1st Annual Southeastern Biogeochemistry Symposium

April 5-6,2014

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Keynote Speaker

Dr. William Schlesinger

Cary Institute of Ecosystem Studies

"Coupled Biogeochemical Cycles"

Dr. William H. Schlesinger is the President of the Cary Institute of Ecosystem Studies. Previously he served in a dual capacity at Duke University, as both the James B. Duke Professor of Biogeochemistry and Dean of the Nicholas School of the Environment and Earth Sciences.

A graduate of Dartmouth College (A.B.) and Cornell University (PhD.), he has been investigating the link between environmental chemistry and global climate change for over 30 years. His recent work focuses on understanding how trees and soil influence atmospheric carbon dioxide levels.

He is the author or coauthor of over 200 scientific papers on subjects of environmental chemistry and global change and the widely-adopted textbook Biogeochemistry: An analysis of global change (Academic Press, 3rd ed. 2013). He has published editorials and columns in the Charlotte Observer, Chicago Tribune, Los Angeles Times, Philadelphia Inquirer, and the Raleigh News and Observer.

Schlesinger was among the first to quantify the amount of carbon held in soil organic matter globally, providing subsequent estimates of the role of soils and human impacts on forests and soils in global climate change. He was elected a member of The National Academy of Sciences in 2003, and was President of the Ecological Society of America for 2003-2004. He is also a fellow in the American Academy of Arts and Sciences, the American Geophysical Union, the Soil Science Society of America and the American Association for the Advancement of Science.

His past work has taken him to diverse habitats, ranging from Okefenokee Swamp in southern Georgia to the Mojave Desert of California, and three times as a Duke alumni tour guide to Antarctica. His research has been featured on NOVA, CNN, NPR, and on the pages of Discover, National Geographic, the New York Times, and Scientific American. Schlesinger has testified before U.S. House and Senate Committees on a variety of environmental issues, including preservation of desert habitats, global climate change and carbon sequestration.

Schedule

Saturday April 5, 2014

Time	Event	Location
9:00 AM - 10:30 AM	Check In	CULC Atrium
10:30 AM - 10:45 AM	Introduction and Welcome	CULC 144
10:45 AM - 11:30 AM	**Keynote: William Schlesinger "Coupled Biogeochemical Cycles"**	CULC 144
11:30 AM - 1:00 PM	Oral Session I	CULC 144
1:00 PM - 2:00 PM	Lunch	Tech Green
2:00 PM - 4:00 PM	Oral Session II	CULC 144
4:00 PM - 6:00 PM	Poster Session I	CULC Rooftop (5th Floor)
6:00 PM - 8:00 PM	Reception and hors d'oeuvres	CULC Rooftop (5th Floor)

Sunday April 6, 2014

Time	Event	Location
8:30 AM -9:00 AM	Breakfast Buffet	CULC Atrium
9:00 AM -10:30 AM	Oral Session III	CULC 144
10:30 AM -12:30 PM	Poster Session II	CULC Atrium
12:30 PM -1:00 PM	Awards Presentation	CULC 144

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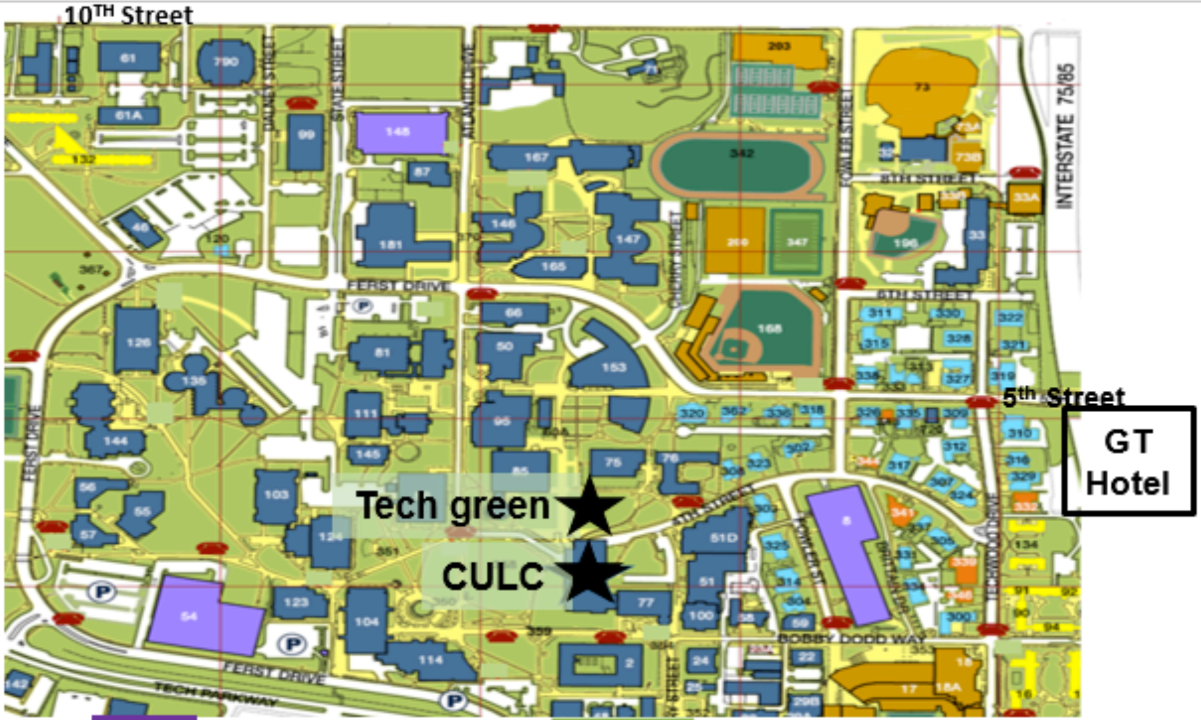
Maps



CULC 1ST floor map

CULC 5th floor map

Oral Session I
11:30AM-1:00PM
Saturday April 5
CULC 144

11:30 AM
Oil in the beach: The microbial response to hydrocarbons parallels changes in oil chemistry

Will A. Overholt*, Kala P. Marks, Luis-M Rodriguez-R, Christopher Hagan, John Kaba, Kostas Konstantinidis, Markus Huettel, and Joel E. Kostka

