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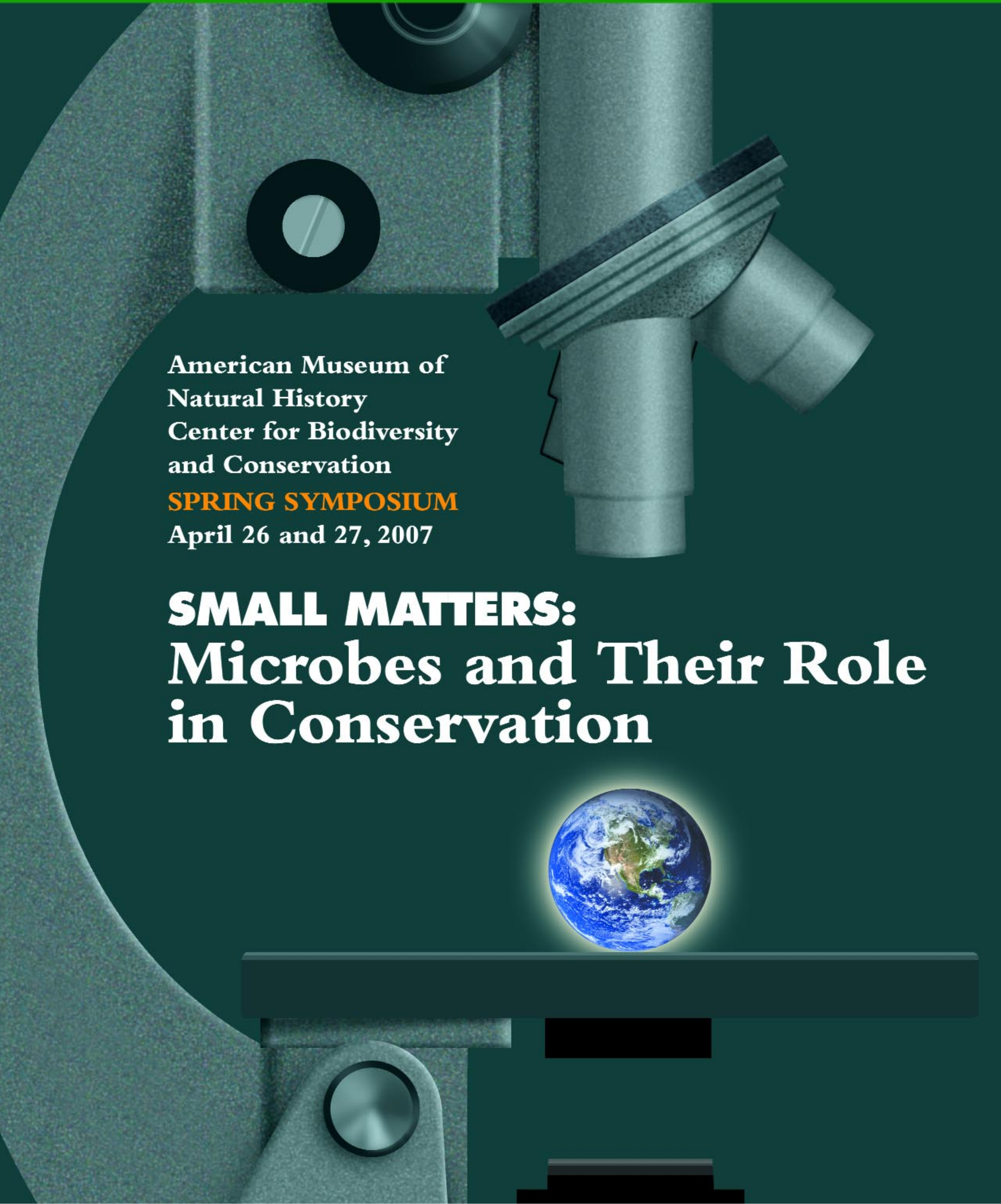

**American Museum of**
**Natural History**
**Center for Biodiversity**
**and Conservation**
**SPRING SYMPOSIUM**
**April 26 and 27, 2007**

# SMALL MATTERS: Microbes and Their Role in Conservation

AMERICAN MUSEUM OF NATURAL HISTORY

# SMALL MATTERS: Microbes and Their Role in Conservation

**Small Matters: Microbes and Their Role in Conservation** is sponsored by the American Museum of Natural History's Center for Biodiversity and Conservation, with support from the National Science Foundation, the Mack Lipkin Man and Nature Series, and the Joseph and Joan Cullman Conservation Foundation, Inc. Additional support is provided by the Wildlife Conservation Society and anonymous donors.

The Mack Lipkin Man and Nature Series was established in honor of Dr. Mack Lipkin, Sr., by his many friends and admirers. Dr. Lipkin was a physician who was a gentle and powerful force towards advancing the most humane and caring practices of medicine. The Museum is proud to welcome three leading scientists as the 2007 Mack Lipkin Man and Nature Series Fellows: Rita Colwell, Claire Fraser-Liggett, and James Staley.

The Center for Biodiversity and Conservation was established with a leadership grant from The Starr Foundation and the support of many other generous foundations, corporations, and individuals. Many people contributed to the planning and execution of this symposium, and while they are far too numerous to list individually, the Center for Biodiversity and Conservation extends its thanks to all of them.

For their significant role in shaping the form and content of this symposium, we especially wish to acknowledge the symposium's Steering Committee and Content Advisors, who are named in the back of this program. We also wish to acknowledge the valuable contributions of Kevin Frey, Amy Johnson, and the Museum's Volunteer Office.

