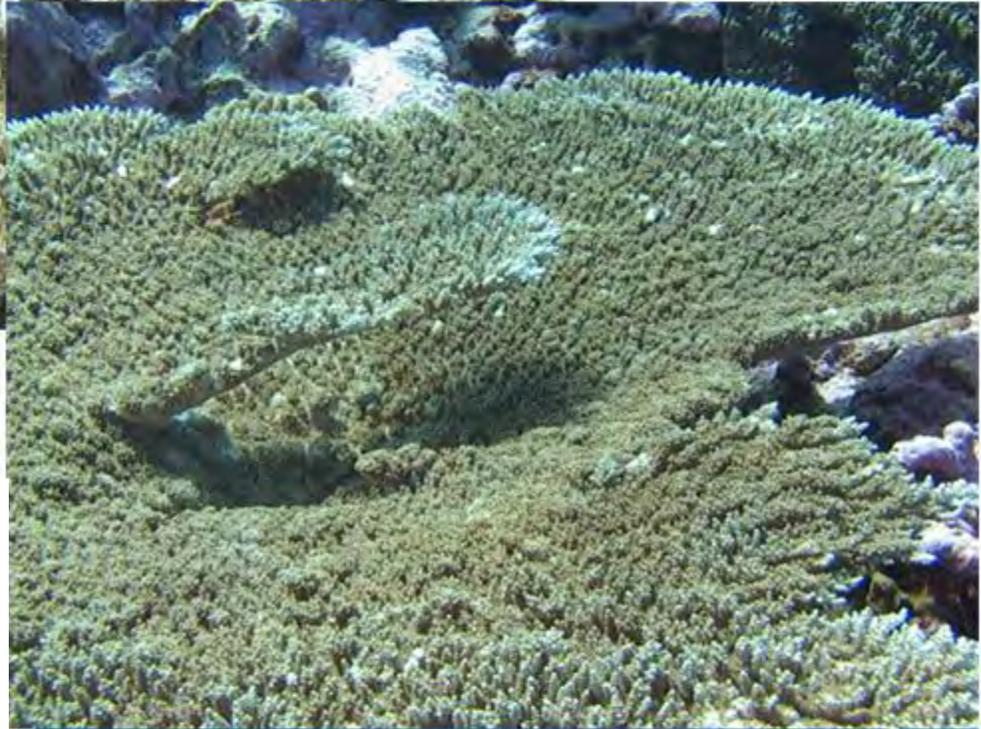
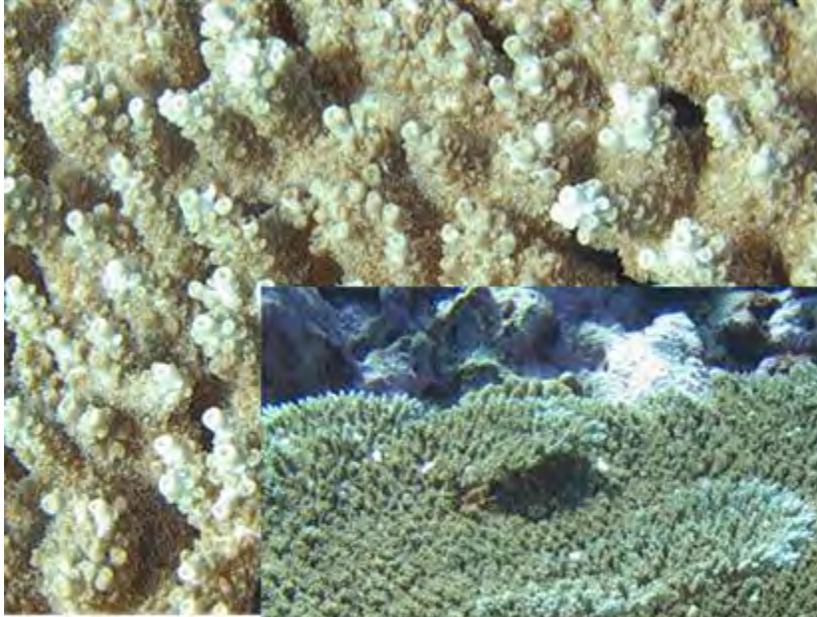
Forest Rohwer, Robert A. Edwards, and Anca Segall, San Diego State University (NSF 1046413)

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.



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 range of 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 (GFCR). Over 65% of GFCR plant species are endemic, an extraordinary level for a continental region.