Georgia Institute of Technology

Environmental microbiology and biogeochemistry were coupled to investigate the effects of oil on native Gulf coast beach microorganisms, and to identify dominant oil-degrading taxa. Results indicate a rapid depletion of hydrocarbons, and a concomitant increase in oxygen consumption rates in beach sands after the oil arrived. This was paralleled by a bloom in bacteria, a sharp decrease in taxonomic diversity, and a succession of microbial populations in the oiled sands. Oil stimulated Gamma- and Alphaproteobacterial lineages, and negatively impacted Archaeal groups similar to Nitrosopumilus that likely provided key ecosystem functions. Twelve metagenomes were generated in order to interrogate shifts in the functionality of microbial communities with time as the communities recovered. Comprehensive iTag (>300 samples) and metagenomic datasets reveal similar shifts in community structure with time. Genes involved in hydrocarbon utilization were substantially enriched relative to housekeeping genes in oiled samples. By June 2011, extractable hydrocarbons were close to detection limits, and the microbial community structure and taxonomic diversity was similar to pre-spill samples. Overall, multiple lines of independent evidence describe the microbial response to hydrocarbon discharge as a succession dynamics model driven by nutrient availability and hydrocarbon chemistry.

11:45 AM
The influence of the Amazon River on the biogeochemistry of dissolved organic matter in the tropical North Atlantic Ocean

Michael Seidel*, Nicholas D. Ward, Patricia L. Yager, Edward J. Carpenter, Helga R. Gomes, Alex V. Krusche, Thorsten Dittmar, and Patricia M. Medeiros

University of Georgia

The Amazon River annually exports 22 Tg of dissolved organic matter (DOM) into the tropical North Atlantic (TNA). Yet, our knowledge about the biogeochemical cycling of DOM in the river to ocean continuum is still very limited. We present results from the first study that covers the upriver station at Óbidos to the outer parts of the river plume in the TNA. To unravel the biogeochemical processes in the continuum we link the molecular DOM composition using ultrahigh-resolution mass spectrometry to geochemical tracer and biological analyses. Compositional DOM changes in the plume appear to be mainly driven by the dilution of riverine with oceanic waters. However, using incubation experiments we find that about a third of the riverine DOM compounds are photo- and biodegradable within days. Furthermore, the compositional DOM variability within the plume is significantly determined by bacterial productivity suggesting continuous microbial degradation of terrestrial-derived DOM in addition to rapid turn-over of autochthonous DOM from phytoplankton blooms. Our results show that DOM cycling within the river to ocean continuum is much more complex than previously thought.

12:00 PM
The aquatic priming effect: Evidence for the influence of labile organic matter on the remineralization of semi-labile organic matter

Lauren Mach*, Andrew Steen, and Alison Buchan

University of Tennessee, Knoxville

The priming effect (PE) is a natural phenomenon first described in soil systems whereby the addition of labile organic compounds and/or nutrients stimulates the microbially mediated remineralization of recalcitrant compounds. The PE has been overlooked in aquatic systems and may explain the disappearance of terrestrially-derived dissolved organic matter (t-DOM) in the coastal ocean, which receives labile OM inputs from coastal vegetation and phytoplankton. In order to examine whether the PE may occur in the southeastern US coastal ocean, we examined the effect to which different labile sources of carbon and nutrients stimulated the mineralization rates of plankton-derived semilabile OM by a natural Georgia coastal microbial community. Addition of a protein source (BSA) and inorganic phosphorus stimulated microbial mineralization of semilabile OM, whereas addition of a labile carbon substrate (acetate) alone repressed mineralization of OM relative to a no-addition control. Addition of inorganic nitrogen alone or inorganic nitrogen plus inorganic phosphorus had no clear effect on semilabile OM mineralization. These data suggest coastal microbial community members can be ‘primed’ by the addition of labile carbon and nutrient sources and provides a basis for developing a mechanistic understanding of t-DOM transformations by these populations.

12:15 PM

Probing the photochemical reactivity of deep ocean refractory carbon: A lesson from superoxide and hydrogen kinetics

Leanne C. Powers*, William L. Miller, Jade K. Enright, and Lydia C. Babcock-Adams

University of Georgia

A comprehensive understanding of the global sources and sinks of marine dissolved organic carbon (DOC) has been hampered by the lack of information on organic carbon dynamics in the deep sea. Surprisingly, one proposed removal process is by photochemical reactions once deep ocean refractory carbon (DORC) mixes to the sunlit surface waters (Mopper, Nature 1991). Photochemical reactions involving DOC create intermediates that reduce oxygen to superoxide (O_2^-), which then can form hydrogen peroxide (H_2O_2). These two reactive oxygen species play a significant role in environmental redox kinetics but their link to DOC oxidation is not fully understood. To better quantify the removal processes of DORC, shipboard irradiations were used to determine H_2O_2 production rates and O_2^- steady-state and dark decay dynamics. Results indicate that surface and deep water samples have similar initial H2O2 production rates but for long term irradiations (>24 hours), some deep water samples stop H_2O_2 production. Superoxide steady-state concentrations decrease during long exposures, and modeled decay suggests that precursors for O_2^- production are consumed and/or new reactive intermediates (antioxidants) increase the oxidative sink for O_2^-.

12:30 PM

Changing organic matter chemistry associated with increasing greenhouse gas production along a permafrost thaw progression

Suzanne B. Hodgkins* Malak M. Tfaily, Carmody K. McCalley, Tyler A. Logan, Patrick M. Crill, Scott R. Saleska, Virginia I. Rich, William T. Cooper, and Jeffrey P. Chanton

Florida State University

Methane (CH_4) and carbon dioxide (CO_2) release due to permafrost thaw represents a major potential climate change feedback, but the magnitudes of these fluxes, and the biogeochemical processes underlying them, are still uncertain. We examined peat and pore water biogeochemistry along a permafrost thaw gradient from recently- to fully-thawed sites in Stordalen Mire, northern Sweden, using a combination of anaerobic incubations and organic chemistry analyses of peat and dissolved organic matter (DOM). Anaerobic incubations revealed increasing CH_4 and CO_2 production potentials and CH_4/CO_2 ratios along the thaw progression ($p<0.0001$), which were coupled with several proxies for decomposition rates in field samples. Fourier transform infrared spectroscopy (FTIR) revealed increasing peat humification rates with thaw. Ultrahigh resolution mass spectrometry of DOM revealed an increasing proportion of lipid-like, protein and amino sugar-like, and other low-O/C-ratio compounds with thaw, which was highly correlated with the abundance of a microbially-derived fluorophore as revealed by fluorescence pectroscopy ($p<0.0001$), suggesting increased microbial activity with thaw. These changes are likely driven by increasing litter quality due to shifts from Sphagnum- to sedge-dominated plant communities. These results imply that changes in plant community associated with permafrost thaw can lead to per-volume increases in CH_4+CO_2 production rates and CH_4/CO_2 ratios.

