SMALL MATTERS:
Microbes and Their Role in Conservation

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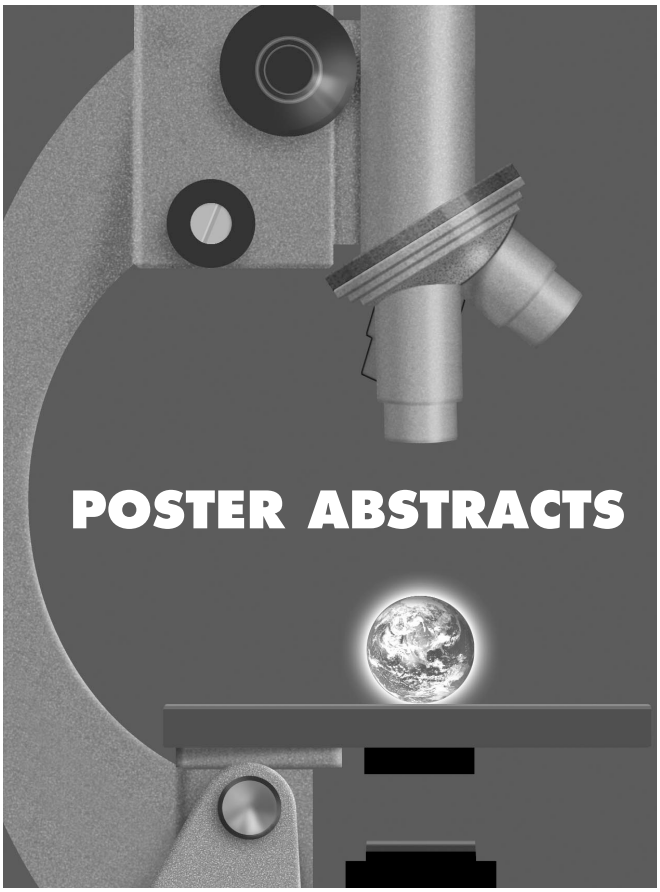

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Posters on display during the symposium are organized alphabetically, by first author, beginning to the left on entering the Hall of Northwest Coast Indians.

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METAGENOMICS REVEALS UNEXPECTED DIVERSITY OF β-LACTAM ANTIBIOTIC RESISTANCE GENES IN PRISTINE ALASKAN SOIL

A golden era of antibiotics is coming to a close in part because of the prevalence and spread of antibiotic resistance. Resistance to many new antibiotics arises quickly, and spreads easily because of the transfer of DNA among bacteria. It is important to address how and from where resistance arises in order to understand and prevent resistance in the clinic. Soil, for example, has been implicated as a potential reservoir of antibiotic resistance genes. However, the few studies of resistance in soil have focused on agricultural or polluted soils; therefore the diversity of resistance genes in a pristine soil is virtually unknown. Furthermore, most studies of resistance rely on culturable bacteria, thereby limiting the analysis to the 1% of soil bacteria that can be cultured on a petri plate. To address the gaps in knowledge and assess the full scope of the diversity of antibiotic resistance in soil, we surveyed β-lactam antibiotic resistance genes from a remote, Alaskan soil from an island in the Tanana River near Fairbanks, Alaska. Metagenomics was used to access the genes from the unculturable bacteria of soil. Metagenomics is the study of the composite DNA from all of the thousands of different bacteria in an environmental sample. This composite, or metagenome, from Alaskan soil was fragmented and cloned, and the resulting clone library was selected on eight different β-lactam (ie: penicillin) antibiotics. Fourteen different antibiotic resistance genes were isolated, and the most common type encoded β-lactamases. βeta-lactamases confer resistance by deactivating the β-lactam molecule. One gene conferred resistance to β-lactams, but was not a recognizable β-lactamase. Pristine soil, therefore, is a reservoir of new and diverse β-lactam antibiotic resistance genes. These data will inform future studies of the sources of antibiotic resistance and strategies for managing antibiotic resistance in medicine.

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THE BIODIVERSITY OF SEA ICE COMMUNITIES IN THE BALTIC SEA

The Baltic Sea is the world's largest brackish water basin. Its water is a mixture of saline water from the Atlantic and fresh water supplied by numerous rivers. The species richness in the Baltic is greatly affected by the salinity of the water. Brackish water bodies (2-15‰), like the Baltic Sea, are considered species poor. Reduced species richness in relation to salinity stress is obvious along the Baltic Sea gradient. The Baltic Sea freezes annually because of its northern location. The ice covers about 200 000 km², which is almost half of the total area of the Baltic Sea. Winter-time was long held to be a dormant period when organisms survived at the limits of their physiological tolerance. However, biological studies on sea ice have shown that there are active algal and protist communities in the sea ice. The biodiversity of these communities has not been assessed before. It has been assumed that sea ice exhibits biodiversity comparable to that found in the underlying water. In this study we have assessed the biodiversity of sea ice communities (0.65-20 µm) using molecular ecological methods based on sequencing of small-subunit ribosomal RNA gene clone libraries. The results of our study show that the sea ice communities in the Baltic Sea are extremely diverse compared to the Baltic Sea water. This suggests that ice communities may be important in the over-wintering of microscopic algae and protists and that the biodiversity of eukaryotes in the Baltic Sea may be underappreciated if only measured from the water. Our study highlights the loss that is likely to face us when the ice cover is diminishing or disappearing as a result of the climate change and the rising temperatures. It highlights an imperative need to understand biodiversity before its loss on a global scale.

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DISTRIBUTION, DIVERSITY AND SULFIDOGENESIS OF PROKARYOTES IN THE UZON CALDERA

Prokaryotes are known to be exceptionally diverse, yet the mechanisms shaping the distribution of this diversity are not

well-defined. Importantly, the diverse metabolic activities of prokaryotes can influence local and global biogeochemical cycles. Thermophilic sulfidogenic prokaryotes, for example, may contribute to sulfide mineralization in volcanically-derived hydrothermal fields such as those in the Uzon Caldera, Kamchatka, and Far East Russia. Here we preliminarily examined some differences among hot pools in Uzon, which may affect the presence and abundance of sulfate-reducing prokaryotes (SRP). Enumeration-enrichment cultures demonstrated that heterotrophic SRP were heterogeneously distributed throughout the caldera and possibly limited by high temperatures. Two geochemically-distinct pools, Arkashin Shaft and Zavarzin II Spring, were selected to compare the activity of SRP and the diversity of Bacteria. We used ^{35}S-radiotracer experiments to determine sulfate-reduction rates (SRR) for different depths in sediment cores from both pools. The absolute value of SRR was higher in Arkashin, 2.0 nmol-cm^{-3}hr^{-1}, than in Zavarzin, 0.3 nmol-cm^{-3}hr^{-1}. In Zavarzin, sulfate-reduction occurred at multiple depths. In Arkashin, sulfate-reduction appeared restricted to a specific depth, possibly due to the presence of alternative electron acceptors. We generated 16S rRNA gene sequence libraries and found that taxonomic groups which include sulfidogenic bacteria, such as the genus Desulfurella*, occurred in both pools. Many of the sequences were not represented by isolated and described species. Estimating the diversity of sequences in each library indicated that higher richness depended on the level of comparison. Surprisingly, Arkashin had more phyla, but Zavarzin had more species. Evidence for sulfide biomineralization in Uzon may help in identification of biomarkers in the rock records of Earth and other planets. Continuing efforts, focused on the isolation of both sulfidogenic and arsenate-reducing prokaryotes and sequencing of Archaeal 16S rRNA genes, should provide additional insight to the distribution and diversity of prokaryotes in terrestrial thermal environments.*

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Biogeochemical Interactions during Microbial Iron and Nitrogen Cycling in Anoxic Sediments

Redox cycling of iron (Fe) plays a major role in the fate of many compounds in terrestrial and aquatic ecosystems. While nitrate (NO_3^-) is also present in many such environments, much remains to be learned about the complex biogeochemical interactions between Fe and N during redox cycling in anoxic sediments. Although NO_3^- reduction typically precedes Fe(III) reduction in sediments, we have shown that NO_3^- reduction rates can be inhibited by small amounts of Fe(II) produced during minimal Fe(III) reduction. This inhibition is explained by a chemical reaction between sorbed Fe(II) and biogenic nitrite (NO_2^-) resulting in formation of Fe(III) (oxy)hydroxide cell coatings that block NO_3^- transport into the cell. Evidence is provided by SEM and TEM analyses and by chelators which relieve inhibition by preventing the required Fe(II) sorption. Although this abiotic reaction between Fe(II) and NO_2^- is relatively fast, Fe(II) reacts with NO_3^- much more slowly and the microbial oxidation of Fe(II) with NO_3^- is a much more important reaction. Coupled Fe-N redox interactions may lead to novel microbial communities specifically adapted to redox oscillations. Microbial redox processes and communities that develop during either nitrate or iron reduction versus multiple cycles of iron reduction and nitrate-dependent Fe(II) oxidation were examined using river sediment. For the latter systems, NO_3^- and acetate were periodically added allowing four cycles of microbial Fe(III) reduction and Fe(II) oxidation. NO_3^- addition under low-carbon conditions caused rapid microbial Fe(II) oxidation and NH_4^+ accumulation. Microbial communities associated with iron redox cycling were assessed using culture-based and phylogenetic techniques. NO_3^--reducing cultures were dominated by beta-Proteobacteria, Fe(III)-reducing cultures by delta-Proteobacteria, and iron-cycling cultures more diversely populated. These results suggest that repeated iron-cycling results in a diverse community able to take advantage of available energy.

