

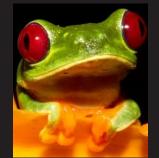
Dimensions of Biodiversity

















National Science Foundation 2010 – 2012 Projects







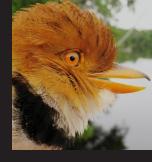
















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Acknowledgements

Many NSF staff members, to 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 fourth 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 14 new projects in FY 2012 bringing the total number of active projects to 41. 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 halfcentury we can no longer afford to wait."

> Dr. Joann P. Roskosi 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 humanand 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.

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. "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

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.

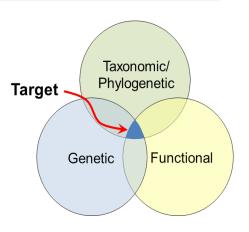


Dimensions of Biodiversity involves five streams of activity. The approach for supporting these activities involves planning and partnering, developing baselines of our current understanding, and assessing progress periodically during the decade in order to align investments with newly-appreciated priorities.

Streams of acti	vity 2020 Goals	
Research	An integrated understanding of the key but unknown dimensions of biodiversity on earth	
Cyberinfrastructure	Informatics and infrastructure that support accessible, interoperable information capability for dimensions of biodiversity	
Collections	Digitization of collections and enhanced physical infrastructure to link to cyberinfrastructure and leverage the enormous investments of the past	
Workforce	A diverse, interdisciplinary, globally-engaged, scientific workforce capable of transforming and communicating our understanding of biodiversity on Earth	
Synthesis	Scientific analyses and syntheses that generate and disseminate useful information for scientists, educators and decision makers	
Approach:		
	ase lining & Assessing Aligning investments nchronizing progress with emerging prioritie	

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

The first of the annual competitions for research awards was held in 2010. In 2010 and 2011 a partnership with NSF-China supported International Research Coordination Network projects. In 2012 the partnership with NSF-China was expanded to include collaborative research projects, and a new partnership



was established with the State of Sao Paulo, Brazil that also supports collaborative research projects. NASA also joined as a partner in 2012, to support research projects that use remote sensing.

- FY 2010: 16 projects (US Total ~\$25.7M: BIO \$18.9M; other NSF \$6.8M; NSF-China: ~\$108K)
- FY 2011: 11 projects (US Total ~\$28.0M: BIO \$17.5M; other NSF \$10.5M; NSF-China: ~\$93K)
- FY 2012: 14 projects (US Total ~\$26.4M: BIO \$21M; other NSF \$4.7M; NASA \$720K; NSF-China: \$2M; Brazil: \$2M
- FY 2013 Partners: NASA (up to \$2M); funding agencies in China (up to \$5.2M) and Brazil (up to \$4M).

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

Tia-Lynn Ashman, University of Pittsburgh (NSF 1241006); Aaron I. Liston, Oregon State University, Richard Cronn, U.S. Forest Service (NSF 1241217)

Species that are polyploidy contain more than two pairs of chromosomes. This project will examine the role that polyploidy has played in the evolution of a group of strawberry species growing in the US and in China.

Research on Airborne Ice Nucleating Species (RAINS)

Brent C. Christner, Louisiana State University (NSF 1241161); David C. Sands, Montana State University, Cindy Morris, INRA-PACA, (NSF 1241054); Boris A. Vinatzer, David Schmale, Virginia Tech (NSF 1241068); Carolyn F. Weber, Idaho State University (NSF 1241069)

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

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

Joel L. Cracraft, American Museum of Natural History (NSF 1241066); Christopher W. Dick, University of Michigan (NSF 1240869); Robert P. Guralnick, University of Colorado (NSF 1241029); Kenneth E. Campbell, LA County Museum of Natural History (NSF 1241042); Andrew V. Brower, Middle Tennessee State University (NSF 1241056); John M. Bates, Field Museum of Natural History (NSF 1241075); Barbara M. Thiers, Scott Mori, New York Botanical Garden (NSF 1241127)

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

Do parallel patterns arise from parallel processes?