12:45PM

Does oxygen exposure time control the extent of organic matter decomposition in peatlands?

Michael Philben*, Karl Kaiser, and Ronald Benner

University of South Carolina

The extent of decomposition was investigated in four peat cores collected along a latitudinal gradient from 56˚N to 66˚N in the West Siberian Lowland. Acid:aldehyde ratios of lignin phenols were significantly higher in the two northern cores compared with the two southern cores, indicating peats at the northern sites were more highly decomposed. Yields of hydroxyproline, an amino acid found in plant structural glycoproteins, were higher in northern cores compared with southern cores. Hydroxyproline-rich glycoproteins are not synthesized by microbes and are generally less reactive than bulk plant carbon, so elevated yields indicated northern cores were more extensively decomposed than the southern cores. The southern were less decomposed despite warmer temperatures, indicating temperature was not the primary control of peat decomposition. The plant community oscillated between Sphagnum and vascular plant dominance in the southern cores, but vegetation type did not appear to affect the extent of decomposition. Oxygen exposure time appeared to be the strongest control of the extent of peat decomposition. The northern cores had lower accumulation rates and drier conditions, so these peats were exposed to oxic conditions for a longer time before burial in the anoxic catotelm, where rates of decomposition are generally an order of magnitude lower.

Oral Session II
2:00-4:00PM
Saturday April 5
CULC 144

2:00 PM
Intense nitrogen cycling in barrier island groundwater revealed by a nitrous oxide hotspot

Charles Schutte* and Samantha Joye

University of Georgia

Anthropogenic nitrogen fixation is roughly equal to the nitrogen fixation of Earth's entire biosphere. Much of this anthropogenic nitrogen is used to fertilize agricultural fields. A portion of this nitrogen runs off and is concentrated in the coastal zone by riverine discharge, damaging water quality. Microbial nitrogen cycling in coastal sediments can mitigate eutrophication by removing bioavailable nitrogen, but it simultaneously generates nitrous oxide, a potent greenhouse gas. Here we report the discovery of a nitrous oxide production hotspot in a shallow barrier island aquifer. We measured nitrous oxide concentrations, production and consumption rates, vertical diffusion fluxes, and flux to the atmosphere across triplicate depth profiles. We observed nitrous oxide concentrations of 225 nM in the brackish groundwater beneath the upper beach, and a flux to the atmosphere of 8570 nmol m^{-2} day^{-1}. While this flux was too low to influence the nitrous oxide budget of Earth's atmosphere, it was driven by an important zone of denitrification that removed bioavailable nitrogen from the coastal environment. We calculate that Georgia's barrier islands have the potential to remove ~1.5% of the annual nitrate loading from the Altamaha River (Georgia's largest watershed) to the ocean.

2:15 PM
Elevated ammonia oxidation rates in Antarctic circumpolar deep water vs. winter water

Bradley B. Tolar*, Meredith Ross, Natalie J. Wallsgrove, Qian Liu, Lihini I. Aluwihare, Brian N. Popp, and James T. Hollibaugh

University of Georgia

We report here the first nitrification rate measurements from the Southern Ocean (south of 60°S) and under 100 m depth. A previous study by our lab (2006) identified differences in the composition of Thaumarchaeota populations in Winter Water (WW) versus Circumpolar Deep Water (CDW), and suggested that these differences might be reflected in Thaumarchaeota ammonia oxidation rates. We found abundant Thaumarchaeota genes (102-108 copies L^{-1}), and transcripts (103-107 copies L^{-1}) and measured oxidation of $^{15}NH_4$ (0.52-140 nM day^{-1}) in samples from the WW and CDW collected in spring (2010) and summer (2011) across the PAL-LTER study area in the Southern Ocean. Thaumarchaeota gene abundances correlated to increased temperature, salinity, and $[NO_x]$ – all properties of the CDW. Analysis of 454 pyrosequencing reads for 16S rRNA and amoA genes showed more diversity in CDW populations. Summer ammonia oxidation rates were detectable in both CDW and WW, though on average rates were higher in CDW (25 vs. 12 nM day^{-1}), indicating a more active community of nitrifying organisms.

2:30 PM
Thaumarchaeota and ammonia oxidizing archaea response to coastal hypoxia

Natalie Ortell*, Kjell Gundersen, and Alice C. Ortmann

University of South Alabama

Ammonia oxidizing Archaea (AOA), members of the Thaumarchaeota, participate in marine nitrogen cycling, converting ammonia to nitrite and providing a link to denitrification and ultimately the removal of nitrogen from marine systems. The gene encoding the α subunit of ammonia monooxygenase (amoA) is commonly used as a marker for microbial ammonia oxidation. The objective of this study was to characterize the thaumarchaeal community and to determine the potential for nitrification under coastal hypoxic conditions. Surface and bottom samples were collected during two summers from the Mississippi Bight water column. Thaumarchaeota 16S rRNA and archaeal amoA genes were quantified using qPCR. Thaumarchaeota contributed more to the total prokaryote community in bottom waters. Abundances of Thaumarchaeota and amoA increased with distance from the coast (Wilcoxon, $p < 0.05$). A significant negative relationship was detected between dissolved oxygen and Thaumarchaeota and amoA abundance (Spearman's, $\rho = -0.58$ and -0.27, respectively). The amoA to Thaumarchaeota ratio was less than 1:1 in the majority of samples and did not differ between hypoxic and normoxic conditions (Wilcoxon, $p > 0.05$). These results suggest that Thaumarchaeota are important members of coastal hypoxic environments, however, not all Thaumarchaeota appear to be AOA.