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Identification of the Natural Bacterial Microbiota on the Skin of Eastern Newts, Bullfrog tadpoles and Redback Salamanders

Amphibian populations in several regions of the world appear to be declining due to infectious diseases. While many studies have identified the pathogens associated with specific declines, very few studies have attempted to identify the natural microbiota that is present on amphibian skin. Knowledge of the natural microbiota that healthy individuals carry may, in some cases, provide valuable background information so that pathogens can be more readily identified. In addition, it may be possible in the future to utilize the beneficial bacteria from amphibian skin as probiotics for the prevention and/or treatment of disease in amphibians. In this study, we used traditional culturing methods

to isolate the natural bacterial microbiota found on the skin of apparently healthy adult eastern newts (Notophthalamus viridescens)*, larval bullfrogs* (Rana catesbieana) *and redback salamanders* (Plethodon cinereus) *living in natural field sites in Virginia. Using a combination of biochemical tests and fatty acid methyl ester (FAME) profiles, we positively identified five bacterial species from newts, three bacterial species from bullfrogs and four bacterial species and one yeast from redback salamanders. In a parallel study, we used Biolog EcoPlates to examine the physiological profiles of bacterial communities at six sites with newt and bullfrog tadpole populations. A cluster analysis resulted in two main groupings: one for all the water samples and one for all the skin swab samples from the amphibians. This result suggests that only a sub-set of bacteria in the environment are able to successfully colonize amphibian skin. Future studies will focus on the interactions between these skin bacteria and potential pathogens and on the impact of environmental stressors on the skin microbiota.*

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From Culture to Transplantation: Microbial Profiling for Coral Reef Restoration

Coral aquaculture and transplantation are currently being employed to address worldwide decline of coral reefs and promote reef ecosystem recovery. Issues that arise with these restoration strategies include possible introduction of diseases onto natural reefs and the vulnerability of transplanted corals to bleaching and disease. Although these efforts are promising, current approaches have yet to incorporate analyses of coral-associated microbes as a health indicator before transplantation. Corals contain native bacteria (100 million/square inch) within their mucus layer, which provide protection and allow for adaptation to environmental conditions. Shifts from ambient bacterial communities to opportunists and/or pathogens have been observed in bleached and diseased corals. While visual and histological assessments are currently implemented, incorporating molecular profiling and culture-based methods can provide a microbial baseline and ascertain whether a cultured coral is compromised, before any disease symptoms present. Scleractinian corals from the Florida Keys are fragmented, cultured, and transplanted back into the wild through a joint project with The Florida Aquarium, University of Florida Tropical Aquaculture Facility, Florida Keys National Marine Sanctuary, and Mote Marine Laboratory. To complement their efforts and assist in developing a health certification process, we are monitoring coral-associated bacterial composition in the natural environment, under culture conditions, and following transplantation back into the Florida Keys. This novel approach utilizes two molecular profiling methods, Automated Ribosomal Intergenic Spacer Analysis (ARISA) and Terminal Restriction Fragment Length Polymorphism (T-RFLP) to identify components of the coral-associated bacterial community that can be used to assess the health and predict the future success of the transplanted corals. Results from this project will provide insight into the stability of coral-bacterial associations, and provide managers with preliminary information on the condition of corals to be used for transplantation, and therefore will have direct implications for coral restoration and conservation.

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The Global Viral Metagenome Project

Viruses are major cogs in the engine of evolution and critical elements in the web of life on earth. The need to understand this most numerous and most diverse class of biological entities on our planet is clear. However, most viral sequencing efforts have focused on the small subclass of viruses related to disease processes. Recently, metagenomes from viral samples taken mostly from seawater have been obtained, and in all cases, the great majority of genes observed were unlike anything seen before. In contrast to plants, animals, and bacteria, viruses remain largely unknown, a major gap in our understanding of our planetary biome. The Global Viral Metagenome Project seeks to comprehend the diversity of viruses by mounting a massively parallel effort to sequence and analyze viral genomes from different places on earth. The project anticipates the day when sequencing costs have dropped sufficiently to permit the processing of an environmental sample for a few hundred dollars. However, technological advances will not remove the need for a large number of human eyes to examine the sequences and, aided by computational tools, make sense of them, for at present, only humans can recognize significance in unanticipated patterns. The need for large numbers of participants in

a great diversity of sites is being met by high school and university students working collaboratively on the global effort. The collaboration relies on a publicly accessible web-based environment that brings computational tools and creative programming within reach of those without computational experience and on a curriculum and social structure that facilitates peer-to-peer mentoring across national boundaries. At this pilot stage, participating schools include those in China, Israel, Pakistan, Sweden, U.K, and the U.S. Students may also gain from their experience a model for how important problems may be solved in ways that transcend nationality.

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453/Sanger Genome Sequence of the Oral *Bacterium Aggregatibacter Aphrophilus NJ8700*

Aggregatibacter aphrophilus*, formerly named* Haemophilus aphrophilus*, is a member of the* Pasteurellaceae *family in the g-subdivision of the Proteobacteria. Its natural ecological niche is the oral cavity that is part of a complex ecosystem in which a rich and diverse microbiota has evolved. The rationale for sequencing this commensal species is that an understanding of commensals versus pathogens in the context of the Pasteurellaceae family and an understanding of the oral biofilm networks through comparative genomics will advance our knowledge of ecosystems and community interactions. Bacterial populations in the oral cavity function as a coordinated community that uses intra and interspecies communication. Channels of communication include metabolite exchange, cell-cell recognition, genetic exchange, and signaling molecules produced by the host and by other bacteria in the community. Completion and full annotation of the genome sequence of* A. aphrophilus NJ8700 *and comparison to other oral cavity bacteria will advance our understanding of microbial community ecology and biology, specifically in the following areas: (i) comparative genomics among commensals and pathogens in the* Pasteurellaceae *family that will in particular exploit the close relationships of* A. aphrophilus *to* Aggregatibacter actinomycetemcomitans*; (ii) comparative genomics of communication systems among early colonizers and bridge bacteria such as secretion systems, genes encoding quorum-sensing systems, and genetic exchange; (iii) comparative and evolutionary studies of phage/prophages among the* Pasteurellaceae *and colonizers of the oral cavity; (iv) microbial evolution of the* Pasteurellaceae *in the g-subdivision of Proteobacteria. We also assess the potential role of* H. aphrophilus NJ8700 *and its genomic characterization as a model system for community analysis.*

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Ecological Implications for Conservation: Healthy Ecosystems are Good for Your Health

Control and prevention of directly transmitted zoonoses remain intractable problems in public health. We investigated whether there was a relationship between human health and environmental health, such that humans would derive a direct, tangible benefit from conservation of biodiverse ecosystems. We therefore tested ecological factors, particularly biodiversity, and their effects on the risk of human disease, specifically Hantavirus*. We hypothesize that there is an inverse relationship between biodiversity of the mammal populations and the prevalence of zoonotic disease, so that when biodiversity increases, the incidence of Hantavirus in the ecosystem decreases. To test this hypothesis, a web-sampling grid was placed in five natural areas in and around Portland, Oregon. A "web" consists of 12 100-meter trap lines radiating from a center point and covering 3.14 Hectares. In order to trap as many different species as possible, 352 live-traps of four different trap types were placed on a web for four nights at a time and checked daily. Each park was trapped nineteen times over the course of three years. Biodiversity was calculated with a Simpson's Index, which takes into account both the number of species (richness) and the number of individuals within each species (evenness). Blood samples from captured animals were tested for hantaviral antibodies using ELISA. We captured 5058 specimens and found* Hantavirus*–positive deer mice* (Peromyscus maniculatus)*, the natural host, in all parks. Using a regression, we found a strong significant negative relationship between site biodiversity and percent infection rate: more precisely, as biodiversity decreased, the prevalence of Hantavirus in the ecosystem increased, and exponentially so when diversity became very low, a phenomenon we describe as a zoonotic release. Biodiverse ecosystems therefore appear to provide a direct service to humans through disease suppression, further supporting the need for their conservation.*

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ASSESSING DIVERSITY OF PLANKTONIC CILIATE COMMUNITIES IN MARINE COASTAL WATERS

Planktonic ciliates play a critical role in marine food webs because they serve as a trophic link between smaller planktonic microbes, and larger metazoan organisms. Most of our understanding of the diversity and distribution of these organisms is based on data from culture-dependent studies. We applied molecular methods to analyzing the diversity of ciliates in the groups Choreotrichia and Oligotrichia, the predominant heterotrophic ciliates in the plankton. We generated small subunit rDNA clone libraries from ciliate communities collected in marine waters and sediments from different coastal New England locations across time. Using these data, we obtained a snapshot of ciliate diversity in each collection. Our data reveal (1) most sites are marked by a few common haplotypes and many rare haplotypes, though the identity of the common haplotypes varies by site and time; (2) the greatest diversity of haplotypes fall within the Oligotrichia (Class Spirotrichea); (3) very few haplotypes are shared between samples and (4) there is not clear pattern of diversity associated with geography or time. Together, these data suggest that heterotrophic ciliates are quite diverse along the North Atlantic coast, and that the abundance of ciliates is driven by multiple factors. We are now embarking on additional studies to disentangle the driving patterns of marine ciliate diversity.

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REPRODUCTIVE ISOLATION RAPIDLY EVOLVES IN AN RNA VIRUS

The primary mechanism for virus speciation is thought to be differential adaptation to divergent hosts. However, it is not known whether the adaptation per se causes a barrier to gene flow (i.e. beneficial mutations have pleiotropic effects on gene exchange) or neutral mutations accumulate that happen to affect gene exchange (cause reproductive incompatibility). The first explanation has an explicit role for natural selection in speciation, while the latter is in line with older evolutionary theory on the origin of eukaryotic species, as articulated by Dobzhansky and Muller. We tested the molecular basis for reproductive isolation, a critical first step in speciation, by monitoring the process of speciation in laboratory populations of an RNA virus that undergoes genetic exchange only when multiple virus genotypes co-infect the same host. We subjected four populations of the RNA bacteriophage f6 to 150 generations of natural selection on a novel host. Although there was no direct selection acting on host range in our experiment, three out of the four populations lost the ability to infect one or more alternative hosts. In the most extreme case, one of the populations evolved a host range that does not contain any of the hosts infectible by the wild type f6. Whole genome sequencing and competitions between isogenic phage strains confirmed that the resulting reproductive isolation was due to a single nucleotide change, highlighting the ease with which an emerging RNA virus can decouple its evolutionary fate from that of its ancestor. Our results confirm the biological credibility of simple 'no-gene' mechanisms of assortative mating, in which assortative mating arises as a pleiotropic effect of genes responsible for ecological adaptation. In addition, our study highlights the power of microbial experiments to bridge studies of microevolution and macroevolution.