The overall 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 levels ranging from the intraspecific to the community. 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.



Above: *Protea aurea* from Blesberg, Western Cape Province, South Africa. 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. Photo by Jane Carlson

Right: *Pelargonium sericifolium* from South Africa. Pelargoniums are the ancestors of cultivated 'geraniums'. These plants are marked by their diversity in growth form, leaf shape and flower types. Photo by Carl Schlichting.



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)

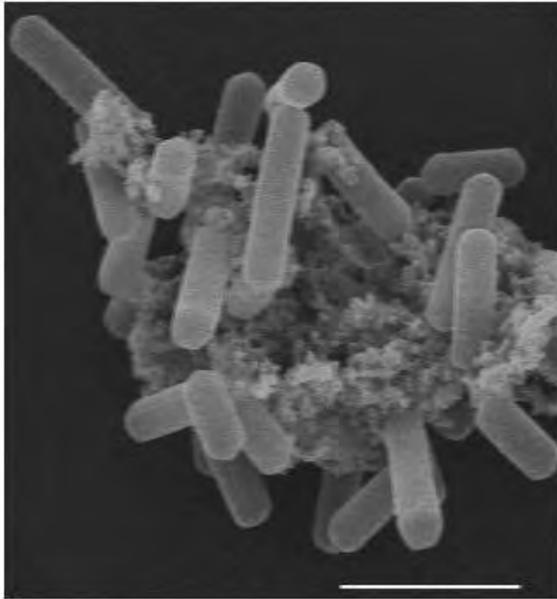
Stahl and others will examine the diversity and function of ammonia oxidizing Archaea (AOA) in the ocean and determine the role of these newly discovered organisms in structuring the diversity of phytoplankton.

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 and having 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* comprise one of three primary lineages of evolutionary descent 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

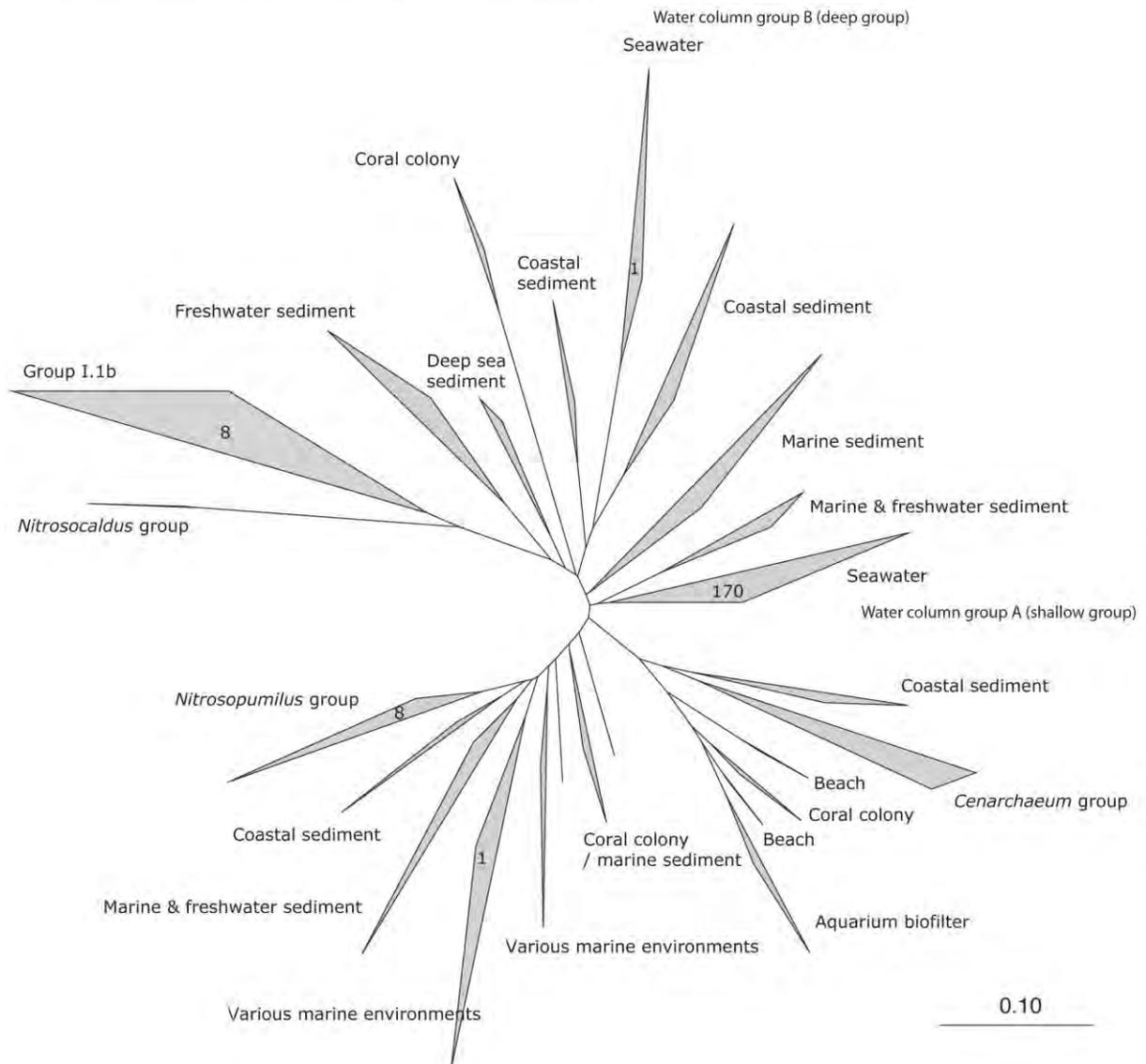
available to nitrite oxidizing bacteria and some phytoplankton. In addition to their ability to deprive other marine organisms of ammonia, genetic analyses points to an unusual copper-based system of respiration that may render them more competitive in iron limited environments. The implication is that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