2:45 PM

Detecting nitrous oxide reductase (nosZ) genes in soil metagenomes: Method development and implications for the nitrogen cycle

Luis Orellana*, Luis Rodriguez-R, Steve Higgins, Joanne Chee-Sanford, Robert Sanford, Kirsti Ritalahti, Frank Löffler, and Konstantinos Konstantinidis

Georgia Institute of Technology

The key enzyme for mitigating N_2O emissions is nitrous oxide reductase (NosZ), which catalyzes N_2O reduction to N2. We have recently described a novel group of "atypical" NosZ encoded on the genomes of denitrifiers and incomplete denitrifiers, most of which were missed in previous PCR-based surveys. We analyzed the abundance and diversity of both types of *nosZ* genes in whole-genome shotgun metagenomes obtained from sandy and silty soils that typify the US corn belt. We defined appropriate cutoffs for detecting typical and atypical *nosZ* fragments based on in-silico generated metagenomes. Based on the determined cutoffs, more than 71 distinct reference representatives, encoding typical and atypical NosZ, were detected in both soils. Remarkably, more than 70% of the total *nosZ*-encoding reads in both soils were classified as atypical. Approximately 12% of the *nosZ* reads were taxonomically assigned to the Anaeromyxobacter genus, indicating their potential relevance for N_2O reduction. Further analyses indicated that atypical *nosZ* genes were more abundant than typical ones in publicly available soil metagenomes, underscoring the ecological importance of atypical *nosZ*. Our work provides a bioinformatic strategy to detect target genes in short-read metagenomes and has implications for better understanding N-cycling in soils.

3:00 PM

Metatranscriptomics identifies metabolic partitioning among microbial size-fractions in a marine oxygen minimum zone

Sangita Ganesh*, Laura A. Bristow, Bo Thamdrup, and Frank J. Stewart

Georgia Institute of Technology

Oxygen minimum zones support diverse microbial communities with roles in major elemental cycles. Recent work has shown that association with suspended particles is a strong determinant of microbial community structure and function in OMZs. However, the extent to which physiological activity varies in situ between particle-associated and free-living OMZ microbial communities is not well understood. We analyzed community gene expression (metatranscriptomes) in size-fractionated communities from the anoxic OMZ off Mexico. Microbial biomass was sampled from the oxycline and OMZ at two sites and fractionated into three size classes (>30 µm, 1.6-30 µm, 0.2-1.6 µm) y filtration. Community RNA from each fraction was analyzed using shotgun Illumina sequencing. Here, we describe transcriptional differences across size fractions and depths, and between coastal and offshore sites differing in nutrient and oxygen conditions, placing specific emphasis on genes mediating microbe-microbe interactions and pathways of dissimilatory nitrogen and sulfur metabolism. Results are discussed relative to metagenomic patterns of community metabolic potential, as well as coupled process rate measurements. These data highlight the potential for particle-associated microorganisms to influence community biogeochemical transformations in OMZs.

3:15 PM

The influence of rapid, millennial-scale climate change on nitrogen isotope dynamics of the Cariaco Basin during marine isotope stage 3

Kelly Gibson*, Robert Thunell, Eric Tappa, Larry Peterson, and Martha McConnell

University of South Carolina

Understanding the changes to the nitrogen cycle on millennial scales and shorter can help to determine the influence of rapid climate changes on the fixed nitrogen pool, and feedbacks between its sources and sinks, but millennial-scale records of $\delta^{15}N$ variability are sparse. We present here a sedimentary $\delta^{15}N$ record from the Cariaco Basin from Marine Isotope Stage 3 (~35-55 ka). The $\delta^{15}N$ values during stadial periods reflect an imported regional signal and support the argument that there was not an increase in N_2 fixation in the tropics and subtropics during the last glacial period. Millennial-scale increases in $\delta^{15}N$ occur during interstadial periods in conjunction with increased productivity and anoxic-deep water conditions, representing a local increase in water column denitrification. This local pattern of variability confirms that while the global nitrogen budget may be in steady-state on glacial-interglacial timescales, regional changes in $\delta^{15}N$ dynamics also occur in response to rapid, short-lived climate changes. These millennial-scale fluctuations to the sources and sinks of fixed nitrogen occur on timescales relevant to present society, particularly as anthropogenic forcing continues to influence the climate system at rates comparable to, if not faster than, periods of rapid climate change in the past.

3:30 PM
Sinking particulate phosphorus in the Cariaco Basin, Venezuela

Annie Opseth*, Claudia Benitez-Nelson, Melissa Bennett, Robert Thunell, and Wendy Plessinger

University of South Carolina

In an effort to better understand the biogeochemical cycling of phosphorus (P) in the Cariaco Basin, the chemical composition and the sinking flux of particulate P was examined using sediment trap data collected from the Cariaco Time-Series (1995-2010). Total, inorganic and organic P composition and fluxes were determined on sediment trap samples using a modified Aspila method and sequential extraction techniques. In agreement with more recent studies, particulate inorganic P (PIP) was found to dominate the total particulate P (TPP) pool. TPP versus particulate N (PN) and particulate organic C (POC) suggest that a significant fraction of the PIP pool is biologically derived. However, the remaining PIP pool, particularly when TPP fluxes and % PIP concentrations are high suggest that PIP is derived from a wider range of sources. Preliminary data suggests that the high PIP fluxes are due to three P phases: labile, oxide bound and authigenic P. Strong associations with carbonate and terrestrial material, especially during non-upwelling when biological activity is reduced, suggests that this PIP is derived from land and the remobilization of relict sediments initially deposited on the continental shelf. Such sources must therefore be considered when examining P biogeochemistry and its potential impact on ecosystems.

3:45 PM
P-NEXFS analysis of aerosol phosphorus delivered to the Mediterranean Sea

Amelia F. Longo*, Ellery D. Ingall, Julia M. Diaz, Michelle Oakes, Laura E. King, Athanasios Nenes, Nikolaos Mihalopoulos, Kaliopi Violaki, Anna Avila, Claudia R. Benitez-Nelson, Jay Brandes, Ian McNulty, and David J. Vine

Georgia Institute of Technology

Biological productivity in many ocean regions is controlled by the availability of the nutrient phosphorus. In the Mediterranean aerosol deposition is a key source of phosphorus and understanding its composition is critical for determining its potential bioavailability. Aerosols were investigated in air masses originating in either Europe or North Africa using Phosphorus Near Edge X-ray Fluorescence Spectroscopy (P-NEXFS). These air masses are the main source of aerosol deposition to the Mediterranean Sea. Here we show that aerosols originating in Europe represent significant source of bioavailable phosphorus to the Mediterranean. European aerosols deliver on average 3.5 times more soluble phosphorus than North African aerosols and furthermore are dominated by bioavailable, organic phosphorus compounds. The ultimate source of organic phosphorus does not stem from common emission sources, such as coal, gasoline, and diesel emissions, volcanic ash, biomass burning or pollen. Rather, phosphorus associated with bacteria best explains the presence of organic phosphorus in Mediterranean aerosols. Because long-term changes in wind direction are predicted to increase delivery of European aerosols to the Mediterranean Sea, biological production will likely increase over time in this oligotrophic region.