Michael N. Dawson, John Berman, University of California Merced (NSF 1241255); Julian P. Sachs, University of Washington (NSF 1241247)

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

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

Angela E. Douglas, Gregory Loeb, Cornell University; John Jaenike, University of Rochester (NSF 1241099) This project will examine the microbial communities in the gut of fruitflies to understand how the fruit fly hosts and bacteria influence each other, and how this type of interaction may contribute to the process of evolution of hosts and the diverse assemblages of microbes that live within them.

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Community assembly and decomposer function of aquatic fungi along a salinity gradient 20

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

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

A community level approach to understanding speciation in Hawaiian lineages

Rosemary G. Gillespie, John Harte, Rasmus Nielsen, Patrick O'Grady, University of California Berkeley (NSF 1241253); Daniel S. Gruner, University of Maryland (NSF 1240774); Kerry L. Shaw, Cornell University (NSF 1241060); Donald K. Price, University of Hawaii (NSF 1241228)

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

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

Bruce A. Hungate, James Caporaso, Paul Dijkstra, Jane Marks, Egbert Schwartz, Northern Arizona University (NSF 1241094); Lance Price, Translational Genomics (NSF 1241115)

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

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

Anthony R. Ives, Volker Radeloff, University of Wisconsin (NSF 1240804); Kerry M. Oliver, University of Georgia (1240892); Jason Harmon, North Dakota State University (NSF 1241031)

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

The role of biodiversity for microbial adaptation to anthropogenic perturbations 28

Konstantinos T. Konstantinidis, Jim Spain, Eberhard Voit, Georgia Tech (NSF 1241046)

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

Historical and contemporary influences on elevational distributions and biodiversity tested in tropical Asia 30

Thomas E. Martin, Robert Fleischer, Ellen Martinsen, University of Montana (NSF 1241041); Frederick H. Sheldon, Louisiana State University (NSF 1241059); Robert G. Moyle, University of Kansas (NSF 1241181)

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

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

Hans W. Paerl, University of North Carolina (NSF 1240851); Wayne S. Gardner, University of Texas at Austin (NSF 1240798); Steven W. Wilhelm, University of Tennessee (NSF 1240870); Ferdinand L. Hellweger, Northeastern University (NSF 1240894)

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

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

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Nathan Swenson, Michigan State University (NSF 1241136)

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

Oligotrophic phytoplankton community response to changes in N substrates and the resulting impact on genetic, taxonomic and functional diversity 36

Jonathan P. Zehr, Kbigniew Kolber, University of California Santa Cruz (NSF 1241221); Kevin R. Arrigo, Stanford University (NSF 1241093); Matthew Church, University of Hawaii (NSF 1241263)

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

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

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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

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

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

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

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 48

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

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

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

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.

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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.

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

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

Steering Committee:

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

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

<u>OTHER COUNTRIES</u>: 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.

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.

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.

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.

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

Richard Lankau, University of Georgia (NSF 1045977)

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

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

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

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

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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 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

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

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

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

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

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.

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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) 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 84

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

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

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

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.

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

<u>US TEAM</u>: 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)

<u>CHINA TEAM</u>: 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.

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

Tia-Lynn Ashman, University of Pittsburgh (NSF 1241006); Aaron I. Liston, Oregon State University, Richard Cronn, U.S. Forest Service (NSF 1241217))

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

All flowering plants possess two or more copies of every chromosome. Polyploidy is thought to be a main driver of plant speciation, biological adaptation and range expansion. How chromosome doubling contributes to biodiversity, and which genomic mechanisms or functional traits underlie the success of polyploids, remain unanswered questions.

This project will focus on wild species of strawberry (genus Fragaria). Nearly half of the 20 species of wild strawberry are polyploid and the genus has centers of diversity in China and North America. Strawberries possess numerous features (small genome, clonal propagation, availability of synthetic neopolyploids, sensitivity to climate change due to early-spring flowering and northern latitude or high elevation distribution) that make them an outstanding model system to better understand how genome doubling contributes to biodiversity. Research will focus on seven 'trios' of polyploid species and their diploid progenitors, native to North America, Europe and East Asia. Extensive field work will be conducted in China, focused on East Asian species that are poorly known ecologically and taxonomically.