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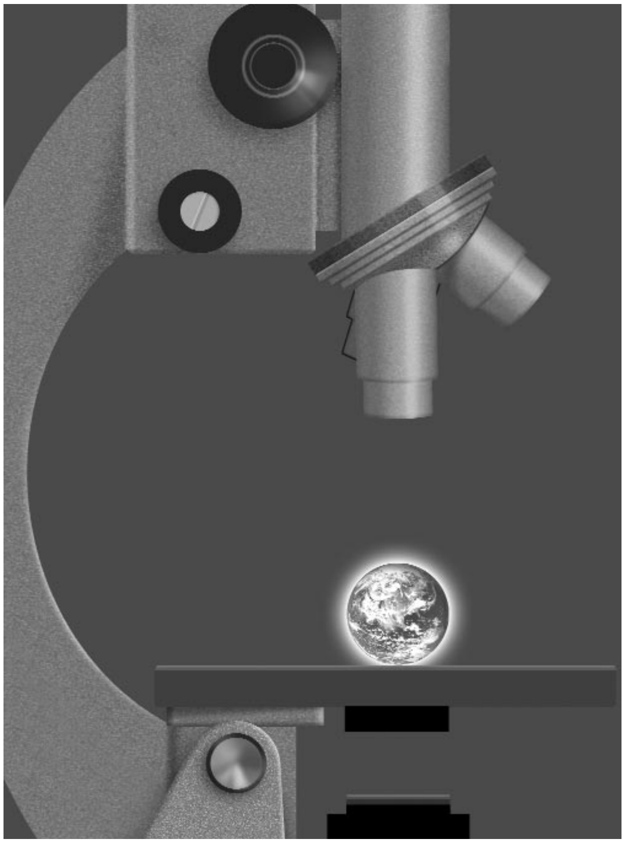
SPRING SYMPOSIUM

American Museum of Natural History
Center for Biodiversity and Conservation
April 26 and 27, 2007

# SMALL MATTERS:
# Microbes and Their Role in Conservation



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American Museum of Natural History
Center for Biodiversity and Conservation

National Science Foundation

# SMALL MATTERS: MICROBES AND THEIR ROLE IN CONSERVATION

## SPRING SYMPOSIUM

*April 26 and 27, 2007*

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Note: Additional symposium information, including participant bios and publications, can be accessed via the CBC website at http://cbc.amnh.org/symposia/microbes

American Museum of Natural History

## SPRING SYMPOSIUM

Microscopic life forms — including bacteria, archaea, single-celled eukaryotic organisms, and (by some definitions) viruses — comprise the vast majority of life on the planet, and are a vital part of functioning, healthy ecosystems. Yet surprisingly little is known about their true diversity and the multitude of roles that they play in the ecosphere. What we do know tends to come from either those organisms that can be cultured in the laboratory (which include less than one percent of all microbial species) or those that directly affect humans, either by causing illness or enhancing our lives in some way. However, in recent years, the revolution initiated by the use of DNA sequences to discover and describe microbe diversity has drastically altered our view of the microbial world and its players. This ability to move beyond the lab and broaden exploration of new habitats has led to the discovery of novel biochemical processes, including new forms of photosynthesis, and even electricity-generating bacteria. But as our understanding of microbes increases, and their once-hidden potential is revealed, our world is entering a period of rapid environmental upheaval, and it will be crucial to understand how these changes will affect microbial life, both now and in the future.

As we strive to meet the challenges of the biodiversity crisis, we wonder how much microbial diversity is being lost, and what the ramifications of those losses might be, such as missed opportunities for advances in medicine or energy production. And if a species of animal or plant goes extinct, how many unique symbiotic microorganisms might also be lost? It is indisputable that biological diversity is fundamental for healthy ecosystems, but it is not clear how the diversity of microorganisms factors into this equation.

In recent decades, we have made significant progress toward integrating ecological and evolutionary processes within biodiversity conservation initiatives. Yet, in the quest to maintain the diversity of life on Earth, the smallest members of the biosphere — representing the overwhelming majority of life forms — have been largely overlooked. By exploring the gap that exists between conservation biology and microbial research we hope to reveal complex patterns of interdependency among organisms, an understanding of which will be necessary to diminish the loss of biodiversity and allow for the simultaneous restoration of damaged systems. This symposium aims to coalesce our knowledge of microbes and their varied interactions with other species and with ecosystems. Within the field of conservation biology today, microbial diversity and ecology are among the most important emerging areas of research and planning. A greater recognition and understanding of these “small matters” may be critical in the conservation of Earth’s biodiversity.

# Center for Biodiversity and Conservation
# Twelfth Annual Symposium
# American Museum of Natural History
# Kaufmann and Linder Theaters

## DAY ONE
## THURSDAY, APRIL 26, 2007

8:00 – 9:00 a.m. REGISTRATION

9:00 a.m. – 12:30 p.m.

## SESSION I
## STANDING ON THE SHOULDERS OF THE TINY: DETECTING AND DESCRIBING MICROBIAL DIVERSITY

### INTRODUCTORY REMARKS

**ELLEN V. FUTTER,** *President, American Museum of Natural History*

**AND MICHAEL J. NOVACEK,** *Senior Vice President and Provost of Science, American Museum of Natural History*

### SESSION INTRODUCTION

Moderator: **SUSAN PERKINS,** *Assistant Curator, Invertebrate Zoology and Sackler Institute for Comparative Genomics, American Museum of Natural History*

### KEYNOTE PRESENTATIONS

The Tree of Life and the Diversification of Eukaryotes

**LAURA A. KATZ,** *Associate Professor, Department of Biological Sciences, Smith College; Graduate Faculty Member, Organismic and Evolutionary Biology and Microbiology, University of Massachusetts Amherst*

It's a Jungle in There: Microbial Diversity in the Human Body

**DAVID A. RELMAN,** *Associate Professor, Microbiology and Immunology, and Assistant Professor of Medicine, Division of Infectious Diseases, Stanford University*

BREAK (20 minutes)

Allopatric Origins of Microbial Species: Evolution of Genome Diversity in Microbial Island Populations

**RACHEL J. WHITAKER,** *Assistant Professor, Department of Microbiology, University of Illinois at Urbana-Champaign*

Genomic Windows on Microbial Species

**JAMES M. TIEDJE,** *Director, Center for Microbial Ecology, Michigan State University, East Lansing*

Microbial Macroecology: Patterns in the Distribution of Microbial Biodiversity

**BRENDAN J. M. BOHANNAN,** *Associate Professor, Center for Ecology and Evolutionary Biology, University of Oregon, Eugene*

Diversity and Biogeography of Marine Viruses

**MYA BREITBART,** *Assistant Professor, College of Marine Science, University of South Florida*

12:30 – 2:00 p.m. LUNCH BREAK

2:00 – 5:00 p.m.