Poster Session I
(First author last names A-M)
4:00-6:00 PM
Saturday April 5

Microbial antimony respiration: New insights into the biogeochemistry of a poisonous element

Christopher A. Abin* and James T. Hollibaugh

University of Georgia

Antimony (Sb) is a toxic metalloid that belongs to Group 15 of the periodic table. In nature, Sb can exist in either the +3 (antimonite) or +5 (antimonate) oxidation states. Although a great deal of research has been devoted to the biogeochemical cycling of metalloids such as arsenic and selenium, very little information exists regarding the fate and transport of Sb in the environment. Microbe-Sb interactions remain poorly understood and a majority of the work has focused on characterizing microorganisms that oxidize antimonite, thus neglecting the reductive side of the cycle. For the first time, we have isolated an obligately anaerobic bacterium that is capable of respiring antimonate using simple organic acids as electron donors. The reduction of antimonate is accompanied by a concomitant rise in the concentration of antimonite, which precipitates from solution as orthorhombic and cubic microcrystals of antimony trioxide. Further phenotypic analyses have revealed that the isolate is capable of respiring other toxic oxyanions such as arsenate, selenate, selenite, and tellurate. This discovery not only enhances our understanding of the biogeochemical cycle of Sb, but also adds Sb to the growing list of elements capable of serving as terminal electron acceptors for microbial respiration.

Microbial and phytoplankton community changes in response to high inputs of dissolved organic nitrogen from submarine groundwater discharge

Jennifer S. Anders*, Justin D. Liefer, William C. Burnett, Hugh L. MacIntyre, and Behzad Mortazavi

University of Alabama/Dauphin Island Sea Lab

Submarine groundwater discharge (SGD) is now recognized as an important source of nutrients to coastal environments. Nitrogen fluxes from SGD are often comparable to, if not greater than, N loading from nearby rivers. SGD is distinct from other coastal freshwater inputs due to its diffuse nature and in the quantity and composition of nutrients it delivers. The subsequent effect of SGD on the ecology of microbes is poorly understood, even though in coastal Alabama it has been linked to potentially toxic blooms of diatoms. Biweekly monitoring of groundwater from a coastal lagoon indicates that 60-90 percent of the total dissolved nitrogen is in the form of dissolved organic nitrogen (DON), averaging 150 μM. SGD DON can exceed estuarine surface water concentrations by 2 orders of magnitude. Surface water bioassays treated with DON concentrated from groundwater had significantly increased Chl a concentrations over the control treatments by the end of a 6 day incubation. The diatom community abundances tripled in the groundwater DON treatments during the first 48 hours and by the second day were 2 times higher compared to the control treatments. This talk will address some of the consequences of DON fluxes for microbial and phytoplankton communities in SGD dominated coastal systems.

Regional and depth-related differences in the capabilities of Arctic microbial communities to degrade organic matter

John Paul Balmonte* and Carol Arnosti

University of North Carolina Chapel Hill

Rapid decrease in Arctic sea-ice cover is expected to alter many aspects of Arctic ecosystems. Alterations in carbon cycling, in part due to changes in productivity, are likely to ensue. The central role of bacteria in carbon cycling and their sensitivity to subtle variations in environmental conditions suggests a probable change in microbially-driven processes as well. To investigate how microbial heterotrophic processes vary with changes in Arctic sea-ice, we compared the enzymatic capabilities of natural microbial communities from regions of no-, partial-, and full-ice coverage, covering sites and depths not previously investigated, from 79°N to 88°N. Seawater samples spanning the entire water column, as well as surface sediments, were collected and incubated with a suite of fluorescently-labeled polysaccharides and peptide substrates. Patterns of enzymatic hydrolysis rates will be used to investigate depth-related changes and spatial differences in organic carbon processing, providing a baseline for future comparisons as well as insight into the potential impacts of diminishing sea-ice coverage on carbon cycling in the Arctic.

Degradation of *Spartina alterinflora*-derived dissolved organic matter by marsh sediment communities

Scott Beeler*, Audrey Paterson, and Annette Engel

University of Tennessee, Knoxville

Microbial degradation of dissolved organic matter (DOM) in estuarine systems, which is important to geochemical processes and microbial community function and diversity may be impacted by a variety of factors. The introduction of oil from the Deepwater Horizon oil spill in April 2010 to Louisiana marshes is thought to be one such factor. We experimentally investigated the potential impact that the level of oiling may have had on DOM biodegradation rates. Sediments with active microbial communities were collected from two sites with different oiling histories, from inland and marsh edge, at depths of 0-1 cm and 9-10 cm. Batch microcosms of sediments and seawater were enriched with DOM leachate made with marsh grass, *Spartina alterniflora*. DOM biodegradation was evaluated over a one-month period using fluorescence spectroscopy. Biodegradation rates were highest for all sites and depths between one day and two weeks, with similar rates measured for all sites except for inland sediment from the heavily oiled site. This implies the level of oiling may have affected the ability of the microbial communities to degrade vegetation-derived DOM. Further work is needed to determine the effects these changes have on large-scale geochemical processes and microbial community composition in the marshes.

Is urea a driver for Microcystis blooms in Lake Erie?

Bernard S. Belisle*, Morgan M. Steffen, Helena L. Pound, Sue B. Watson, Rick A. Bourbonniere, and Steven W. Wilhelm

University of Tennessee Knoxville

The Great Lakes basin holds nearly 20% of the world's potable freshwater, making it one of the largest freshwater systems. Over the last decade, Lake Erie has experienced extensive annual cyanobacterial harmful algal blooms (cHABs) dominated by events of the toxic cyanobacterium *Microcystis aeruginosa*. It is still unclear what causes *Microcystis* blooms to occur, but there is broad agreement that eutrophication of freshwater systems from anthropogenic sources (urban, industrial, etc.), has led to their proliferation. In particular, the organic compound urea has been implicated as an important source of nitrogen in the environment. Currently, urea constitutes more than 50% of the nitrogen used for agricultural fertilizer, and its usage has increased more than a 100-fold over the past four decades. To identify the potential role of urea in driving blooms of *Microcystis* in Lake Erie, environmental measurements of urease enzymatic activity, phytoplankton biomass, nutrient concentrations, and phytoplankton community composition were measured during a bloom event. Additionally, 48-hour in situ microcosm experiments, spiked with various nitrogen species (urea, nitrate, ammonium, and environmental control), were performed to enable comparison of phytoplankton biomass and community composition. Subsequent research into nitrogen utilization by cyanobacterial species may contribute to future mitigation of bloom events.