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A CASE FOR CONSERVATION MICROBIOLOGY: ECOLOGICAL SPECIFICITY AND EVOLUTIONARY STASIS IN GLOBALLY DISTRIBUTED MARINA BACTERIA

Bacteria are commonly thought to evolve rapidly in nature, through nucleotide sequence change and acquisition of novel functions by lateral gene transfer (LGT). This 'rapid evolution' view suggests that bacterial species lost due to environmental change will quickly be replaced by ecologically similar species that will evolve to fill the open niches. To challenge this view, we examined the phylogenetic structure and ecological incidence of two closely related, phenotypically similar species of deep, cold-dwelling, luminous bacteria, Photobacterium kishitanii *and* Photobacterium phosphoreum. *Relationships of 184 strains isolated from a variety of habitats over 70 years were tested through parsimony analysis of sequences of the* gyrB, recA, *and* luxA *genes. The two species were unequivocally distinct phylogenetically, each exhibited remarkably little phylogenetic divergence regardless of source habitat or geographic origin, and no evidence for LGT of these genes was detected.* Photobacterium kishitanii *was identified as the apparently exclusive bioluminescent symbiont of many deep-sea fishes (multiple specimens of 24 tested species*

in six families of five teleost orders). Photobacterium phosphoreum*, despite its phenotypic similarity, has not yet been found as a bioluminescent symbiont of these or other fishes. The time span, range of geographic locations and diversity of ecological sources from which these bacteria were isolated argue against purifying selection or intra-clade recombination as explanations for the phylogenetic coherence each exhibits. The data suggest instead that* P. kishitanii *and* P. phosphoreum *have evolved primarily through a gradual accumulation of mutations, giving rise to bacterial lineages that apparently have maintained a high degree of habitat specificity and phylogenetic coherence over ecological time. Environmental perturbations affecting survival of* P. kishitanii *therefore could have an impact on the symbiotic hosts of this bacterium, unless* P. phosphoreum *or other luminous bacteria are able to establish bioluminescent symbioses with these fishes in the absence of P. kishitanii.*

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Molecular Phylogenetic Analysis of Class Colpodea (Phylum Ciliophora) Using Increased Taxon Sampling

To further the understanding of the ecology and conservation needs of organisms it is helpful to know their evolutionary relationships. Here we analyze the sister-group relationships of the ciliate class Colpodea (phylum Ciliophora), which is a group of ubiquitous, primarily terrestrial microbes, although some are found in freshwater or marine environments. The Colpodea provides an ideal case in which a molecular genealogy can be compared to a detailed taxonomy of a microbial group. The class has been extensively monographed and there are about 200 described species. Using small-subunit rDNA, taxon sampling is increased from pervious analyses to include all orders within the class, more species within previously sampled orders, and more species within the largest genus, Colpoda*. Our results show that the class Colpodea is paraphlyletic with respect to part of the class Nassophorea, but there is little bootstrap and posterior probability support. Orders Bursariomorphida, Grossglockneriida, and Sorogenida are monophyletic. These orders, though, are nested within the remaining orders. Orders Bryometopida, Colpodida, and Cyrtolophosidida, as well the genus* Colpoda*, are paraphyletic (where not all descendants are included in the group). This extensive paraphyly at the ordinal level and, in the case of* Colpoda*, at the genus level, point to a need to increase molecular sampling and maybe a reevaluation of the morphologically-based taxonomy.*

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Emergence of a Planetary Methane Ecology: Evolution of Aceticlastic Methanogenesis in *Methanosarcinaevia* Horizontal Genetransfer from *Clostridia*

Biogenic methane production (methanogenesis) is a metabolic process unique to a paraphyletic group of Archaea known as methanogens. Aceticlastic methanogenesis is a specific type of methanogenesis carried out exclusively by euryarchaea of the family Methanosarcinacaea*, and responsible for the vast majority of the biogenic methane production on Earth. This process requires two enzymes for the conversion of acetate to acetyl-CoA, acetate kinase (AckA), and phosphoacetyl transferase (PtaA). The methyl group from acetyl-CoA is subsequently reduced to methane via several steps conserved in other methanogens. While the* Methanosarcinacaea *are the only Archaea that possess AckA or PtaA, these genes are ubiquitous throughout the Bacteria. However, in bacteria these genes are used in other pathways, typically producing acetate. Phylogenetic analysis confirms that AckA and PtaA were both horizontally transferred in a single evolutionary event, from an organism related to the cellulolytic* Clostridia *to the ancestor of the* Methanosarcinacaea*. Cellulolytic* Clostridia *have an extensive acetate metabolism, and contain adjacent copies of AckA and PtaA in the order identical to that in* Methanosarcinacaea*. As this clade is highly derived, with a cellulolytic lifestyle presupposing the existence of significant plant biomass, it is likely that this transfer event occurred within the last 350 My, causing a profound change in global methane biogeochemistry within this time.*

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Placement of Diverse Amoebae on the Eukaryotic Tree of Life

The diversity of microorganisms and the need for their conservation can only be realized through an increased knowledge of the relationships among these organisms and between these organisms and their macrobial relatives. Our understanding of

these relationships is limited, however, in part due to the few comparable morphological characters and paucity of molecular data for many groups. Amoebae are a polyphyletic group of eukaryotic microbes that suffer from these limitations. The amoebae include such well-studied organisms as Dictyostelium*, a social slime mold that may hold the key to the evolution of multicellularism and the human pathogens* Entamoeba histolitica *and* Naeglaria fowleri*. However, the amoeboid form confounds morphological studies many amoeboid lineages remain unsampled. As part of an ongoing project "Assembling the Eukaryotic Tree of Life", we have sequenced the SSU rRNA gene and four protein-coding genes from several amoebae of* incertae sedis*, including* Arcella hemisphaerica*,* Arachnula *sp.,* Nolandella *sp.,* Pessonella *sp.,* Trichosphaerium *sp. and a* Rhizamoeba*-like amoebae. In doing so we have greatly increased the molecular data available for this group. We believe increased taxon-sampling will allow further elucidation of the relationships within this group of amoeboid organisms.*

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Hidden Diversity of Allogromiid Foraminiferans

Foraminiferan protists are abundant meiofaunal predators, feeding upon organisms ranging in size from bacteria to small metazoans. An accurate assessment of foraminiferal numbers and trophic interactions is important for understanding nutrient flow in the oceans. Foraminiferal species distribution and richness has traditionally been assessed by examining the shells (tests) built by most of the known species. Unfortunately, certain groups of foraminiferans, particularly the allogromiid taxa, are often difficult or impossible to detect in this manner. A previous environmental DNA survey showed that in a deep-sea-like high-latitude environment (Explorers Cove, Antarctica), at least 75% of the foraminiferal species present were not identified by traditional techniques, and most of these cryptic species were allogromiids. However, the relevance of this result to other environments was not known, because other studies also reported more allogromiid taxa from high-latitude benthic settings. In order to investigate whether this domination of the foraminiferal assemblage by allogromiids is a feature of high-latitude environments alone, we used a series of targeted DNA-based surveys and allogromiid-focused morphological searches at several well-studied locations along the US eastern seaboard. Both survey methods revealed the presence of large numbers of new allogromiid taxa, constituting a majority of the foraminiferans detected at many sites. Morphological screens and specific PCR primers targeted against particular foraminiferal clades also documented substantial differences in the allogromiid assemblage between the locations. This evidence that low-latitude sites exhibit considerable cryptic foraminiferal diversity has significant implications for benthic trophodynamics and reconstruction of paleoenvironments.

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The Role of Bacteria in Treating Amphibians Exposed to a Lethal Fungal Pathogen: An Experimental Study of the Efficacy of Probiotics in Conservation Biology

Amphibian populations around the world are suffering from widespread population reductions and extinctions. One agent of extinction is a fungal pathogen, Batrachochytrium dendrobatidis*. This fungus causes chytridiomycosis infections in which zoosporangia live in the skin surface and release zoospores onto the surface of the amphibian. The pathogen must interact with the community of microbes that normally live on amphibian skin. Our work has shown that the normal bacterial flora on amphibian skin can inhibit the growth of* B. dendrobatidis *on an agar plate. We conducted an experiment to determine if an inoculation of a known anti-chytrid species in the genus* Pedobacter *could help clear a* B. dendrobatidis *infection on* Plethodon cinereus*, the eastern red-backed salamander. The experiment was repeated with another known anti-chytrid species related to* Pseudomonas reactans*. In the first experiment, eighteen days after inoculation, a 29% reduction in infection rate of* B. dendrobatidis *was seen in salamanders that had been inoculated with* Pedobacter *as compared to a control group. Interestingly, essentially all salamanders eventually cleared infection whether they were inoculated with* Pedobacter *or not. In the second experiment, the application of* P. reactans *actually hindered clearance of the chytrid on the skins of* P. cinereus*, leading to a significant statistical interaction ($P = 0.03$). We suggest that a probiotic application of Pedobacter can help clear* B. dendrobatidis *infections, but that not all species that are anti-chytrid in vitro will be effective in vivo. Analysis of DGGE gels indicated that*

application of P. reactans *changed the bacterial community structure of the skin. It is possible that* P. reactans *competitively displaced anti-chytrid species from the skin, leading to an increase in B. dendrobatidis. Future work will focus on the efficacy of application of "probiotic" bacteria as a potential aid in protecting amphibian populations from the negative effects of chytridiomycosis.*

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Symbiotic Bacterial Communities of Three Flea Species: Diversity, Species Interactions, and Population Dynamics

All animals harbor a community of microbial endosymbionts that play integral roles in organismal function. Here, we use more than 300 16S rDNA sequences to investigate the symbiotic communities of three flea species: Oropsylla hirsuta, Oropsylla montana*, and* Xenopsylla cheopis. Oropsylla hirsuta*, a host-specific flea of black-tailed prairie dogs* (Cynomys ludovicianus)*, were collected from prairie dog colonies in Boulder County, Colorado;* Oropsylla montana*, a ground squirrel flea, were collected from a rock squirrel* (Spermophilus variegatus) *in Boulder County, Colorado; Xenopsylla cheopis, the Oriental rat flea, were collected from a long term (>30 years) captive colony of the Center for Disease Control. We find that the diversity of bacteria associated with fleas is relatively low. Possible reasons for this low diversity include nutrient poor blood as the energy source, the innate immune response of blood, and the relatively small size of fleas. While communities have low diversity, the bacterial community differs greatly in composition among individual fleas. Communities within individual fleas do not seem to randomly assemble from the regional species pool; individual fleas tend to be dominated by one bacterial lineage. Inter-specific competition, precedence effects related to the timing of colonization, or pulses of nutrients may explain the dominance of a single lineage. We find that the transmission strategy of the lineage (vertical or horizontal) affects its distribution. The same strain of* Bartonella*, a horizontally transmitted lineage, is found in both* Oropsylla *species, but each flea species harbors its own very divergent members of the vertically transmitted* Rickettsiales. *Finally, we use mismatch distributions of DNA sequences from the dominant lineages and infer that these lineages are going through rapid population expansions.*

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Studies on the Role of Fungi in Conservation of Wheat Straw for Mushroom Production