## SESSION II
## CAN'T LIVE WITH 'EM? DISEASES AND OTHER HARMFUL MICROBES — BUT ARE THEY A NECESSARY EVIL?

Moderator: **MARK SIDDALL,** *Associate Curator, Invertebrate Zoology and Sackler Institute for Comparative Genomics, American Museum of Natural History*

### KEYNOTE PRESENTATIONS

The Role of Parasites and Pathogens in Food Webs

**ANDREW DOBSON,** *Professor, Ecology and Evolutionary Biology, Princeton University*

Microbial Diversity, Biogeography, Climate, and Health

**RITA R. COLWELL,** *Distinguished University Professor, University of Maryland College Park and Johns Hopkins University Bloomberg School of Public Health, and Chairman, Canon U.S. Life Sciences, Inc.*

BREAK (20 minutes)

Harmful Algal Blooms — Increasing Prevalence of Microbial Toxins and Impacts

**PATRICIA M. GLIBERT,** *Professor, Center for Environmental Science, University of Maryland*

Biodiversity Loss and the Rise of Zoonotic Pathogens

**RICHARD S. OSTFELD,** *Senior Scientist, Institute of Ecosystem Studies*

Plant-Soil Biota Interactions and Plant Invasions

**KURT O. REINHART,** *Ecologist, Department of Biology, University of Indiana*

Socio-Economic and Environmental Drivers of Emerging Infectious Diseases in Humans

**KATE JONES,** *Academic Fellow, Institute of Zoology, Zoological Society of London*

## THE 2007 MACK LIPKIN MAN AND NATURE SERIES

5:00 p.m.
Reception and Poster Session
(Hall of Northwest Coast Indians)

7:00 p.m.
Panel Discussion (Lefrak Theater)

## SAVE THE MICROBES, SAVE THE WORLD: THE FATE OF MICROBIAL LIFE ON A CHANGING PLANET

### AN EVENING PANEL DISCUSSION

Moderator: **JULIE BURSTEIN,** *Executive Producer, Public Radio International and WNYC Radio ("Studio 360")*

**RITA COLWELL,** *Distinguished University Professor, University of Maryland College Park and Johns Hopkins University Bloomberg School of Public Health, and Chairman, Canon U.S. Life Sciences, Inc.*

**CLAIRE FRASER-LIGGETT,** *Director, Institute of Genome Sciences, University of Maryland School of Medicine*

**JAMES T. STALEY,** *Professor of Microbiology, and Director, Astrobiology Ph.D. Program, University of Washington*

# Center for Biodiversity and Conservation
# Twelfth Annual Symposium
# American Museum of Natural History
# Kaufmann and Linder Theaters

## DAY TWO
## FRIDAY, APRIL 27, 2007

9:00 a.m. – 12:30 p.m.

## SESSION III
## CAN'T LIVE WITHOUT 'EM? THE ROLE OF MICROBES IN THE SUSTAINABILITY OF LIFE ON EARTH

### SESSION INTRODUCTION

**ELEANOR J. STERLING,** *Director, Center for Biodiversity and Conservation, American Museum of Natural History*

Moderator: **ROB DESALLE,** *Curator, Invertebrate Zoology and Sackler Institute for Comparative Genomics, American Museum of Natural History*

### KEYNOTE PRESENTATIONS

Of Microbes and Macrobes: Are Microorganisms Ecologically Different from Their Plant and Animal Descendents?

**SHAHID NAEEM,** *Professor of Ecology and Chair, Department of Ecology, Evolution, and Environmental Biology, Columbia University*

Microbes and Biogeochemical Processes: Dumb, Black-Box Bioreactors in the Dirt?

**PETER M. GROFFMAN,** *Senior Scientist, Institute of Ecosystem Studies*

A Sea of (Genomic) Change: Ecological and Evolutionary Dynamics in Planktonic Microbial Communities

**EDWARD F. DELONG,** *Professor, Division of Biological Engineering and Department of Civil and Environmental Engineering, Massachusetts Institute of Technology*

BREAK (20 minutes)

## SESSION IV
## THE INTERSECTION OF MICROBIOLOGY AND CONSERVATION: CASE STUDIES

Moderator: **FELICITY ARENGO,** *Associate Director, Center for Biodiversity and Conservation, American Museum of Natural History*

The 5,000 Virus Genome Project: Using New Sequencing Technology to Answer Questions in Biodiversity and Ecology

**MARILYN J. ROOSSINCK,** *Scientist, Plant Biology Division, The Samuel Roberts Noble Foundation*

Lessons from Oligotrophs

**STEPHEN J. GIOVANNONI,** *Pernot Professor, Department of Microbiology, Oregon State University*

The Direct and Indirect Effects of Parasites on Plant Community Restorations

**BITTY A. ROY,** *Associate Professor, Center for Ecology and Evolutionary Biology, University of Oregon, Eugene*

12:30 – 2:00 p.m. LUNCH BREAK

2:00 – 3:10 p.m.