Dissolved organic phosphorus isolation: Implementation of a bench-top electrodialysis-reverse osmosis unit

Doug Bell*, Ellery Ingall, Amelia Longo, Luke Chambers, and Claudia Benitez-Nelson

University of South Carolina

The combination of electrodialysis and reverse osmosis (ED/RO) has shown promise as a novel technique for the isolation of marine dissolved organic matter (DOM). The advantage of the ED/RO technique is the production of a salt-free, concentrated DOM isolate with minimal size-fractionated losses. We have recently designed and constructed a bench-top ED/RO instrument to assist in the examination of the natural distribution and biological production of dissolved organic phosphorus (DOP) using liquid and solid-state 31P NMR. The objective of this study was to maximize the RO concentration component for DOM isolation and to determine the effect of RO (if any) on sample integrity. All representative DOP compound standards (phosphoester, phosphonate, and polyphosphate) were shown to have recoveries of $\geq$ 90% following a weak alkaline soak (sodium hydroxide, pH 10-11) of the RO membrane. Solid-state 31P-NMR spectra for each recovered DOP compound were indicative of unaltered compound structure. These results suggest that a weak alkaline soak following RO concentration can give high sample recovery while still maintaining sample integrity. However, as evident from the concentration of lake water using RO, recovery in natural samples declines due to the inherent complexity of the sample matrix.

Seasonality influences allochthonous organic matter and microbial community diversity in a cave stream

Kathleen Brannen* and Annette Summers Engel

University of Tennessee, Knoxville

Although microbial communities in cave streams rely on the input of allochthonous inorganic and organic nutrients, the dogma has been that cave systems support stable subsurface ecosystems. However, due to seasonal differences in allochthonous organic matter input from photosynthetically derived material, as well as hydrologic changes that occur seasonally, we hypothesized that microbial communities change over time based on the nature and type of organic matter, as well as due to hydrology (e.g., antecedent moisture). Microbial diversity based on amplicons of 16S rRNA genes was evaluated across seasons from samples taken along a sinking stream, and in the context of geochemical (e.g., pH, temperature, dissolved oxygen, dissolved cations and anions, total inorganic and organic carbon) and hydrologic (i.e. rainfall) controls. Statistical significance was assessed by using

RDA. Between surface and subsurface sites, variations in the relative distribution of Proteobacteria positively correlated with TOC, but the distribution of Bacteroidetes and Actinobacteria positively correlated with rainfall amount the week before sampling. Our results suggest that seasonal differences in microbial community diversity in cave streams is dependent on TOC and rainfall. Despite being a common trend observed in surface environments, this trend must be functionally different in the dark cave environment.

The role of vegetation in methane flux to the atmosphere: Should vegetation be included as a distinct category in the global methane budget?

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Currently, the global annual flux of methane to the atmosphere is fairly well constrained at ca. 645 Tg CH_4 yr^{-1}. However, the relative magnitudes of the fluxes generated from different sources remain poorly resolved. Of the identified natural sources, the contribution of vegetation to the global methane budget is arguably the least well understood. Historically, reviews of the contribution of vegetation to the global methane flux have focused on the role of plants as conduits for soil-borne methane emissions from wetlands, or the aerobic production of methane within plant tissues. Many recent global budgets only include the latter pathway in estimating the importance of terrestrial vegetation to atmospheric CH4 flux. However, recent experimental evidence suggests several novel pathways through which vegetation can contribute to the flux of methane. Herein, we provide a comprehensive estimate of the role of vegetation in the global methane budget. This first, albeit uncertain, estimate indicates that vegetation may represent up to 22% of the annual flux of methane to the atmosphere, contributing ca. 31-143 Tg CH4 yr-1 to the global flux of this important trace greenhouse gas. Overall, our findings emphasize the need to better resolve the role of vegetation in the biogeochemical cycling of methane.

Maximizing the recovery of dissolved organic matter from saltwater samples

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Dissolved organic matter (DOM) plays a major role in global carbon cycling in aqueous environments. Insufficient techniques to fully isolate DOM from natural samples with high salt concentrations have thus far hampered natural organic matter characterization. Here, an electrodialysis and reverse osmosis (ED/RO) system was constructed and optimized to concentrate DOM from small volume (2 to 10 L) samples by removing water and dissolved salts. Samples of coastal seawater and cultured algal filtrates were processed under numerous system operating conditions in order to optimize DOM recoveries. DOM recoveries are up to 53% and 70% for seawater and algal filtrates, respectively. The recoveries with this ED/RO system are typically 2 to 3 fold higher than those obtained through tangential flow ultrafiltration. These ED/RO recoveries are comparable to PPL resin extraction methods; however, PPL techniques may preferentially extract a subset of compounds most easily bound by the resin. Future modification to the ED/RO system including pulsed application of the electric potential across the ED membrane stack and processing samples in conjunction with PPL extractions and will likely result in further improvements of DOM recovery.

Relationships among *Prochlorococcus* ecotypes across oceanic temperature ranges

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Prochlorococcus, a cyanobacterium, is the numerically dominant photosynthetic organism of open ocean ecosystems. With the completion of several recent cruises, we now examine ecotype diversity of open ocean latitudinal transects spanning the world's two largest oceans, the Atlantic and Pacific. Quantitative PCR analyses confirmed the numerical domination by the eMIT9312 or the eMED4 ecotype, regardless of the presence of other known *Prochlorococcus* ecotypes and a strong influence of temperature on this relationship. Furthermore, temperature stands out as the primary factor that functionally influences ecotype diversity in the surface mixed layer. With the advent of axenic Prochlorococcus, we have investigated the competitive interrelationships between eMED4 and eMIT9312 in laboratory cultures at different temperatures. This data correlates well with observed field data, and together these data may provide a framework for future community and competitive laboratory studies, as well as contribute to a greater understanding of genetic diversity projections of field populations in increasingly warm ocean environments.