Fungi have been reported as efficient degraders of cellulosic materials. A technology has therefore been developed which envisages the use of fungi in degrading wheat straw (or other agricultural wastes or by-products) for compost production used for growing Agaricus bisporus *– which is famous as white button mushroom throughout the world. This mushroom is being grown in Northern parts of India from Sept. to March under natural climatic conditions. The compost used for its growth is prepared by heterogenous solid state fermentation in which indigenous Thermophilic & Mesophilic fungi actionmycetes and bacteria place significant role in succession and conserve the wheat straw in to useful compost used as substrate for mushroom cultivation. The present was therefore conducted with the objective to isolate and identify the mycoflora which play major role in composting and growth of mushroom. Fresh wheat straw supplemented 2% nitrogen level was randomly sampled for isolation of mycoflora at six turns from six zones identified in accordance to physical and microbiological status of the stack, yielded 220 isolates under twenty species belonging to three major groups of moulds, such as dematiaceous fungi, Aspergilli, and mucoraceous fungi. Of these,* Alternaria sp., A. chlamydospora, Helminthosporium sp., Chaetomium virescens, Humicola sp., Humicola Sp2, Humicola sp3, Aspergillus japonicus, Syncephalastrum sp., Mucor sp. *and* Fusarium moniliforme *were recorded as additions to, mushroom compost mycoflora. Growth of Twenty cultures was further screened on cut, supplemented and sterilized straw in the laboratory. The vegetative and reproductive growth of A.* bisporus *was also studied on fungal impregnated straw. Based on in vitro yield of fruit bodies and rate of growth, the fast growing cultures, i.e.* A. fumigatus, A. niger, Humicola sp.*, and* C. globosum *were bulk multiplied and added to compost at third turn which reduced the composting period by 8-9 days along with statistically significant increase (11%) in yield of mushroom crop. This study therefore can be used not only to be conserve the wheat straw but also results in enhanced yield of mushroom.*

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A Practical Method for Identification and Description of Microbial Eukaryotes Using the Testate Amoeba Centropyxis as a Case Study

Traditional descriptions of a number of microbial eukaryotes are usually made in the context of a non-standardized discipline. Assigning types or following standardized rules for description and nomenclature was not common practice in early works, making identification and comparison to recent works laborious and often subjective. Hence impeding advances in building biodiversity knowledge about these organisms. Here we are interested in developing a more precise method in order to facilitate identification and description of microbial eukaryotes. We analyzed twelve nominal taxa of the genus Centropyxis *Stein, 1857 to compare how traditional taxonomic practices conflict with contemporary ones. We collected over 2000 specimens at the Tiete River, Sao Paulo, Brazil, and made morphological measurements of discreet and continuous characters using a compound microscope and a Scanning Electron Microscope; ecological data was observed regarding habitat exploration. These datasets were analyzed and compared to previous literature in order to verify the consistency of described species, varieties and forms. We encountered transitional forms that undermine the distinctions stated for three species and nine varieties. Moreover, a number of problems in the traditional descriptions for these organisms — namely lack of types, non-standardized descriptions and the existence of several infrasubspecific taxa — are incongruent with modern surveys. We suggest an explicit and standardized taxonomic practice in order to enhance our taxonomic concepts for microbial eukaryotes, that relies on a comprehensive listing of all taxa that as been described under the same or different names. This differs from a common revision in that it relies on the usage of names and concepts implied by the authors instead of typification. This will allow advances in describing the biodiversity of microbial eukaryotes and more precise inferences for studies in related areas.*

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Symbiont Modifies Host Life History Traits That Affect Gene Flow

*Maternally-transmitted bacterial symbionts are common in insect herbivores and can influence host survival and fecundity under a variety of conditions. Symbiont-mediated effects on host life history strategies, however, are largely unknown. Here we show that the facultative bacterial symbiont "*Candidatus *Regiella insecticola" strikingly alters both dispersal and mating in the pea aphid,* Acyrthosiphon pisum*. Pea aphids containing* Regiella *produced only half the number of winged offspring in response to crowding and, for two out of three aphid lineages, had altered timing of sexual reproduction in response to conditions mimicking seasonal changes, as compared to aphids lacking* Regiella*. These symbiont-associated changes in dispersal and mating may have played a key role in the initiation of genetic differentiation and in the evolution of pea aphid – host plant specialization. As symbionts are widespread in insects, symbiont-induced life history changes may have promoted specialization, and potentially speciation, in many organisms.*

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Phytoplankton in a Turbulent, Turbid Environment: Potential Effects of Climate Change in the Lower Hudson and East Rivers

The occurrence of 29 dominant species of phytoplankton in an 8-year series of weekly samples from 2 sites in Lower Manhattan was analyzed by correspondance analysis and other multivariate methods. Hudson River sample points formed distinct clusters with respect to salinity and temperature, whereas samples from the East River, using the same taxa, did not. These data suggest significant differences in organization of the phytoplankton communities at these two sites due to hydrodynamic differences: the Hudson is typically highly stratified, whereas the

East River is dominated by turbulent mixing. Distributions of individual taxa in the ordination plane were also studied, allowing a characterization of them with regard to hydrographic variables, revealing differences in some dimensions of niche space. On the basis of these results, we can make tentative predictions regarding changes in the dominant phytoplankton species in these habitats as a result of rising temperatures and salinities, due to climate change and rising sea level.

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Species Identification of Avian Malaria Parasites: Morphology, Host Association, Genes, and Phylogeny

Species identification remains a standing challenge for those working with microbial organisms and is a major issue in public health, veterinary medicine, and conservation biology. Here I evaluate different tactics used in the identification of an important group of protists, the malaria parasites of birds (genera Plasmodium *and* Haemoproteus*). The avian malaria parasites are common in bird families worldwide and exhibit variable host breadth and pathogenicity. Host shifts and subsequent host population decline have been documented, but studies on the distribution of these parasites both among hosts and geographic regions have been severely limited by the lack of reliable criteria for species identification. The evolutionary significance of characters traditionally used to identify malaria parasite species, including morphology as seen under the light microscope, life history traits, and host association has recently been called into question by molecular studies. Additionally, molecular studies, primarily using gene sequences from the mitochondrial cytochrome b gene, suggest there is a greater cryptic diversity of the parasites than recognized by traditional means, perhaps 10,000 or more species infecting avian hosts worldwide. I investigate the diversity of the avian malaria parasites and combine traditional approaches with gene sequence data from four genes across the parasites' three genomes (mitochondrion, nucleus, and plastid). Included is a large sample of birds (3000 birds, 30 families, 10 orders) from eastern and western North America, Israel, and Malaysia. Species identifications based upon the criteria of morphology, host association, genetic divergence, and reciprocal monophyly are compared. My goal is to evaluate the utility of different characters and criteria in the species identification of the avian malaria parasites and to identify an appropriate method for identification of avian malaria parasite species.*

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The Evolution of Virus Synchrony and the Conservation of Small Populations

Species that exhibit a strong Allee affect, the positive relationship between population density and fitness of individuals, are more susceptible to the threats affecting small populations. Effective density increases with the temporal synchrony of key life history events. Therefore, understanding the evolution of synchrony will improve our ability to conserve small populations, predict the spread of invading species, and understand the process of adaptation to new environments. Here we use a virus model system to examine the role of ecological history in selecting for synchronous cell lysis, the time of first reproduction for viruses in a population. Positive selection for increased synchrony should occur when viruses reproductively benefit from intracellular interactions with other genotypes. We predicted that frequent co-infection should select for low variability in lysis times among individual viruses, because this increases the probability of mutually-beneficial genetic complementation, the masking of deleterious alleles during co-infection. We tested the hypothesis by measuring lysis time for RNA phages evolved for 300 generations in the presence or absence of frequent co-infection. Results confirmed that the high-level co-infection viruses showed greater synchronicity of lysis time. In addition, partial genome sequencing suggested that this result was not driven by low genetic diversity among individual viruses isolated from the co-infecting populations. Our study demonstrates the fundamental need for organisms as simple as viruses to evolve phenological synchrony, and that ecological history can determine whether or not individuals in a population are selected to synchronize their reproduction.

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Spatio–Temporal Patterns of Soil Microbial Dynamics and Net Nitrogen Mineralization in Longleaf Pine Flatwoods along Florida's Gulf Coast

Little information exists on spatio-temporal patterns of soil characteristics in longleaf pine flatwoods communities along

the lower coastal plain of the Gulf coast. The Pt. Washington longleaf pine restoration study conducted through the University of Florida is focused on determining the effects of post–site preparation, low level herbicide applications on longleaf pine growth & survival, plant species richness, and soil nutrient cycling. As part of the study, a monitoring program was designed to answer these questions by detecting patterns of development from data collected on forest structure, plant species richness, and a set of soil quality factors including soil microbial biomass as environmental indicators. Three representative sites along a spatial gradient from Pensacola to Tampa Bay, (720 km), each containing stands of three distinct successional stages (age groups) were used in this study to represent a chronosequence of 120 years. Soil organic matter (SOM) was measured by the Walkley-Black method. Soil microbial biomass was determined through chloroform fumigation-extraction (CFE), and the fungal biomass was estimated by extracting ergosterol from soil samples. Preliminary results indicated that pioneer plant species dominated the early successional stages of stand development, but species composition resembled that of typical flatwoods communities within thirty years of age. SOM declined along a moisture gradient analyzed from cypress swamps through wet savannas to the drier flatwoods. Soil bacterial biomass initially increased after a disturbance as soil organic matter accumulated, but decreased as the fungal-to-bacterial biomass ratio rose with longleaf pine basal area. The numbers of nitrifying bacteria were higher in young longleaf pine forests than in forests greater than 90 years. Net nitrogen mineralization levels were high and variable after disturbance but decreased as the forest cover matured and fungi dominated the microbial biomass. As longleaf pine forests reached 90 years old, net-nitrogen mineralization rates became more stable in magnitude and variability. It appears that longleaf pine flatwoods stands reach a steady state equilibrium in terms of our indicators at a threshold age of ninety years after establishment.