## SESSION IV continued

### Shedding New Light on a Dark Topic: The Microbial Wonderland of Caves

**DIANA NORTHUP,** *Visiting Associate Professor of Biology, and Professor Emerita, Centennial Science and Engineering Library, University of New Mexico*

### Viruses, Microbes, and the Decline of Coral Reefs

**FOREST ROHWER,** *Assistant Professor, Department of Biology, San Diego State University*

### Sex, Drugs, and Penguins: A Study of Antibiotic Resistance in Antarctica

**ROBERT V. MILLER,** *Regents Professor and Head, Department of Microbiology and Molecular Genetics, Oklahoma State University*

**BREAK** (20 minutes)

3:40 – 5:00 p.m.

## CAPSTONE PANEL DISCUSSION

Moderator: **GEORGE AMATO,** *Director, Sackler Institute for Comparative Genomics, American Museum of Natural History*

**DURLAND FISH,** *Professor of Epidemiology, Yale University*

**JESSICA L. GREEN,** *Assistant Professor, School of Natural Sciences, University of California, Merced*

**MICHELE K. NISHIGUCHI,** *Associate Professor of Evolutionary Biology, Department of Biology, New Mexico State University*

**PAUL TURNER,** *Associate Professor of Ecology and Evolutionary Biology, Yale University*

**BESS B. WARD,** *Chair, Department of Geosciences and William J. Sinclair Professor of Geosciences, Princeton University*

**CLOSING REMARKS**

**ELEANOR J. STERLING,** *Director, Center for Biodiversity and Conservation, American Museum of Natural History*

AVAILABLE ON LINE

Speaker abstracts and participant bios and publications are posted on our website: http://cbc.amnh.org/symposia/microbes/

## Brendan J. M. Bohannan

Associate Professor, Center for Ecology and Evolutionary Biology, University of Oregon, Eugene

### MICROBIAL MACROECOLOGY: PATTERNS IN THE DISTRIBUTION OF MICROBIAL BIODIVERSITY

*The variety of life has long fascinated biologists. One of the most intriguing aspects of this variety is that it is not randomly distributed — there are* patterns *in the distribution of life's diversity. Such patterns include diversity-energy, diversity-area, and diversity-latitude patterns, among others. The study of these patterns in plant and animal life has been called "macroecology," and it has played an important role in conservation. The study of "microbial macroecology" is in its infancy. Recent research has documented spatial and temporal patterns in the distribution of microbial life, in many cases qualitatively similar to those documented for plants and animals. These observations raise the intriguing possibility that there are biodiversity scaling rules common to all forms of life.*

## Mya Breitbart

Assistant Professor, College of Marine Science, University of South Florida

### DIVERSITY AND BIOGEOGRAPHY OF MARINE VIRUSES

*Viruses are the most abundant biological entities in the marine environment, and play important roles in biogeochemical cycling, horizontal gene transfer, and defining bacterial community composition. Metagenomic analyses of viruses collected from throughout the world's oceans have recently provided insight into the identity, diversity, and biogeography of marine viruses. The majority of the viral sequences were not similar to those in the current databases, but there was a distinct shared "marine" quality amongst the identifiable sequences. Despite the shared qualities, different marine regions had different assemblages of viruses. Cyanophages and a newly discovered clade of single-stranded DNA phages dominated the Sargasso Sea sample, whereas prophage-like sequences were most common in the Arctic. However, most of the differences between viral communities were explained by variation in the relative abundance of the most common viral types, rather than exclusion of certain viral genomes. Mathematical modeling suggested that the global marine virome contained hundreds of thousands of species. These results support the idea that viruses are widely dispersed throughout the oceans and that local conditions enrich for certain viral types through selective pressure.*

## Rita R. Colwell

Distinguished University Professor, University of Maryland College Park and Johns Hopkins University Bloomberg School of Public Health, and Chairman, Canon U.S. Life Sciences, Inc.

**KEYNOTE PRESENTATION**

### MICROBIAL DIVERSITY, BIOGEOGRAPHY, CLIMATE, AND HEALTH

*Vector-borne diseases have long been recognized to be climate driven, but it is now clear that many infectious diseases are intricately related to weather patterns, climate, and seasonality. Epidemics of cholera, a devastating disease occurring predominantly in third world countries, has been shown to be directly correlated with environmental parameters including sea surface temperature, sea surface height, and salinity, among others. Recent studies incorporating satellite sensing technology, ground truth measurements, and microbiological analyses have provided the basis for predictive modeling of cholera epidemics in Bangladesh, India, and East Africa. From these studies, it is clear that microbial diversity and biogeography will play an increasing role in understanding human health and infectious diseases. Currently under way is analysis of more than 30 strains of* Vibrio cholerae *and related spp., from widely diverse geographical sources, to address the genomic basis of biogeography at the species level.*

## Edward F. DeLong

Professor, Division of Biological Engineering and Department of Civil and Environmental Engineering, Massachusetts Institute of Technology

**KEYNOTE PRESENTATION**

### A SEA OF (GENOMIC) CHANGE: ECOLOGICAL AND EVOLUTIONARY DYNAMICS IN PLANKTONIC MICROBIAL COMMUNITIES

*Modern genetics, molecular biology, and genomics have their roots in a reductionist world view that dissects its understanding of Biology from the component molecular and cellular parts list — typically at the sub-cellular level. One of the larger lessons learned from comparative genomics, however, is that microbial genomes are not static entities, nor do they evolve in a vacuum. Rather, microbial community processes, including (but not limited to) lateral gene transfer, intra- and inter-species interactions, metabolic complementation and cross-feeding, competition, predation, etc., shape what genome is. Genome, in reality, is a verb, not a noun. Recently, applications of environmental genomics offer a window into this genome dynamism, and the processes that drive microbial ecology and evolution in natural environments. A few examples from ocean-going microbial community genomic surveys help to illustrate these points.*