This research will establish whether similarities in functional diversity and ecological amplitude of polyploid species are the result of common rules of genetic diversity, chromosome structure or gene expression in a polyploid genome, or whether multiple genetic and genomic pathways lead to successful responses to environmental change. Deep phylogenetic and population genomic sampling will determine whether multiple independent origins contribute to functional and genetic diversity of natural polyploids. The characterization of trait and gene expression in natural and synthetic polyploids, and their diploid progenitors, under climatically diverse experimental gardens (eastern USA, western USA, China) will identify how functional and genetic diversity are distributed in a polyploid/diploid lineage. The integration of these results will inform efforts to predict the effect of whole genome duplication on ecological and evolutionary responses to environmental change in numerous other plant lineages.

This project will accelerate our understanding of how genome doubling confers success, and how it contributes to biodiversity across geographic and evolutionary scales. Moreover, this deeply integrated comparative study of the wild relatives of the cultivated strawberry – a polyploid species of world-wide economic importance – will provide foundational knowledge and contribute unparalleled resources that may be harnessed in efforts to ensure sustainability of strawberry and related crops (e.g., cherry, peach, pear, apple) in the face of abiotic stress. The work will promote training by broad participation and international collaboration, and novel hands-on science curriculum for middle school and undergraduate students.



Above: Eagle Glacier and River, Juneau Alaska, a high latitude site of *Fragaria chiloensis*. [Arlo Midgett]



Above: Fragaria chiloensis fruit at Honeyman State Park, Florence, Oregon. [Tia-Lynn Ashman]



Strawberry polyploidy project collaborators at the H.J. Andrews Experimental Forest. Jacob Tennessen, Rich Cronn, Aaron Liston, Tia-Lynn Ashman, Chris Edwards. [Aaron Liston, Oregon State University]

Research on Airborne Ice Nucleating Species (RAINS)

Brent C. Christner, Louisiana State University (NSF 1241161); David C. Sands, Montana State University, Cindy Morris, INRA-PACA, (NSF 1241054); Boris A. Vinatzer, David Schmale, Virginia Tech (NSF 1241068); Carolyn F. Weber, Idaho State University (NSF 1241069)

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

Microorganisms are abundant in the atmosphere and widely distributed by air currents, yet little is known about the abundance, diversity, and flux of microorganisms in the atmosphere. Numerous studies have provided evidence that microorganisms in the atmosphere may affect cloud development, cloud chemistry, and thus weather patterns. Ice formation in clouds is important in the processes leading to precipitation, but at temperatures warmer than -36oC (-33°F), water drops in clouds require particles, ice nucleators, to initiate freezing. The most active naturally occurring ice nucleators are microorganisms with the capacity to catalyze freezing at temperatures near -2°C (28oF). This is accomplished by a specialized protein that serves as an 'ice template', aligning water molecules in a fashion that promotes freezing.

RAINS is motivated by the potential of ice nucleating microorganisms to significantly impact meteorology and use atmospheric precipitation as a dispersal strategy. Goals of this study are to: (1) characterize the taxonomic diversity in the lower atmosphere and precipitation (including precipitation that occurred between 1794 AD and present and which is preserved in glacial ice), (2) determine the genetic diversity of microbial assemblages and individual ice nucleating bacteria in the lower atmosphere, and (3) examine the role of precipitation and biological ice nucleation in disseminating microbes via the atmosphere. RAINS will be transformative in determining which microbial taxa are carried to the Earth's surface via precipitation, which of these microbes are ice nucleators and may contribute to inducing precipitation, and which of these taxa present possible inoculum sources for diseases that impact humans, domestic animals, and plants.

RAINS will increase knowledge on the biodiversity and nature of the most active ice nucleators in the planetary boundary layer of the atmosphere, where important meteorological phenomena occur. Ice nucleation may allow certain microorganisms and plant pathogens to efficiently 'cycle' between the atmosphere and surface habitats, and RAINS will contribute to ongoing efforts to assess the movement of ice nucleating microorganisms at the geographical scale. Outreach efforts will take these advances into high school and college classrooms in the form of hands-on research experiences for students at both levels and will serve as the basis for high school educators to develop unique classroom activities. In addition, an international network of scientists collecting field data on the relationship between biological ice nucleator abundance, cropping patterns and precipitation in dry land regions will be established. RAINS will sponsor an international conference that brings together 10 young career scientists in the network to highlight the advances of these investigations and identify the outstanding scientific questions.

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