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Global Analysis of Bacteria Biogeograpghy and Dispersal

Knowledge about dispersal is key to understanding how microbes interact with their environment. Evidence from protists and spore-forming bacteria suggests microbes can easily move across the globe and colonize appropriate habitats regardless of distance. However, new data suggest some extremophiles, such as bacteria surviving in hot springs, have limited ranges due to how far they can disperse. More research on dispersal will tell us if all bacteria are found everywhere on Earth within their appropriate habitat. Will we find identical bacteria from biomes in the United States versus the same biomes across the globe? How large a geographic area should we examine to find all species of bacteria in the world? To answer these questions, I have constructed a database from the scientific literature of 9,400 16S DNA sequences across 59 eubacteria genera. This database includes the date of isolation, geographic location, and ecological environment where researchers isolated the DNA or bacteria. I examined the relationship between date, location, and genetic distance within a genus-level phylogenetic tree, and many of the genera have non-random correlations between these factors. Further research will attempt to separate sampling artifacts in this database as well as find how rapidly bacteria from each genus spread across the globe. Of course, all types of bacteria cannot be treated as having the same properties. The 59 genera allow me to calculate correlations between dispersal ability and physical phenotypes, such as ability to grow anaerobically or the ability to produce spores. Perhaps these relationships will allow researchers to make generalizations concerning dispersal across all types of bacteria.

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Stress, Immunity, and Blood Parasites in a Free-Living Population of White-Crowned Sparrows

Life history theory assumes that reproduction is expensive and competes for resources with other costly activities, such as immune defense. Human-induced environmental variability may exacerbate this trade-off when resources become limiting. Evidence from laboratory and field studies show that habitat degradation increases stress levels, parasite loads, and malnutrition of animals. This study conducted during summers 2003 and 2004 examined the mechanisms through which food availability, stress, and parasite load interact to impact individuals within a wild population of White-crowned Sparrows (Zonotrichia leucophrys oriantha) *during the breeding season. I experimentally reduced host parasite loads and manipulated food availability to study the effects on circulating corticosterone, immune function, and blood parasite loads. A standard stressor was applied to each bird to measure mean change in baseline corticosterone and post-stressor corticosterone to assess an individual's sensitivity to a stressor. Birds were injected with a non-pathogenic foreign protein (PHA) in the wing web and swelling was measured to assess strength of the cell-mediated immune response. I collected blood samples to quantify blood parasite intensities. Males were more sensitive to*

the applied stressor during the early breeding season than late breeding season. Infection status with blood parasites significantly increased baseline corticosterone, and drug treatment significantly lowered mean baseline corticosterone in males. Males were more sensitive than females to the applied stressor overall. Both food and drug treatments impacted immune responsiveness. Birds who received food supplements had significantly higher wing web swellings than birds who did not receive food supplements. Additionally, birds who received antiprotozoal drug treatment had significantly lower swellings than birds who did not receive drug.

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Lack of Effects of Elevated N and CO_2 on Soil Microbial Diversity in a North American Grassland Model System

Soil microbes such as bacteria and fungi are critical in processes including nutrient cycling and symbiotic interactions. The structure of the microbial community influences the nature and magnitude of these processes, and can thereby lead to shifts in aboveground community structure; the influence of global change factors such as elevated nitrogen and carbon dioxide on microbial community structure may therefore have far-reaching effects on biodiversity. We examined the impact of direct increases in N supply and atmospheric CO_2 enrichment on the diversity of two soil microbial groups, bacteria and arbuscular mycorrhizal fungi, using community DNA fingerprinting (Terminal Restriction Fragment Length Polymorphisms) in a series of experimental grassland plots. Despite the treatments having been applied over a period of 7 years, we observed few differences in species composition or relative abundance between treatments. These results suggest that these two soil microbial groups exhibit stability (resistance) in the face of two prominent features of global change in these ecosystems, at least over the time period studied. Our current research focuses on examining linkages between the aboveground and belowground communities by determining whether evidence exists for interactions between these global change factors and the functional diversity of the aboveground plant community.

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Permafrost: A Depository or Subzero Incubator for Psychrophilic Microorganisms?

Permafrost (P) is widespread in the Arctic, sub-Arctic, and Antarctica occupying > 20% of the world's land surface. In conservation biology, P is usually considered a natural depository of ancient organisms trapped in ice thousands of years ago. P is generally believed to be completely inactive. This is wrong. We found detectable microbial activity measured as $^{14}CO_2$ uptake or oxidation of ^{14}C-ethanol and glucose in P-samples incubated at temperatures from -1 down to -80°C. Activity was stimulated significantly by volatile C-substrates (ethanol, methane). To characterize microorganisms responsible for subzero activity, we used culture-independent techniques (PLFA, PCR-SSCP). Ethanol induced growth of several unknown eubacteria affiliated with alpha-, beta- and gamma-proteobacteria, Firmicutes *and* Bacteroides-Flavobacterium-Cytophaga *phyla as well as one ascomycete related to* Rhinocladiella atrovirens. *Two isolation techniques were used: i) frozen cellulose powder mixed with ethanol-mineral medium, and ii) supercooled liquid media stabilized with glycerol. The first technique allowed enrichment and isolation of basidiomycetous yeasts* Mrakia *and* Leucosporidium *as well as ascomycetous fungi Geomyces sp. Use of supercooled liquid led to isolation of various bacteria* (Polaromonas, Pseudomonas, Arthrobacter, Cryobacterium, Collimonas Rhodococcus, Sinorhizobium *and* Flavobacterium). *Growth of fungi was exponential with generation times 14-34 d, while bacteria displayed progressively declining growth. All isolated organisms displayed true growth at -17 to 0°C with yielding 0.27-0.52 g of cell C (g of C-ethanol)$^{-1}$ similar to that found above zero. The 'state of maintenance' implying zero growth with some non-zero catabolic activity was not confirmed. A significant fraction of psychroactive microorganisms remain unculturable. Some of them were shown to be vulnerable even to moderate warming above zero. Under anticipated climatic changes accompanied by P-degradation, these vulnerable organisms could perish. We suggest depositing of P samples at temperatures below -100°C to preserve samples for comparative taxonomic studies in the future.*

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Evaluating Support for the Current Classification of Eukaryotic Diversity

Perspectives on the classification of eukaryotic diversity have recently shifted from a system emphasizing macrobial clades (animals, plants, fungi) toward a system of six supergroups that unites diverse microbial and macrobial lineages. These supergroups are widely acknowledged in the literature and textbooks. However, it remains unclear whether they capture evolutionary relationships accurately. We analyze two facets of supergroup robustness: taxonomic stability and support from molecular analyses. Comparison of supergroup classification reveals considerable taxonomic instability in all groups (Parfrey LW, Barbero E, Dunthorn MS, Lasser E, Bhattacharya D, Patterson DJ, Katz LA, PLoS Genet 2(12): e220). Additionally, in analysis of molecular genealogies, we find variable support for each of the supergroups that differs according to the taxonomic area targeted and the origin of the genes used in the analysis (organellar versus nuclear). Destabilizing factors include issues of eukaryotic complexity, limited data, nomenclatural ambiguity, and sparse taxonomic sampling. We argue that low taxonomic sampling of diverse free-living microbial lineages is the most critical factor; as such taxa are substantially underrepresented in molecular genealogies. We remain optimistic that increased taxon sampling and further efforts will produce a robust taxonomic framework on which knowledge of eukaryotic diversity can be assembled.

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Between- and Within-Lake Comparison of Bacterial Assemblages in the Illinois River Floodplain

As investigators move towards developing a more complete picture of microbial diversity, it becomes necessary to examine distinct habitats within seemingly homogenous systems. In this study, we assessed the diversity of bacterioplankton assemblages in shallow lakes of the Illinois River floodplain system. The objective was to compare the bacterial assemblages: 1) between lakes that are isolated vs. those that seasonally flood (i.e., water mixing among lakes and the river) and 2) within lakes with respect to suspension status (free-living vs. particle associated) and water column position (bottom vs. subsurface, subsurface vs. air-water interface). Subsurface and bottom water samples were collected from three connected and three unconnected lakes. Bacteria from each sample were separated into particle-associated (> 3 micrometer) and free living by filtration. Air-water interface and subsurface water samples were collected from one of the unconnected lakes. DNA was extracted and 16S rDNA PCR amplicons (primers 338F and 518R) were separated by denaturing gradient gel electrophoresis (DGGE). DGGE fingerprints were analyzed using the Pearson Coefficient (PC) in unweighted pair group method analysis. Assemblages in all lakes were surprisingly similar in composition. The greatest differences in assemblage profiles were due to water column position. This division was especially clear among particle associated bacteria; the PC within subsurface and bottom groups was 0.30 and 0.46 respectively while the PC between groups was <0.01. Additionally, three of seventeen phylotypes observable at the air-water interface were not detected in the subsurface. This work suggests that while environmental characteristics may select for similar assemblages on the landscape level (i.e., lakes within the river system), assemblage differences are likely due to within-lake factors such as degree of association (i.e., on particles or on water surface vs. freely suspended) and depth-dependent physicochemical conditions.

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Metals Transformation by a Phylogenetically Distinct Anaerobe, Strain UFO1

Metal-transforming microorganisms play an important role in metals cycling and the immobilization of toxic metals in the environment, offering potential strategies for bioremediation. Well-characterized microorganisms, such as Geobacter spp. *and* Shewanella spp.*, can couple the transfer of electrons to energy generation through the process of dissimilatory metal reduction. Fermentative microorganisms are capable of using metals as an electron sink, but have largely been ignored for their role in metals cycling. We have isolated a novel, fermentative bacterium capable of metals transformation, Strain UFO1. This strain is a member of the newly described genus* Pelosinus*, which is most closely related to* Acetonema *and phylogenetically distant from other*

well known metal-reducers. Direct reduction of Fe(III)-nitrilotriacetic acid occurred in the presence of lactate. Additionally, strain UFO1 reduced the humic acid analog anthraquinone-2, 6-disulfonate (AQDS) to its reduced form, AH_2DS, using a variety of electron donors including lactate and H_2. Ferrihydrite was not directly reduced in the absence of an electron-shuttling moiety. Synchrotron-XPS spectra revealed the mineral transformation of ferrihydrite from Fe(III) to Fe(II) by a culture of UFO1 containing lactate and AQDS, suggesting that the reduction of insoluble Fe(III) was shuttle-mediated. Reduction of 1, 3, and 5 ppm Cr(VI), occurred within 24 hours using lactate; in the presence of 1 mM AQDS, 3 and 5 ppm Cr(VI) were reduced to 0.1 ppm within 2 hours. Soluble U(VI) was removed from solution in the presence of Strain UFO1, which appears to be mediated via phosphate release and precipitation of uranyl phosphate. The characterization of Strain UFO1 contributes to a broader understanding of the diversity of organisms involved in metals transformation. The phylogeny and ecophysiology of Strain UFO1 call for its conservation as an important part of the microbial community.