## Andrew Dobson

Professor, Ecology and Evolutionary Biology, Princeton University
Coauthors: **Armand Kuris, Ryan Hechinger**, and **Kevin Lafferty**

**KEYNOTE PRESENTATION**

### The Role of Parasites and Pathogens in Food Webs

*Food webs are the last frontier of ecological knowledge. Their mathematical structure is more complicated than that of galaxies and atoms, yet we have only recently realized that parasites and pathogens play a major role in determining the structure of food webs. Dr. Dobson will describe examples from intense quantitative studies of salt marsh food webs along the coast of California and Baja Mexico that include data on parasites. The results suggest that parasites may form as much as 50 percent of the biological diversity within a web and that their biomass may exceed that of the major vertebrate taxa. Moving inland, he will then describe the potential role that pathogens play in modifying the plant community structure in California grassland ecosystems.*

## Stephen J. Giovannoni

Pernot Professor, Department of Microbiology, Oregon State University

### Lessons from Oligotrophs

*The introduction of new culturing procedures has led to a dramatic increase in the number of important bacterioplankton groups that are being cultivated and studied in a laboratory setting. Among the most significant new isolates are members of the SAR11* (Pelagibacter) *clade.* Pelagibacter *accounts for approximately 25 percent of microbial plankton cells in the ocean surface layer, and may exceed 50 percent of the cells in temperate ocean gyres during summers. The* Pelagibacter *genome is only 1,308,506 bp, but it is sufficient to encode all of the functions needed for this free-living cell to play a dominant role in the oxidation of the oceanic dissolved organic carbon pool.* Pelagibacter *is an obligate oligotroph that so far can only be grown on natural seawater, where it replicates reliably and reaches densities of about 106 cells/ml, similar to native populations. In contrast to parasitic Bacteria and Archaea with small genomes,* Pelagibacter *has complete pathways for most fundamental metabolic functions, including biosynthetic pathways for all twenty amino acids.* Pelagibacter *also expresses the light-dependent proton pump Proteorhodopsin. It has no pseudogenes, introns, transposons, extrachromosomal elements or inteins, few paralogs, and the shortest intergenic spacers yet observed for any cell. Metagenomic data is providing an opportunity to investigate the SAR11 genome diversity. Analysis of Venter's Sargasso Sea SAR11 metagenomic data suggests that ocean gyre populations of SAR11 are similar to coastal isolates in conserved, core regions of the genome, but differed markedly in islands of genomic variability. The largest variable genomic island lies between the 23S and 5S rRNA genes, and encodes genes for cell surface properties. Extraordinarily high allelic variation and genome rearrangements appear to mask the conservation of many genome properties in native SAR11 populations, leading to overestimates of species diversity.*

## Patricia M. Glibert

Professor, Center for Environmental Science, University of Maryland

### Harmful Algal Blooms — Increasing Prevalence of Microbial Toxins and Impacts

*Harmful Algal Blooms (HABs), formerly often called "red tides," are proliferations of microscopic or macroscopic algae that have many deleterious impacts on the environment. These impacts include development of high biomass and scums, shading of submerged aquatic plants, direct toxicity to fish and shellfish, oxygen depletion, alteration of food webs, and suffocation of fish from mucus production and gill interference. The range of toxins produced by HABs is quite extensive, including brevetoxins, the cause of neurotoxic shellfish poisoning (NSP); saxitoxins, the cause of paralytic shellfish poisoning (PSP); okadaic acid, the cause of diarrhetic shellfish poisoning (DSP); domoic acid, the cause of amnesic shellfish poisoning (ASP); and azaspiracid, the cause of azaspiracid shellfish poisoning (AZP), and numerous others. Over the past few decades, the world's coastal waters have experienced an increase in the number and type of HAB events. As with all blooms, their proliferation results from a combination of physical, chemical, and biological mechanisms and their interactions with other components of the food web that are, for the most part, poorly understood. Although some of the factors contributing to national – and global – expansion are natural, such as biological species dispersal, many others are considered to be a result of human activities. Increases in nutrient loading, changes in agriculture and aquaculture practices, overfishing, ballast water discharge, and global climate change may all be important in the global increase in HABs.*

## Peter M. Groffman

Senior Scientist, Institute of Ecosystem Studies, New York

**KEYNOTE PRESENTATION**

### MICROBES AND BIOGEOCHEMICAL PROCESSES: DUMB, BLACK-BOX BIOREACTORS IN THE DIRT?

*Microbes carry out a vast array of biogeochemical processes that are critical to a variety of ecosystem services related to the production of food and fiber and water and air quality. These processes include the degradation of organic matter and the recycling of nutrients contained therein, and also the production and consumption of water and air pollutants, including trace gases that influence the chemistry and physics of the atmosphere. Analysis of these processes is complicated by the impressive physiological flexibility of microbes, the difficulty of studying their activity* in situ*, and the close coupling between microbial and plant processes in nature. It has been particularly challenging to determine the importance of diversity in regulating microbial processes. As a result it is currently not clear if microbial communities and their activity can be treated as simple black-box bioreactors, or if understanding and management of microbial processes requires a detailed understanding of community structure, diversity, and dynamics.*

## Kate Jones

Academic Fellow, Institute of Zoology, Zoological Society of London
Co-Authors: **K.E. Jones, N. Patel, M. Levy, A. Storeygard, D. Balk, J.L. Gittleman,** and **P. Daszak**