Dominance of *Methanosaeta* populations at high acetate concentrations during unstable anaerobic digestion

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Anaerobic digestion is an ideal biological waste treatment process capable of simultaneous pollution mitigation and renewable energy recovery. Despite the apparent advantages of anaerobic digestion as compared to aerobic processes, the broader adoption of anaerobic digestion technology for waste treatment has been hindered by concerns of potential process instability resulting from the susceptibility of methanogenic microbial populations to changes in process conditions, such as fluctuations in the concentration of acetate, which is a key substrate for methanogenesis. Therefore, to enhance the process stability of anaerobic digestion, the objective of this study was to identify methanogenic populations that can potentially thrive at fluctuating concentrations of acetate. Triplicate continuous anaerobic digesters fed with animal waste were established at 35°C. All digesters exhibited stable operation with consistent pH, methane yield, and acetate level prior to step-wise increases in substrate loading rate that eventually resulted in process disruption. 16S rRNA gene clone library and quantitative real time PCR assays were used to monitor the dynamics of various methanogenic populations in response to changes in process conditions. Chemical analyses indicate that acetate concentration remained constantly below 0.5 mM before spiking to ~40 mM as a result of substrate overloading. As expected, *Methanosaeta*-related populations, known to be competitive for acetate at low concentrations, were indeed the dominant methanogens at low acetate concentrations. However, *Methanosaeta* populations remained dominant even at higher acetate levels, outcompeting *Methanosarcina*-related methanogens known to be more competitive than *Methanosaeta* at high acetate conditions. Furthermore, analysis of enrichments developed with 20 mM acetate consistently resulted in *Methanosaeta* as the overwhelming majority. Thus, the *Methanosaeta* populations dominating the methanogen community in this study appear to be more ecologically important than *Methanosarcina* throughout the acetate concentration range relevant to anaerobic digestion. Ongoing effort is focused on the characterization of physiological features that may contribute to the surprising competitiveness of these Methanosaeta populations.

Influence of iron and external biotin on biotin metabolism in marine diatoms

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Diatoms are crucial contributors to the ocean biological carbon pump, yet in large regions of the open ocean diatom growth is limited by iron availability. In addition to trace metals, B-vitamins are critical for diatom growth due to their role in cellular metabolic pathways and have been shown to likewise limit growth. Since there is an iron requirement for biotin (vitamin B_7) synthesis, production of the vitamin in diatoms may be affected by iron-limitation. A combination of culture-based physiology and molecular approaches were used to quantify the expression patterns of diatom genes involved in biotin synthesis and uptake of biotin from the surrounding environment when exposed to a matrix of growth conditions. Our results indicate that low-iron conditions with biotin present in the growth medium suppresses biotin synthesis in the oceanic diatom *Pseudo-nitzschia granii*, and a metabolic shift from biotin biosynthesis to uptake of the vitamin from the growth medium may occur. Variations in biotin synthesis and utilization by biotin-producing diatoms could also have significant consequences on the availability of the vitamin to other members of the microbial community.

Shewanella oneidensis requires homocysteine for anaerobic biofilm formation

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The gram-negative, γ-proteobacterium *Shewanella oneidensis* MR-1 forms biofilms on silicate surfaces under aerobic growth conditions. The ability of S. oneidensis to form biofilms under anaerobic growth conditions, however, is not well understood. To test the hypothesis that LuxS (which converts S-ribosyl homocysteine to homocysteine in the activated methyl cycle) is required for biofilm formation under anaerobic growth conditions, an in-frame *luxS* deletion mutant was constructed and tested for anaerobic biofilm formation capability. Results of biofilm formation assays and direct visualization via confocal laser scanning microscopy indicated that the *luxS* mutant was unable to form biofilms on bare or Fe(III)-coated silicate surfaces under anaerobic growth conditions. The *luxS* mutant retained wild-type biofilm formation activity, however, when supplied with exogenous sulfur-containing metabolites (homocysteine, methionine, cystine, cysteine, glutathione, dithiodoglycolic acid) and non-sulfur-containing metabolites with the capacity to accept sulfhydryl groups (serine and homoserine), but not non-sulfur-containing metabolites (alanine, lysine). These results suggest that anaerobic biofilm formation by *S. oneidensis* requires homocysteine, and that homocysteine production deficiencies may be overcome by supplying S. oneidensis with exogenous metabolites that feed into the homocysteine-producing activated methyl cycle.

Comparisons of different proxies in tracing terrestrial organic matter in sediments of active margins, New Zealand

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Recent studies continue to show that separating sources of terrestrial organic matter (TOM) associated with litter (TOML) versus soil (TOMs) can be problematic in coastal sediments. Here, we provide a comprehensive comparison of lipids with other organic proxies to further address this issue. In this study, 25 surface sediment samples were collected from three fjord systems in Fiordland, New Zealand. As expected, C/N ratios and $\delta^{13}C$ were useful for tracing TOM inputs, but could not separate TOML from TOMS. A significant correlation was found between $\lambda8$ and $\delta^{13}C$ (R2 0.853), with only weak correlations with 3,5-dihydroxybenzoic acid (3,5-Bd, R2 0.490) and BIT index (R2 0.309, e.g., Smith et al, 2010), which are typical TOMS indices. Therefore, $\lambda8$ appeared to be tracking TOML. TOMS indices, 3,5-Bd and p-hydroxyacetophenone (PON), correlated significantly with the ratio of terrigenous to aquatic fatty acids (TARFA, R2 0.664), and the carbon preference index (CPIL, R2 0.714), while $\lambda8$ showed weaker correlations with TARFA (R2 0.331) and CPIL (R2 0.543). This suggested that fatty acids proxies (TARFA and CPIL) were tracking TOMS more effectively here.

Interactions of airborne microbial communities with clouds: A perspective from metagenomics

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Bacteria contribute to the biological aerosols in the atmosphere and it is thought to influence cloud formation and precipitation. Previous studies found that several bacterial species are good ice nuclei due to an outer-membrane protein that serves as a nucleation center. However, the impact of bacterial cells in cloud formation remains poorly characterized. Most studies in aerobiology were conducted on surface air and assessed the 16S rRNA gene while the microbial communities at higher altitudes, which are more relevant for cloud formation, remain uncharacterized. To study the bacterial communities in the troposphere we collected samples from over 10km, two major tropical hurricanes and low altitudes during two NASA campaigns. Metagenomic sequencing was performed for four samples, three high altitudes and one low altitude using Ilumina-GAII technology. Taxonomic analysis showed that Proteobacteria is the most abundant phylum, but that Bacteroidetes and Actinobacteria are the second most abundant in the high and low altitude samples, respectively. To understand how bacterial cells may influence cloud formation, the *inaZ* gene was searched in all metagenomes, but detected only at low altitude. Metagenomic analysis of bacterial communities in the atmosphere would provide quantitative insights in the distribution of proteins related to cloud formation and cloud chemistry.