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Diversity of Root Pathogenic Fungi in the Los Tudtlas Biosphere Reserve, VeraCruz, Mexico

Root pathogenic fungi (RPF) have been studied mainly as a cause of disease and economic losses; however they may play ecological and evolutionarily important roles in the natural plant communities and in the soil microbial communities through multitrophic interactions with soil microorganisms and plant roots. RPF have been recorded as a major factor in the establishment and change of natural plant communities and agriculture landscapes; Eucalyptus *forests in Australia devastated by the root rot caused by* Phytophthora cinnamomi *is an example. General objective of this study was to assess diversity, abundance and root damage caused by the main RPF in four land use types. Rainforest, agroforestry, grassland and maize were sampled at each one of three regions. From 32 plots, eight subsamples were taken at the first 20 cm of depth. Different selective media for isolation and culture of RPF were used. Soil dilution plate technique was applied for isolation and quantification of the soil population density in rhizosphere soil. Disease infection was assessed plating ten 1.0 cm long pieces of feeding roots in each of one plate with selective media. Seventeen genera of fungi are represented, each with several morphospecies; the highest number of morphospecies were detected in agroforestry and grassland, followed by rainforest and maize. A similar number of isolates were obtained from rhizosphere soil (inoculum potential activity) and roots (inoculum effectiveness). The highest number of soil fungi isolates (saprophytic, pathogenic and antagonistic) was detected in the less disturbed region.* Fusarium spp. *is the most abundant genera and may be useful as a bioindicator of the soil health. RPF inhabit and cause disease in all four land use types but the difference may be in the grade of damage caused by the RPF in the plant community, in response to the community structure and the presence of natural enemies.*

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Assessment of Cryogenic Practices to Preserve Bacterial Assemblages: A Study of Central Park, NY Sediment

Effective methods exist for preservation of single bacterial species, however preserving complex assemblages has not been adequately addressed. This research focuses on developing best practices for preservation and archival of microbial communities. This study compared three different cryotechniques used to preserve a bacterial assemblage. Sediment (n=1) (Rowing Pond, Central Park, NY [2005]) was divided into the original (O), unfrozen sediment and three treatments stored in liquid nitrogen. The frozen treatments were: Mr. Frosty (MF; freeze rate ~1 °C/min), 30% glycerol (G), and 10% dimethylsulfoxide (DMSO). Total DNA was extracted from aliquots of each treatment and 16S rDNA was amplified to construct Bacteria clone libraries (~1.4 kb, 150 clones/treatment) for sequencing. Additionally, bacteria from all treatments were cultured by spread plate technique on nutrient agar. DNA was extracted from 50 CFUs per treatment (10-4 dilutions) and 16S rDNA was amplified and sequenced. Sequences were BLASTED in GenBank and used to construct phylogenetic trees to associate unidentified bacteria with known taxonomic groups. Culture-independent, genus-level analyses indicated that MF and G (56% and 51% of O) recovered

slightly more genera than DMSO (41%), and select genera were unique to each treatment (e.g., O: Flavobacterium*; G:* Caulobacter*). Phylum and class level analyses were similar across all treatments. Culture-dependent results (n=2; p=0.075) showed that MF and G (80% and 61% of O [4.5 x 10^3 CFU/g], respectively) yielded fewer CFUs/g than DMSO (133%). However, initial BLAST results indicated that cryotreatments MF and DMSO seem to recover the majority of the assemblage initially present in O. Although culture-independent analyses indicated that complete assemblage retrieval may not be possible from one cryotreatment, culture-dependent data indicated that all treatments may similarly recover cultured bacteria present in O. Results indicate progress toward cryogenic preservation of assemblages and help establish the framework for future directions in long-term testing.*

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Patterns of Bacterial Diversity and Distributions across the Ants

Ants are a dominant feature of almost all terrestrial ecosystems and are among the most abundant groups of metazoans on the planet. Although a few lineages are known to harbor symbiotic bacteria, we know little about the prevalence and diversity of bacteria across this family, the forces that shape the diversity and distributions of bacteria, or the roles that microbial associates play in ant biology. To address these shortcomings, we studied the bacterial flora of several hundred ant species from 148 genera spanning 19 of the 20 subfamilies within the family Formicidae. Through a combination of PCR screening, sequencing, and phylogenetic analyses of 16S rRNA genes, we identified 58 distinct bacterial associates from the ants. These microbes were classified into 15 orders and eight classes within the Actinobacteria, Bacteroidetes, Proteobacteria, *and* Firmicutes. *Over 2/3 represented novel species and several could not be assigned to currently defined bacterial orders. Though the functions of these bacteria remain elusive, we have identified several candidate gut symbionts from the* Entomoplasmatales *and* Rhizobiales. *The phylogenies and distributions of these and other microbes supported a common trend of specialization, with related microbes infecting related hosts.* Rhizobiales *were prevalent within ecologically similar ants from the tribe Cephalotini and the genus* Dolichoderus. *They were also identified in unrelated ants which overlapped in both lifestyle and diet. Given these patterns and the results of prior research, we hypothesize that* Rhizobiales *have played important roles in facilitating convergent evolution in ant diets, enabling several unrelated lineages to specialize on nitrogen poor food sources. In summary, our findings indicate that: 1) Host ecology and evolution have influenced the ecology and evolution of their bacterial associates. 2) Many novel and functionally significant bacteria await discovery within the ants. 3) Symbioses with bacteria are a common and underappreciated component of ant biology.*

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High Rates of Evolution in Small Single-Stranded DNA Viruses

Much is known about the nature and diversity of mutation and nucleotide substitution rates in RNA viruses. However, the DNA viruses for which rates have been estimated are almost exclusively limited to those that have codiverged with their host organisms, as molecular clocks of these viruses can be calibrated from host divergence times. Rates inferred from these are low (~10^{-7} to 10^{-9} substitutions/site/year), yet little is known about the long-term rates of other DNA viruses. To determine the substitution rates of a unique family of small single-stranded (ss)DNA viruses, the Parvoviridae*, specifically canine parvovirus (CPV) and human B19 erythrovirus, we employed a Bayesian Markov Chain Monte Carlo approach that considers variations in phylogenetic branch lengths among temporally-sampled viruses and explores different models whose parameters include tree topology and population dynamics. CPV recently emerged from feline panleukopenia parvovirus (FPLV), yet while FPLV has remained endemic in its host populations, we show that CPV has undergone an epidemic-like pattern of logistic/exponential growth, effectively doubling its population size every few years. This rapid population growth was associated with a lineage of CPV that acquired a broader host range and greater infectivity. CPV's rate of evolution, during emergence, was ~10^{-3} substitutions/site/year, with intraclade rates of FPLV and CPV ~10^{-4} substitutions/site/year. B19 showed similar rates. That these divergent viruses, with very different lifestyles, both exhibit elevated rates of evolution suggests these rates may be characteristic of all autonomous parvoviruses. While they are replicated with cellular machinery, their substitution rates appear to be much more rapid than those of both their hosts and codivergent DNA viruses and closer to the rates of RNA viruses. It may be the case that rapid rates of evolution characterize all ssDNA viruses, as suggested by the high levels of diversity found among these viruses.*

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MICROBIOTIC SOIL COMMUNITY EFFECTS OF TREE GROWTH ACROSS TWO SITES IN PANAMA

Tropical deforestation causes biodiversity loss and has implications for ecosystem functional changes. Panama's annual forest loss of 1.6% exceeds averages both worldwide and in the tropics. Selection trials are underway as part of a larger effort to abate this trend by promoting silviculture over agriculture and cattle ranching as a more economically attractive land use. One important component of economic feasibility is tree growth performance. While growth performance associated with soil physical properties (e.g. nutrient availability and structure), climate (e.g. temperature, moisture and PAR) and some aspects of soil microbial communities (e.g. mycorrhizas) is well documented, the relative importance of these components is not. In this study I addressed how much these components may affect tree growth by asking the following questions: 1) How much is the soil as a whole (nutrients, structure and microbiotic community) responsible for differences in seedling growth versus the climate as a whole; 2) How important is the microbiotic community component in the overall soil effect on seedling growth; 3) Can the microbiotic soil community from nearby forest soil be used to inoculate trees planted in grass-dominated fallows? To address these questions, we conducted a tree growth experiment in a nursery in Panama comprised of three treatments: (1) three species of seedlings grown in (2) steam-sterilized and fertilized soils taken from the (3) wettest (Soberania – 1700mm rainfall) and driest (Rio Hato – 1100 mm rainfall) sites in a selection trial run by PRORENA of the Smithsonian Tropical Research Institute. Sterilization eliminated the entire microbiotic soil community, so these questions address community level effects, including decomposers, nitrogen-fixers, symbionts and pathogens, among other groups. Seedlings of three species of economic interest were used in this study: Enterolobium cyclocarpum (corutu), Guazuma ulmifolia (guazimo) *and* Ochroma pyramidale (balso). *These species are also important in the recovery of abandoned pasture lands, often being the first to recolonize them. We measured growth rates and leaf areas of the potted plants for over six months. Our results suggest that a significant fraction of growth differences can be explained by soil effects. Additionally, the community of soil microorganisms plays an important role in growth performance, but effects vary with tree species. Some of these differences are consistent with previous work on mycorrhizal dependence. Finally, forest inoculum did not have a significant effect on tree growth, and seemed to retard growth in some instances. These results will inform tropical reforestation efforts, improve crop selection, and point the way for further research.*

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ECOLOGICAL NICHE MODELLING FOR DRIVER SPECIES OF FOREST FLOOR ECOSYSTEM: USING GENETIC ALGORITHM (GA)

Ecological niche modelling of a forest floor ecosystem improves the understanding of the driver species. The tool is used to conceptualize the hyper volumetric niche of a species – a paedosphere engineer – important component in nutrient cycling in the soil. The intricate relationship between the living and nonliving world simulated by the ecological niche model with the genetic algorithm helps in identification of species that is driving the community for succession. The habitat suitability for a species has been expressed as a grid ranging from 0 (unstable) -1 (most stable) and has been based on the species habitat requirements.