### SOCIO-ECONOMIC AND ENVIRONMENTAL DRIVERS OF EMERGING INFECTIOUS DISEASES IN HUMANS

*Human emerging or re-emerging infectious diseases (EIDs) are considered to be an extremely significant burden to human public health and economies. A range of socio-economic and environmental factors (such as greater rates of trade and travel, population growth, agricultural changes, increased antibiotic drug use, and climate change) are considered to be among the important drivers of the emergence and re-emergence of these diseases. However, few studies have explicitly analyzed these linkages to build a critical understanding of when, where, and what diseases will be emerging next. Here we investigate the temporal and spatial patterns of the initial occurrence of EID events reported in humans between 1842 and 2004 and examine the links with a range of socio-economic, environmental, and ecological factors. We find that the majority of EID events involve bacterial pathogens, are originally transmitted to humans from wild animal populations (are zoonotic), and their reported rate of emergence or re-emergence has risen significantly this century and reached a peak in 1980 to 1990s. EID events occur mainly at higher latitudes and are concentrated in a few places such as the northeastern U.S., Western Europe, Japan, and southeastern Australia. Controlling for the effect of disease reporting bias, we demonstrate significant positive independent correlations with EID events and human population density and growth, latitude, rainfall, and host biodiversity. Dr. Jones and colleagues anticipate that these analyses will form the starting point of predictive modeling to understand and mediate the consequences of future emerging and re-emerging infectious diseases under different scenarios of global change.*

## Laura A. Katz

Associate Professor, Department of Biological Sciences, Smith College; Graduate Faculty Member, Organismic and Evolutionary Biology and Microbiology, University of Massachusetts Amherst

**KEYNOTE PRESENTATION**

### THE TREE OF LIFE AND THE DIVERSIFICATION OF EUKARYOTES

*Data from microbes have transformed our views on the patterns and processes underlying the diversification of life on Earth. Prokaryotes evolve through a complex interaction between vertical and lateral inheritance of genes. Hence, attempts to catalog prokaryotic diversity and elucidate the ecological principles that drive this diversity must accommodate the varying patterns of inheritance in prokaryotic individuals, populations, and "species." Although data remain sparse for many lineages, the invention of the nucleus in eukaryotes appears to have reduced, though certainly not eliminated, lateral transfers of single genes. Eukaryotes have been impacted by at least two major influxes of genes, in the acquisition of mitochondria and later of chloroplasts. In view of this backdrop of lateral transfer, Dr. Katz and colleagues are working towards reconstructing a eukaryotic tree of life that reflects the portion of eukaryotic genomes that have evolved through vertical processes. By focusing on poorly known lineages of amoebae and flagellates, they are evaluating current taxonomic hypothesis and proposing a new framework for the origin and diversification of eukaryotic life.*

## Robert V. Miller

Regents Professor and Head, Department of Microbiology and Molecular Genetics, Oklahoma State University

### SEX, DRUGS, AND PENGUINS: A STUDY OF ANTIBIOTIC RESISTANCE IN ANTARCTICA

*Widespread use of antibiotics is rapidly and dramatically changing the face of drug resistance in bacteria. To understand how antibiotic use has affected the evolution of drug resistance in bacteria, a "base line" of drug resistance distribution must be obtained. Currently, we do not possess a time machine that will* *allow us to go back in time to a pre-antibiotic era. However, antibiotic use in the Antarctic has been minimal and may afford us with the base-line resistance profile we need. Dr. Miller's research group has been exploring the distribution of antibiotic resistance in populations of Antarctic penguins and in the seawaters surrounding Palmer Station, Antarctica. Some of the questions the group has been addressing include: "What drug resistances are co-inherited?"; "How prevalent is drug resistance?"; "Are these drug resistances transferable by conjugation or other gene transfer mechanism?"; and "Has human habitation at Palmer Station affected the distribution of antibiotic resistance among Southern Ocean microbes?"*

## Shahid Naeem

Professor of Ecology and Chair, Department of Ecology, Evolution, and Environmental Biology, Columbia University

**KEYNOTE PRESENTATION**

### OF MICROBES AND MACROBES: ARE MICROORGANISMS ECOLOGICALLY DIFFERENT FROM THEIR PLANT AND ANIMAL DESCENDENTS?

*At first glance, the living world seems a riot of colors, sounds, smells, shapes, and forms; trillions of organisms belonging to millions of species found in every pore, crack, and crevice of all the sands, soils, and sediments of every surface, in every body of water, and in the air. Life on Earth seems an unruly entanglement of plants, animals, and microorganisms, all feeding, breeding, and having at one another, red in tooth and claw. Though this seems like a formula for utter chaos, biodiversity is surprisingly highly ordered and rich in extraordinary patterns — at least for multi-cellular plants and animals, or the "macrobes." How many big and small, how many fierce and tame, how many rare and common, how diverse, and many other properties of biodiversity are remarkably predictable. Nature is anything but chaotic and it is these remarkable patterns that allow us to manage, restore, and conserve biodiversity. Now, recent advances in molecular methods are telling us that microbes show patterns like macrobes. These astonishing findings, if true, imply that all of biodiversity, from its smallest to its biggest creatures, throughout the whole of the biosphere, is not random but highly structured.*

## Diana Northup

Visiting Associate Professor of Biology, and Professor Emerita, Centennial Science and Engineering Library, University of New Mexico