The proposed 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.



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

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



The role of viruses in structuring biodiversity in methanotrophic marine ecosystems

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

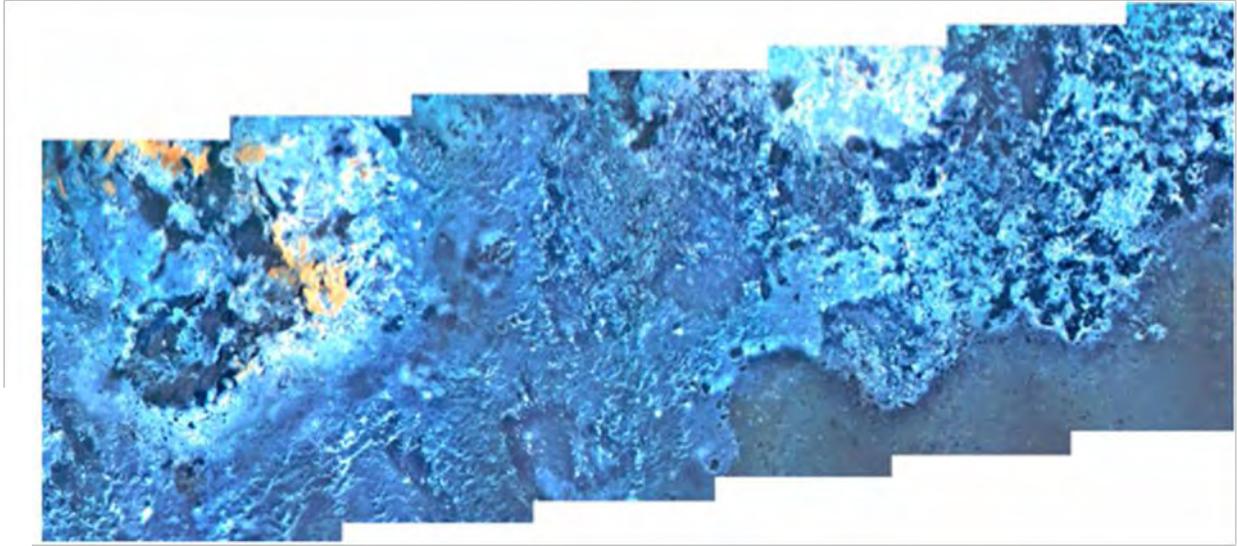
Microbes in ocean sediments form a unique ecosystem; there methane is consumed, preventing large amounts of this potent greenhouse gas from entering the atmosphere. The research will shed light on a dark corner of the biosphere, and could identify new and novel genes that support life in these environments.

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.