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UNDERSTANDING THE DIVERSITY OF *SYMBIODINIUM* IN REEF CORALS OF WEST PAPUA, INDONESIA HELPS SET CONSERVATION PRIORITIES

Coral reefs are under severe threat from climate change. When sea surface temperatures rise above normal for a sustained period, coral bleaching occurs. Coral bleaching is the stress-induced reduction in the density and photosynthetic activity of the coral's single-celled, endosymbiotic algae, a protist in the genus Symbiodinium. *Coral bleaching can lead to the mass*

mortality of reef-corals (>90% in the western Indian Ocean in 1998) placing the very foundation of these already fragile ecosystems at risk. Coral reefs in West Papua region of Indonesia are among the most biologically diverse in the world. As such, they are currently the target of a conservation management plan which aims to promote the establishment of a marine protected area network. Here we present the first data on the distribution of Symbiodinium *on West Papuan coral reefs. These data will help identify areas that may have been subjected to bleaching in the past as well as those that are likely to survive climate change in the near future. These data will be directly applied to the conservation and management of West Papuan coral reefs. In addition, these findings highlight the crucial role that microscopic organisms can play in the stability and diversity of ecosystems.*

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Revealing the Evolutionary History of an Unknown Amoeba: Multigene Analysis of *Corallomyxa Tenera* Sp. Nov.

The microbial world makes up more than 50% of the Earth's biomass. Despite this fact their diversity and taxonomy is poorly known. Here we describe a new amoeboid lineage ATCC® 50975™, isolated from sediment collected from the edge of a man-made salt marsh near Beaufort, North Carolina, USA. A detailed morphological analysis that included transmission electron microscopy (TEM) and light microscopy (LM) demonstrate that this isolate is a new species, herein designated, Corallomyxa tenera*, sp. nov.. This species is characterized by its delicate appearance, short duration of the anastomosing reticulate network and production of round smooth-walled cysts. The new species also lacks some features found in other* Corallomyxa *species including cytoplasmic condensation and an electron dense "chromocenter". The genus* Corallomyxa *is one of the plasmodial, amoeboid organisms whose taxonomic position has been uncertain. We combine morphological description with a multigene analysis to assess its phylogenetic placement within the eukaryotic tree of life. A Bayesian analysis of four concatenated genes (SSU-rDNA, actin, alpha- and beta-tubulin) from a wide diversity of eukaryotes, places the new species together with taxa normally placed in the putative supergroup 'Rhizaria'. All molecular loci refute the traditional placement of* Corallomyxa *within the supergroup 'Amoebozoa', which includes other Mycetozoidea and Lobosea. Maximum likelihood (ML) and Bayesian analyses of the two well-sampled genes, SSU-rDNA and actin, including more taxa from 'Rhizaria' show a close affinity of* Corallomyxa *with Foraminifera,* Gromia *and, for SSU-rDNA, Haplosporidia. We further identify a novel stem, herein designated E23-13-1, in the predicted SSU-rDNA secondary structure that supports this relationship. A hypothesis is presented for the evolution of morphological characters that include anastomosis of psueodopodia, bidirectional streaming of granules, and reticulation and formation of network; and other molecular synapomorphies in a clade containing* Gromia, Corallomyxa, *Foraminifera and Haplosporidia.*

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Environmental Stressors Shift the Microbial and Viral Community on Corals from Oceanic to Pathogenic

Culture-independent analyses of microbial communities on tropical corals have shown that coral-associated Bacteria are distinct from those in the water column; it has been hypothesized that these normal microbial symbionts can provide corals with defenses (chemical, nutritional, or exclusionary) against pathogens. However, there has been an alarming increase in coral disease incidence during the last several decades that has contributed to the decline of coral reefs. In addition many studies have shown that environmental stressors are correlated with this elevation in coral disease and die offs, yet the etiological agents of the majority of these diseases remain unknown. In order to determine how the microbial and viral consortia on and within corals changes in response to environmental stress, Porites compressa *corals were exposed to a variety of conditions known to cause demise of coral reefs, namely: elevated temperature, increased nutrient concentration, dissolved organic carbon (DOC) loading, and reduced pH. Using 454 Life Sciences pyrosequencing, 12 coral-associated microbial and viral metagenomes were generated and analyzed. These datasets demonstrate that the microbial*

community shifts from an oceanic and non-virulent consortia to a heterotrophic and highly virulent consortia within only 16-64 hours of treatment. Also of special interest is the change in herpes-like viruses (HLVs). It was found that all samples contain a large number of sequences similar to a herpes-like virus, and that exposure to reduced pH, elevated nutrient, and high environmental temperatures dramatically increase the relative percent of these sequences. This suggests that corals may experience HLV lytic outbreaks in response to these forms of stress. Overall, these combined data clearly show that degraded environmental conditions can quickly alter the symbiotic balance between the coral host and its natural microbiota, which may ultimately cause disease and death of corals.

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Water Quality Consequences of Microbial Diversity in Wetland Soils

Excess nitrate in water bodies presents a critical water quality problem for both human and ecological health. Microbes perform the key chemical transformations in denitrification, an important mechanism for nitrate removal. Therefore, the composition and diversity of microbial communities may be important determinants of denitrification rates. Theoretically, a high diversity of traits and strategies could confer an 'insurance' and/or 'complementarity' effect that allows a microbial community to perform well (i.e., sustain high denitrification rates) under stressful and/or variable environmental conditions. Plant diversity can have a large impact on microbial community structure because plant litter and root exudates represent important sources of carbon for microbes. Our study 1) characterizes microbial communities using denaturing gradient gel electrophoresis, a molecular fingerprinting method, and 2) measures denitrification potentials using the denitrification enzyme activity method in experimental plots of varying plant diversity in Sandy Creek, a restored wetland in Duke Forest (Durham, North Carolina, U.S.). Sample plots include: unseeded treatments; monocultures of Eupatorium maculatum*; monocultures of* Scirpus cyperinus*; four species polycultures; and eight species polycultures. We analyze these data to determine the importance of plant diversity and composition relative to environmental factors (SOM, soil moisture, nitrate availability) in regulating both microbial community structure and denitrification rates. Given that microbial community structures may shift in response to environmental degradation and that microbial diversity may be an important regulator of denitrification rates, conservation efforts may need to consider not only plant and animal diversity, but also microbial diversity as essential components of wetland ecological integrity.*

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Is the Mercury Resistance *(mer)* System of *Thermus Thermophilus* HB17 an Ancestor to the Broadly Distributed *mer* System among the *Bacteria*?

The mercury resistance system (mer) *is widespread among the* Archaea *and the* Bacteria *and is found in microbes from diverse environments. The evolutionary origin of* mer *is presently unknown. The merA gene encodes for mer's core function, the enzyme mercuric reductase (MerA). Microbes with* merA *remove mercury from their environment by reducing Hg(II) to the volatile Hg(0). Environmental microbes from across large geographical and phylogenetic distances carry diverse* merA *genes that share strong sequence conservation at the core catalytic region. These observations suggest that resistance to mercury is an ancient phenotype. To explore the origins of mercury resistance, complete prokaryotic genomes were searched for* merA *and an alignment of MerA sequences was assembled. Phylogenetic analyses showed that MerA from the hyperthermophile* Thermus thermophilus *HB27 branched externally to all bacterial MerA sequences, suggesting that it might represent an ancestral locus. This is consistent with the hypothesis that metal-microbe interactions evolved in geothermal environments. Mercury resistance in strain HB27 was investigated by constructing a* merA *deletion mutant in which resistance declined fourfold relative to the wild-type and whose crude cell extract lost all mercuric reductase activity. Further characterization showed that unlike similar systems in the* Proteobacteria, mer *in HB27 did not encode for active transport of mercury, was constitutively expressed, and its MerA used NADH preferentially to NADPH as a co-substrate in the reduction of Hg(II). This study supports the hypothesis that* mer *has evolved among thermophilic prokaryotes in geothermal environments, and begins the characterization of a putative model for an ancestral bacterial mercury resistance system.*

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Pigs and Passerines: Environmental Impacts on Gastrointestinal Biota in Wild Birds

Impacts of disease on the ecology of wild birds have been clearly documented. Parasites can drive life-history evolution and have important conservation implications. However, the majority of vertebrate-microbe interactions are more complex, ranging from pathogenic to mutualistic, and are highly context dependent. While livestock microbiota have been intensively studied, the sources and consequences of resident microbiota in wild birds are not well described. We studied patterns in nest microbial communities of wild passerines in Illinois, sampling nest material from cavity nesting (e.g. House Sparrow) and open nesting (e.g. American Robin) species throughout the breeding season. Nest material was agitated in sterile PBS, which was then plated by serial dilution on 10% Tryptic Soy Agar (TSA) and incubated for 5 days at 23˚C to obtain counts. Seasonal increases in cultivable bacterial densities (CFU/gram nest material) occurred for both cavity and open nesting species, although the latter was not significant. Richness (assigned by colony morphotypes on TSA plates) did not correlate to collection date. Density and richness also varied among species and between nesting types. These preliminary patterns suggest that bacterial exposure in the nesting microhabitat varies among species and may be responsive to environmental changes in nest material availability and local habitat contamination. More holistic analysis of these communities by PCR-DGGE are planned to better understand patterns in nest microbial ecology. We place these findings within the context of a developing research program to explore microhabitat and habitat variation in microbial exposures of wild birds and discuss plans to evaluate impacts of environmental modification near swine production facilities on wild bird microbial ecology and gastrointestinal health. Increased understanding of how environment shapes resident microbial communities will contribute to studies of microbial impacts on avian ecology in natural systems and may prove valuable as habitat overlap of wildlife and domestic animals expands.

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Diversity of Mobile Genetic Elements: Influence of Metal Contamination on the Structure and Function of the Gene Cassette 'Floating Genome'

Mobile genetic elements represent a genetic resource through which bacteria may rapidly adapt to living in dynamic conditions. One such element, the integron, incorporates exogenous sources of DNA called gene cassettes into the recipient genome via site-specific recombination. These genetic elements were first discovered due to their role in the acquisition of antibiotic resistance gene cassettes in clinical bacteria. However, more recent evidence indicates that numerous types of gene cassettes can be incorporated into integrons in environmental bacteria, many of which contain a predicted protein of unknown function. Our previous work demonstrates that class 1 integrons are significantly more abundant in metal-contaminated estuarine and riverine habitats than in reference sites suggesting that bacteria possessing integrons are selected for in contaminated systems. Thus the objective of this research is to examine the structure and function of the gene cassette pool in systems with varying degrees of metal contamination to test the hypothesis that a selective pressure shapes gene cassette richness, similarity, and predicted function. Data indicate that while gene cassette richness estimates are similar among contaminated and reference sites, cassette community composition is distinct at each site. The predicted function of these genes includes a wide variety of genes other than those associated with antibiotic resistance and includes many predicted genes with no matches to sequences in available databases. These findings suggest that the gene cassette pool of mobile genetic elements is a diverse resource available to environmental bacteria and may constitute a 'floating genome' distinct from the core content of bacterial genomes.