### SHEDDING NEW LIGHT ON A DARK TOPIC: THE MICROBIAL WONDERLAND OF CAVES

*Contrary to their reputation as dank, slimy holes in the ground, caves are breathtakingly beautiful in the geological sense and fascinating in the microbial realm. Caves provide a wealth of environmental challenges and opportunities for microorganisms due to the total darkness beyond the twilight zone; the generally constant relative humidity and temperature; their patchy, often oligotrophic nature; and the occasional wealth of reduced gases. The cycling of iron, manganese, sulfur, and nitrogen by microorganisms inhabiting caves and the role of microorganisms in precipitating calcium carbonate speleothems are of particular interest to the research team. Using multidisciplinary approaches (microscopy, geochemistry, cultivation, and molecular biology), the team has established that microorganisms in Lechuguilla and Spider Caves (New Mexico) oxidize reduced iron and manganese in the carbonate walls to produce abundant ferromanganese deposits that coat many walls and ceilings of the caves. Some of the genetic sequences recovered from these deposits indicate the possibility of nitrogen cycling, and an abundance of mesophilic Archaea have been identified in one site. In Cueva de Villa Luz (Tabasco, Mexico), studies have revealed sulfate-reducing and sulfur-oxidizing bacteria in the black mud of the stream, and the biofilms that hang from the ceiling ("snotties") and that line the hydrogen sulfide vents ("phlegm balls"). These studies have shed light on nutrient cycling in the subsurface through the windows of caves and have revealed a novel and fascinating community of microorganisms that are worthy of protection.*

## Richard S. Ostfeld

Senior Scientist, Institute of Ecosystem Studies

### BIODIVERSITY LOSS AND THE RISE OF ZOONOTIC PATHOGENS

*The majority of emerging infectious diseases are caused by pathogens that are maintained in wildlife hosts and occasionally transmitted to humans (i.e. zoonoses). Most zoonotic pathogens tend to replicate well in a small number of highly competent "reservoir" species, and human infection occurs when they "spillover" from these reservoirs to us, often aided by a vector such as a mosquito or tick. For many epidemiologically important zoonoses, the wildlife reservoirs tend to be abundant, resilient species that proliferate when human activities degrade or fragment habitats. Examples include Lyme disease, for which the main reservoirs are small rodents such as white-footed mice; and West Nile Virus, for which competent reservoirs include songbirds such as Blue Jays, Common Grackles, American Robins, and House Finches. This talk will present evidence that the loss of biodiversity can increase risk of human exposure to zoonotic pathogens by favoring highly competent reservoirs. High diversity, in turn, creates a "dilution effect" by distributing both vectors and pathogens among a large group of generally poor-quality hosts.*

## Kurt O. Reinhart

Ecologist, Department of Biology, University of Indiana

### PLANT-SOIL BIOTA INTERACTIONS AND PLANT INVASIONS

*Exotic invaders are a major global threat to biodiversity and ecosystem function. Experimental studies find greater damage to invading plant species in their home vs. invaded ranges, but little is known about the biological mechanisms underlying this variation. Here, Dr. Reinhart reports that isolates of the soil-borne* Pythium *pathogens are abundant, but isolates collected from soil surrounding the invasive tree* Prunus serotina *in its native U.S. range caused more root rot (≥151%) and mortality (≥64%) of seedlings than* Pythium *from the non-native European range. These experimental results, along with demographic patterns of* P. serotina *density in nature, strongly indicate that* Pythium *associated with* P. serotina *are causing more mortality in native than non-native ranges. These findings support the Enemy Release Hypothesis, which predicts plants that invade non-native regions experience less density regulation by enemies. However, there were some pathogenic isolates from the non-native range, indicating the potential for pathogens to eventually regulate the density of* P. serotina *in invaded forests. Understanding why invading species are less affected by resident enemies is important for developing strategies to predict and control exotic plants in their new ranges.*

## David A. Relman

Associate Professor, Microbiology and Immunology, and
Assistant Professor of Medicine, Division of Infectious Diseases,
Stanford University

**KEYNOTE PRESENTATION**

### IT'S A JUNGLE IN THERE: MICROBIAL DIVERSITY IN THE HUMAN BODY

*Complex microbial ecosystems occupy the cutaneous and mucosal surfaces of humans. Recent advances have highlighted both the tremendous diversity of these communities and their importance to host physiology, yet it is humbling to think that we currently understand more about the tropical rain forest than we do these communities with whom we share our bodies! Questions remain about the ecological processes that establish and maintain the human microbiota throughout life. Furthermore, basic features of the human microbial ecosystem remain poorly described, including variability in diversity, in space and time. Host individuality imposes a strong signature on patterns of diversity. In turn, our indigenous microbial ecosystem defines who we are as individuals. Assembly of the oral and the gut microbiota may also involve both stochastic historical events and contemporary environmental factors. Approaches that combine community ecology, molecular microbial ecology, and metagenomics may improve our understanding of health and disease within the communal human organism. By understanding the patterns of diversity associated with human health, we may be able to preserve and restore health more effectively. By recognizing the early signs of impending disturbance, we may be able to predict and avoid disease.*

## Forest Rohwer

Assistant Professor, Department of Biology, San Diego State University

### VIRUSES, MICROBES, AND THE DECLINE OF CORAL REEFS

*The roles of microbes in ecosystem health and decline are just starting to be elucidated. Recently, Dr. Rohwer and colleagues have described the abundance, taxonomic composition, and metabolic potential of the microbial communities from relatively pristine to moderately disturbed coral reefs in the Northern Line Islands. The highest human population on Kirimati atoll was associated with a 10-fold increase in both the number of microbes and viruses versus the unpopulated Kingman atoll. The microbial community switched from a co-dominance of autotrophic and heterotrophic Bacteria on Kingman, to primarily heterotrophs, including many pathogen-like microbes* (Escherichia, Streptococcus, Staphylococcus, *etc.), on Kirimati. Coral disease incidences also increased on the human disturbed reef, despite a decline in coral cover. Dr. Rohwer proposes that a general increase in pathogen-like microbes associated with human disturbance leads to opportunistic coral diseases and reef decline.*