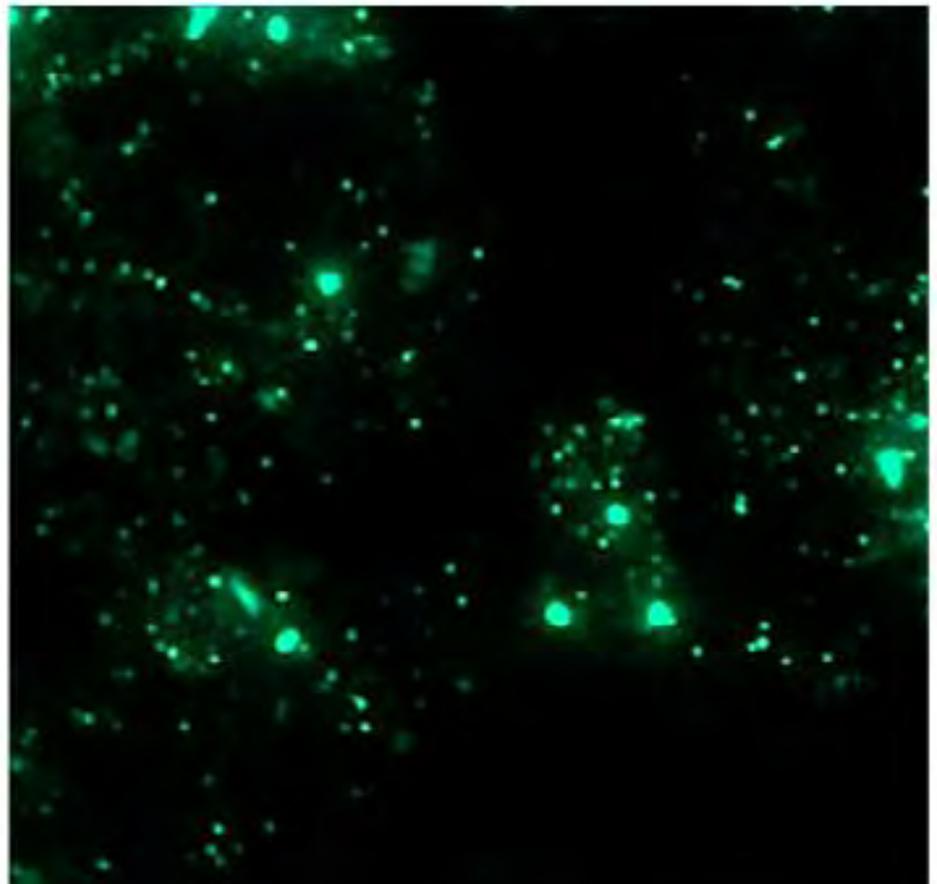
We also know that both the aerobic and the anaerobic microbial communities host huge viral communities—some ten times more viruses than hosts. The prediction that this project will test is that these viruses, as agents

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.



Above: 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. Photomosaic by Oscar Pizarro, University of Sydney.

Right: Epifluorescence microscopy shows bacteria (large green spots) greatly outnumbered by viruses (green pinpoints) in a methanotrophic mat collected off Santa Barbara. Photo by Blair Paul, UCSB



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 others 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.

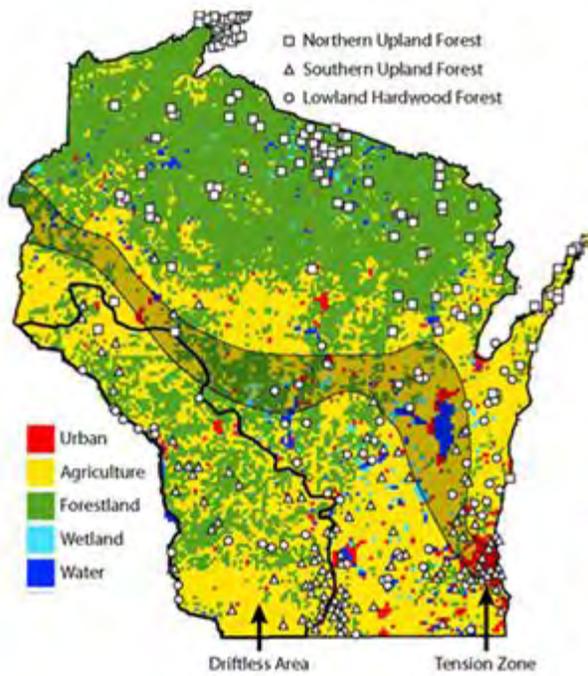
In this project, the researchers will examine the functional traits, phylogenetic relationships, geographic distributions, and patterns of genetic variation in native and introduced plants occupying Wisconsin forests and grasslands. The project team seeks to determine trait evolution and community assembly 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.