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BACTERIAL DIVERSTIY ALONG PHYSICAL AND NUTRIENT GRADIENTS IN STREAM SEDIMENT HYDROLOGIC MARGINS OF HOT AND COLD DESERTS

Microbially-mediated nutrient transformations in stream sediments are of great importance to stream and terrestrial biota, especially in desert systems where water and nutrient availability is low and bacteria are well-adapted to operate under extreme conditions. The desert stream hydrologic margin (HM) is a lateral gradient of sediment water content and solute distribution bridging the aquatic and terrestrial zones, and a hotspot of biological activity and nutrient transformation. We describe the distribution of nitrogen and bacterial communities across this wet-dry gradient at two sites: the Rio Salado (Sevilleta National Wildlife Reserve, New Mexico, USA) and Onyx River (McMurdo Dry Valleys, Victoria Land, Antarctica). Denaturing gradient gel electrophoresis (DGGE) and 16S rRNA clone libraries reveal more heterogeneity in bacterial community composition across this gradient in the cold desert versus the hot desert, though the controls on inorganic nitrogen distribution appear similar. Also, cold desert sediment communities show higher diversity than the hot desert. Up to 22% of sequences per Antarctic site library are most similar to other Antarctic sequences, and this community "endemicity" is highest in wetted sediments. Up to 70% of sequences per New Mexico site library (and up to 20% of Antarctic sites) are most similar to sequences from contaminated or saline habitats, and the proportion of sequences with potential tolerance to extreme conditions is higher in dryer sediments. In addition to their status as biogeochemical hotspots in the landscape, desert stream hydrologic margin environments contain uniquely diverse bacterial communities. Channelization of hot desert streams for water delivery or flood control may endanger both ecosystem function and microbial diversity. Also, rapid summer cooling in the Antarctic Dry Valleys due to climate change diminishes stream flow and threatens to decrease the distribution of endemic bacteria.

AUTHORS	ABSTRACT TITLE	LEAD AUTHOR
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Foissner, Wilhelm	MOLECULAR PHYLOGENETIC ANALYSIS OF CLASS COLPODEA (PHYLUM CILIOPHORA) USING INCREASED TAXON SAMPLING	Dunthorn, Micah
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Gogarten, Peter J.	EMERGENCE OF A PLANETARY METHANE ECOLOGY: EVOLULTION OF ACETICLASTIC METHANOGENESIS IN *METHANOSARCINAE* VIA HORIZONTAL GENE TRANSFER FROM *CLOSTRIDIA*	Fournier, Greg
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Gooseff, Michael N.	BACTERIAL DIVERSITY ALONG PHYSICAL AND NUTRIENT GRADIENTS IN STREAM SEDIMENT HYDROLOGIC MARGINS OF HOT AND COLD DESERTS	Zeglin, Lydia

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Grant, Jessica	PLACEMENT OF DIVERSE AMOEBAE ON THE EUKARYOTIC TREE OF LIFE	Grant, Jessica
Grant, Jessica	REVEALING THE EVOLUTIONARY HISTORY OF AN UNKNOWN AMOEBA: MULTIGENE ANALYSIS OF *CORALLOMYXA TENERA* SP. NOV.	Tekle, Yonas I.
Habura, Andrea	HIDDEN DIVERSITY OF ALLOGROMIID FORAMINIFERANS	Habura, Andrea
Hall, Dana	ENVIRONMENTAL STRESSORS SHIFT THE MICROBIAL AND VIRAL COMMUNITY ON CORALS FROM OCEANIC TO PATHOGENIC	Vega Thurber, Rebecca
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Harris, Reid N.	THE ROLE OF BACTERIA IN TREATING AMPHIBIANS EXPOSED TO A LETHAL FUNGAL PATHOGEN: AN EXPERIMENTAL STUDY OF THE EFFICACY OF PROBIOTICS IN CONSERVATION BIOLOGY	Harris, Reid N.
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Haynes, Matthew	ENVIRONMENTAL STRESSORS SHIFT THE MICROBIAL AND VIRAL COMMUNITY ON CORALS FROM OCEANIC TO PATHOGENIC	Vega Thurber, Rebecca
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Jones, Philip D.	ECOLOGICAL IMPLICATIONS FOR CONSERVATION: HEALTHY ECOSYSTEMS ARE GOOD FOR YOUR HEALTH	Dizney, Laurie
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Kato, Michiko	THE GLOBAL VIRAL METAGENOME PROJECT	Deemy, James

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Katz, Laura A.	ASSESSING DIVERSITY OF PLANKTONIC CILIATE COMMUNITIES IN MARINE COASTAL WATERS	Doherty, Mary
Katz, Laura A.	MOLECULAR PHYLOGENETIC ANALYSIS OF CLASS COLPODEA (PHYLUM CILIOPHORA) USING INCREASED TAXON SAMPLING	Dunthorn, Micah
Katz, Laura A.	PLACEMENT OF DIVERSE AMOEBAE ON THE EUKARYOTIC TREE OF LIFE	Grant, Jessica
Katz, Laura A.	EVALUATING SUPPORT FOR THE CURRENT CLASSIFICATION OF EUKARYOTIC DIVERSITY	Parfrey, Laura Wegener
Katz, Laura A.	REVEALING THE EVOLUTIONARY HISTORY OF AN UNKNOWN AMOEBA: MULTIGENE ANALYSIS OF *CORALLOMYXA TENERA* SP. NOV.	Tekle, Yonas I.
Kaur, Amarjit	STUDIES ON THE ROLE OF FUNGI IN CONSERVATION OF WHEAT STRAW FOR MUSHROOM PRODUCTION	Kaur, Amarjit
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Lahr, Daniel J.G.	A PRACTICAL METHOD FOR IDENTIFICATION AND DESCRIPTION OF MICROBIAL EUKARYOTES USING THE TESTATE AMOEBA *CENTROPYXIS* AS A CASE STUDY	Lahr, Daniel J.G.
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Nerad, Thomas A.	REVEALING THE EVOLUTIONARY HISTORY OF AN UNKNOWN AMOEBA: MULTIGENE ANALYSIS OF *CORALLOMYXA TENERA* SP. NOV.	Tekle, Yonas I.
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Paver, Sara F.	BETWEEN- AND WITHIN-LAKE COMPARISON OF BACTERIAL ASSEMBLAGES IN THE ILLINOIS RIVER FLOODPLAIN	Paver, Sara F.
Paver, Sara F.	ASSESSMENT OF CRYOGENIC PRACTICES TO PRESERVE BACTERIAL ASSEMBLAGES: A STUDY OF CENTRAL PARK, NY SEDIMENT	Rossetto, Michael A.
Picardal, Flynn	BIOGEOCHEMICAL INTERACTIONS DURING MICROBIAL IRON AND NITROGEN CYCLING IN ANOXIC SEDIMENTS	Coby, Aaron J.
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Pop, Mihai	454/SANGER GENOME SEQUENCE OF THE ORAL BACTERIUM *AGGREGATIBACTER APHROPHILUS NJ8700*	Di Bonaventura, Mariapia
Randle, Michelle	BETWEEN- AND WITHIN-LAKE COMPARISON OF BACTERIAL ASSEMBLAGES IN THE ILLINOIS RIVER FLOODPLAIN	Paver, Sara F.
Ray, Allison E.	METALS TRANSFORMATION BY A PHYLOGENETICALLY DISTINCT ANAEROBE, STRAIN UFO1	Ray, Allison E.

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Reich, Peter	LACK OF EFFECTS OF ELEVATED N AND CO_2 ON SOIL MICROBIAL DIVERSITY IN A NORTH AMERICAN GRASSLAND MODEL SYSTEM	Osmundson, Todd
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Robledo-Esqueda, Martha	DIVERSITY OF ROOT PATHOGENIC FUNGI IN THE LOS TUXTLAS BIOSPHERE RESERVE, VERACRUZ, MEXICO	Rodríguez-Guzmán, Pilar
Rodbumrer, Jitsupang	METAGENOMICS REVEALS UNEXPECTED DIVERSITY OF β-LACTAM ANTIBIOTIC RESISTANCE GENES IN PRISTINE ALASKAN SOIL	Allen, Heather K.
Roden, Eric	BIOGEOCHEMICAL INTERACTIONS DURING MICROBIAL IRON AND NITROGEN CYCLING IN ANOXIC SEDIMENTS	Coby, Aaron J.
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Rodríguez-Guerra, Raúl	DIVERSITY OF ROOT PATHOGENIC FUNGI IN THE LOS TUXTLAS BIOSPHERE RESERVE, VERACRUZ, MEXICO	Rodríguez-Guzmán, Pilar
Rodríguez-Guzmán, Pilar	DIVERSITY OF ROOT PATHOGENIC FUNGI IN THE LOS TUXTLAS BIOSPHERE RESERVE, VERACRUZ, MEXICO	Rodríguez-Guzmán, Pilar
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Sánchez-García, Bertha	DIVERSITY OF ROOT PATHOGENIC FUNGI IN THE LOS TUXTLAS BIOSPHERE RESERVE, VERACRUZ, MEXICO	Rodríguez-Guzmán, Pilar

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Shenkin, Alexander	MICROBIOTIC SOIL COMMUNITY EFFECTS OF TREE GROWTH ACROSS TWO SITES IN PANAMA	Shenkin, Alexander
Shrager, Jeff	THE GLOBAL VIRAL METAGENOME PROJECT	Deemy, James
Simon, Mary Alice	THE ROLE OF BACTERIA IN TREATING AMPHIBIANS EXPOSED TO A LETHAL FUNGAL PATHOGEN: AN EXPERIMENTAL STUDY OF THE EFFICACY OF PROBIOTICS IN CONSERVATION BIOLOGY	Harris, Reid N.
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Sinha, B.K.	ECOLOGICAL NICHE MODELLING FOR DRIVER SPECIES OF FOREST FLOOR ECOSYSTEM: USING GENETIC ALGORITHM (GA)	Sinha, B.K.
Sircely, Jason	LACK OF EFFECTS OF ELEVATED N AND CO_2 ON SOIL MICROBIAL DIVERSITY IN A NORTH AMERICAN GRASSLAND MODEL SYSTEM	Osmundson, Todd
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Sizova, Maria V.	PERMAFROST: A DEPOSITORY OR SUBZERO INCUBATOR FOR PSYCHROPHILIC MICROORGANISMS?	Panikov, Nicolai S.
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