## Marilyn J. Roossinck

Scientist, Plant Biology Division, The Samuel Roberts Noble Foundation, Oklahoma

### THE 5,000 VIRUS GENOME PROJECT: USING NEW SEQUENCING TECHNOLOGY TO ANSWER QUESTIONS IN BIODIVERSITY AND ECOLOGY

*Viruses are ubiquitous in life on Earth, but are extremely understudied. Almost all of our knowledge of viruses is derived from those that cause disease in humans and their domesticated plants and animals. Dr. Roossinck has undertaken a study to understand the incidence and diversity of plant viruses. She analyzes dsRNA patterns (a hallmark of RNA virus infection) from plants collected systematically in a biodiversity hot-spot, northwestern Costa Rica, and is determining the sequences of large numbers of these dsRNAs using and adapting 454 LifeSciences technology.*

## Bitty A. Roy

Associate Professor, Center for Ecology and Evolutionary Biology, University of Oregon, Eugene

### THE DIRECT AND INDIRECT EFFECTS OF PARASITES ON PLANT COMMUNITY RESTORATIONS

*Why should we consider plant parasites (pathogens and herbivores) during restoration? On the positive side, we need to remember that parasites are a key element of diversity themselves, comprising approximately half of all biological diversity. Furthermore, pathogen-mediated selection can maintain polymorphism in host genotypes and species; in the absence of parasite-mediated selection or similar stabilizing mechanisms, competitive exclusion will occur, leading to a loss of host diversity. On the negative side, restorations may be vulnerable to parasite attack for a number of reasons:*

1. *They are often planted at high densities with a low diversity of species, which may increase vulnerability to infection.*
2. *Invasive species may bring with them parasites that shift to the non-coevolved natives, or the invasives may be more competent hosts, increasing the overall infection rates in the community, or infection may cause apparent competition.*
3. *Global warming will increase plant water stress, leading to changes in infection rates.*
4. *Global warming will increase fire in some systems, which can alter infection probabilities.*

*Whether or not parasites influence plant restorations depends on the scale (ecological or evolutionary) at which their activities are examined, the degree of host-parasite specificity, whether or not the parasites are native, and interactions with the environment.*

## James M. Tiedje

Director, Center for Microbial Ecology, Michigan State University, East Lansing

### GENOMIC WINDOWS ON MICROBIAL SPECIES

*Defining species has always been difficult in the Bacteria and Archaea since we do not have an accepted species concept. We do give microbes genus and species names based on an operational definition that includes both genetic and phenotypic information but with an arbitrary cut-off that probably does not recognize natural organism clustering and does not recognize the organism's natural ecology. Genomic information provides us the first comprehensive insight into a microbe's full genetic complement, which reveals much about its evolution, its gene content, and probably reflects its ecology. Dr. Tiedje and colleagues have used genomic information from several groups of microbes to obtain better phylogenetic resolution among closely related strains, to learn whether species have a common set of core genes, and to learn the extent of additional genes explored within a species. Burkholderia is one example: a microbial group that most commonly lives on roots of grassy plants, but also causes disease in cystic fibrosis patients, degrades pollutants, prevents as well as causes plant diseases, and fixes nitrogen — even in nodules of legume plants. We term this microbe a versaphile since it can live in so many habitats and perform so many functions. This may be due to its large genome and its arrangement into three replicons allowing for genetic flexibility. Microbes have a 3.8 billion year evolutionary history and would be expected to explore many strategies leading to their current success, and hence it is the differences among microbial groups that will reveal the interesting biology. Dr. Tiedje will also report on the growth in the microbial species detection from the accumulating 16S rRNA gene database, and show that there is no sign yet of nearing a plateau in the discovery of new species, genera, families, or orders.*

## Rachel J. Whitaker

Assistant Professor, Department of Microbiology, University of Illinois at Urbana-Champaign

### ALLOPATRIC ORIGINS OF MICROBIAL SPECIES: EVOLUTION OF GENOME DIVERSITY IN MICROBIAL ISLAND POPULATIONS

*The mechanisms of microbial speciation will emerge by examining the high-resolution structure of diversity within and between microbial populations. Because microbial genomes are so small, these analyses can now be done on the whole genome scale – showing recent genome changes that have occurred as lineages diverge into incipient species.* Sulfolobus islandicus *is a thermophilic Archaea that lives in biogeographically isolated populations in globally distributed geothermal regions. As these isolated populations evolve in local environments, their genomes reflect adaptive changes selected by environmental conditions. Comparative genomics among seven fully sequenced* S.islandicus *strains shows dramatic patterns of genome change that have occurred in the recent evolutionary history of this species as populations diverge in allopatry. These data provide insight into the distribution of diversity within microorganisms that has important implications for understanding allopatric speciation and the "pangenome" diversity. Understanding the distribution of diversity among endemic populations will help to design approaches to conserve the wealth of microbial biodiversity upon which all organisms on Earth depend.*

# Center for Biodiversity and Conservation
# American Museum of Natural History

In 1993, the American Museum of Natural History created the Center for Biodiversity and Conservation (CBC) to enhance the use of scientific data to mitigate threats to biodiversity. The CBC develops strategic partnerships to expand scientific knowledge about diverse species in critical ecosystems, and to apply this knowledge to conservation; builds professional and institutional capacities for biodiversity conservation; and heightens public understanding and stewardship for biodiversity. Working both locally and around the world, the CBC develops model programs that integrate research, education, and outreach so that people — a key factor in the rapid loss of biodiversity — will become participants in its conservation.

The CBC's programs focus on areas of the world where biodiversity is richest and most threatened, as well as on taxa that have traditionally been neglected in the conservation process, such as invertebrates. The CBC has active projects in The Bahamas, Bolivia, Madagascar and southern Africa, the Pacific Islands, Vietnam, and the United States.

Raising awareness and promoting conservation action are also CBC imperatives, and through symposia, workshops, and publications we help to inform the public about biodiversity issues. To make the complex political and economic decisions necessary for the protection of global biological resources, people must have the scientific tools to identify and understand the mechanisms behind the threats to biodiversity. The CBC's role is to equip the world community to use these tools effectively.

Learn more about the CBC at: http://cbc.amnh.org

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