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



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



Left: The four Principal Investigators: Ken Cameron, Don Waller, Ken Sytsma, and Tom Givnish (left to right).

Dimensions of Biodiversity Distributed Graduate Seminar

Julia Parrish, University of Washington (NSF 1050680)

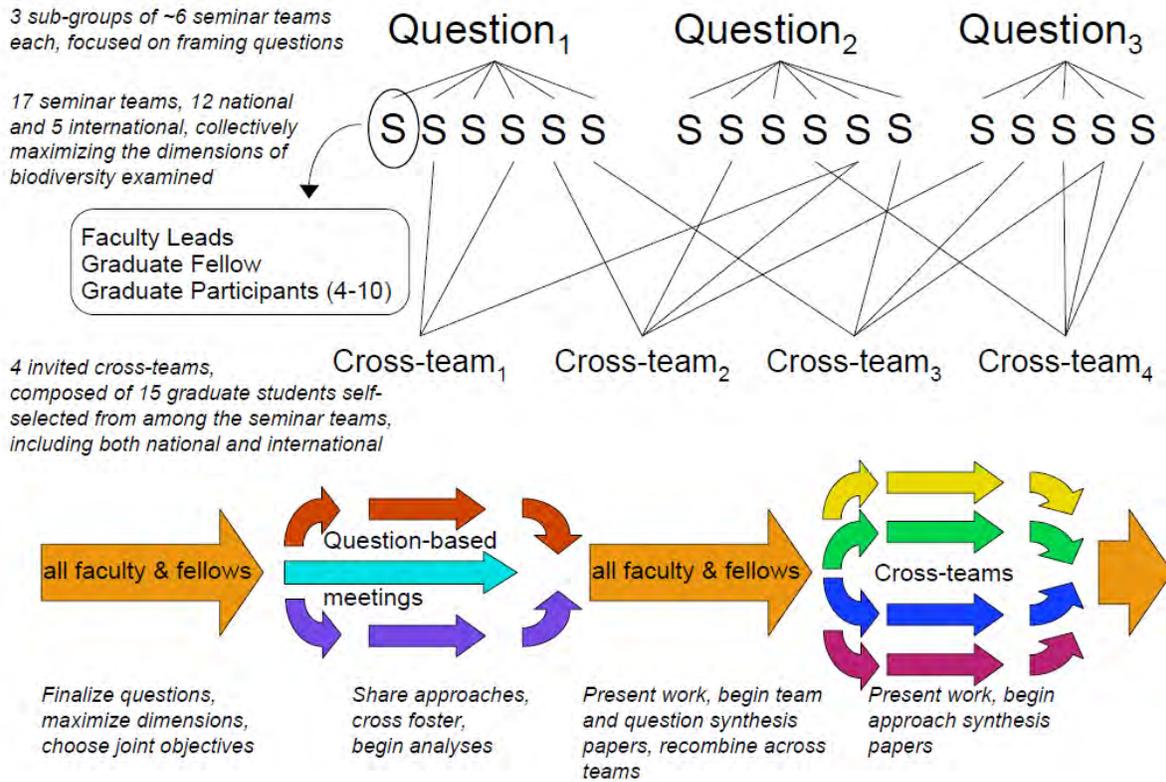
A distributed graduate seminar will provide a baseline for the planned 10-year program. A synthesis of current understanding of the dimensions of biodiversity will be posted on a wiki, crowd-sourced regularly, and “frozen” periodically to allow assessment of progress.

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 15-20 university teams, with international partners on four continents, and more than 100 students chosen from a wide range of disciplines needed to address biodiversity science (e.g., biology, geophysics, economics, anthropology, computer science and health). 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.

This DBDGS will have a fundamental impact on this emerging field through 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 also be exposed to a range of scientific career pathways. 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.

Distributed Seminar Structure:



Above: The structure and schedule for the Dimensions of Biodiversity Distributed Graduate Seminar.

PHOTOGRAPHY CREDITS

Front Cover: Hazel River and unnamed tributary, Culpeper County, Virginia. Photo by P. Firth (NSF).

Back cover: Shoreline and coral reef, Kings Wharf, Bermuda. Photo by P. Firth (NSF).