Characterization of selenium in ambient aerosols and emission sources

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Atmospheric transformations of selenium (Se) in aerosols were investigated using X-ray Absorption Near-Edge Structure (XANES) spectroscopy and X-ray fluorescence (XRF) microscopy. These techniques were used to determine the oxidation state and elemental associations of Se in common emission sources and ambient aerosols collected from the greater Atlanta area. In the majority of ambient aerosol and emission source samples, the spectroscopic patterns as well as the absence of elemental correlations suggest Se is in an elemental, organic, or oxide form. XRF microscopy revealed numerous Se rich particles, or hotspots, accounting on average for ~16% of the total Se in ambient aerosols. Hotspots contained primarily Se0/Se(-II). However, larger, bulk spectroscopic characterizations revealed Se(IV) as the dominant oxidation state in ambient aerosol, followed by Se0/Se(-II) and Se(VI). Se(IV) was the only observed oxidation state in gasoline, diesel, and coal fly ash; while biomass burning contained a combination of Se0/Se(-II) and Se(IV). Differences in Se oxidation state between emission sources and ambient aerosols suggest that either atmospheric processing or unrecognized sources are influencing aerosol Se composition. Although the majority of Se in aerosols was in the most toxic form, the Se concentration is well below the California Environmental Protection Agency chronic exposure limit.

Phosphorus partitioning in the Chukchi Sea: Implications of sea-ice melt

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Phosphorus (P) is a major macronutrient that may influence both biological production and community structure in marine systems. Yet little is known regarding its distribution within marine dissolved and particulate matter, particularly within the Polar Regions. The Chukchi Sea is characterized by declining ice cover and thinning sea-ice due to rising temperatures. As such, polar waters are increasingly being exposed to sunlight, thereby influencing the timing, magnitude, and even composition of the biological food web. In this study, we analyzed multiple water column and ice-core samples collected throughout the Chukchi Sea during the summers of 2010 and 2011 as part of the ICESCAPE (Impact of Climate Change on the Ecosystems and Chemistry of the Arctic Pacific Environment) Program. The goal of this study was to improve our understanding of the source, composition, and distribution of dissolved and particulate P within this increasingly climate impacted ecosystem. Preliminary results suggest that ice melt can be a potentially significant source of P to surface waters depending on sea-ice location.

The influence of aqueous magnesium carbonate saturation on Smectitic interlayer exchangeability, and subsequent $CaCO_3$ structure upon deposition in relation to Ca/Mg concentration

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This project was conceived with the intention of testing the influence of aqueous carbonate over the exchangeability of Ca^{+2} and Mg^{+2} cations within interlayer sites of authigenic, montmorillonite clays; the implications of which impact both ancient and modern day precipitation and diagenesis reactions in alkaline, evaporative lacustrine settings, specifically those associated with the Natron-Magadi Basin. Clay Mineral Society montmorillonite (SWy-2) was first Ca-saturated, from which they were then subject to an array of varying MgCO3 brines of increasing concentration, thus allowing for subsequent Ca^{+2}/Mg^{+2} exchange at interlayer sites, and precipitation of CaCO3 as Ca^{+2} was released. Further testing was done to determine the significance of increased proportion of Mg: Ca in solution on crystallography of the CaCO3 structure (Berner, 1975; Mucci and Morse 1983), regarding formation of High-Magnesium Calcite (HMC), Low-Magnesium Calcite (LMC), and aragonite. XRD, ICP-AES, and XRF were used to analyze both solid clay and carbonate products; MgCO3 brine solutions were subject to ICP-AES, and pH analyses.

Residence times of trace metals in the sea surface microlayer

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The sea surface microlayer is a unique environment; its biological, chemical, and physical properties are very different from the underlying water column. Deposition of atmospheric aerosols provides a major source of trace metals to the oceans and all deposition from the atmosphere to the oceans must pass through the microlayer. A fused silica quartz tube and clean chemistry techniques were used to sample and analyze nine trace metals (Al, Mn, Fe, Co, Ni, Cu, Zn, Cd, and Pb) in the microlayer in an artificial dust deposition experiment. A model was developed from this experiment to calculate the residence times of aerosol derived trace metals in the microlayer. Applications of the residence times will be shown.

Microbial transformation of thioarsenic compounds by haloalkaliphilic phototrophic sulfur oxidizing bacteria

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Thioarsenic compounds are prevalent in arsenic-rich, alkaline, sulfidic waters, such as hypersaline Mono Lake, CA, but bacterial interactions with thioarsenic compounds have been examined only recently. Previous studies of thioarsenic compound transformations have been inconclusive in demonstrating whether or not they are directly oxidized or reduced by bacteria. We obtained an enrichment culture from Mono Lake, CA that is able to directly oxidize the thioarsenic compound monothioarsenate as its sole electron donor for anoxygenic photosynthesis. The culture was able to convert a mixture of thioarsenic compounds photoautotrophically to arsenate in approximately 13 days, and convert 4 mM monothioarsenate to arsenate in approximately 17 days. The culture was dominated by an organism closely related to *Ectothiorhodospira variabilis* and to another *Ectothiorhodospira* sp. previously isolated from Mono Lake. Most other cultures of closely related *Ectothiorhodospiraceae* that we tested were also able to oxidize monothioarsenate. The ability of bacteria to transform thioarsenic compounds directly adds a new component to the well-studied arsenic and sulfur cycles, especially in waters where both occur and where thioarsenic compounds are present.

Influence of naturally occurring thiols on iron and manganese reduction in marine sediments

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While thiols are known to be abundant in marine sediments, their interactions with iron and manganese oxides in environmentally relevant concentrations has not been investigated. These reactions could play an important role in the cycling of carbon and affect the redox state of sediments. In this study, the kinetics of reduction of iron and manganese oxides by glutathione, homocysteine, and cysteine, three common thiols in marine environments was evaluated using voltammetric measurements with Au/Hg amalgam microelectrodes. Pseudo-first order rate constants of 0.075 min-1 and 0.023 min^{-1} were determined for the reduction of iron by cysteine and homocysteine and of 0.32, 0.040, and 0.035 min^{-1} for manganese reduction by cysteine, homocysteine, and glutathione respectively. While metal reduction rates decreased as the complexity of the thiol structure increased, the extent of metal reduction increased, indicating that surface complexes play a large role in the ability of these thiols to reduce metals. Microbial reduction of disulfide was confirmed using S. oneidensis and the participation of thiols in Fe-oxide respiration was investigated in both pure culture as well as marine sediment to evaluate thiol significance in redox biogeochemical processes.

DNA stable isotope probing reveals a prevalence of Type I methanotrophs in an acidic boreal peatland

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Although comprising a small portion of the Earth's surface, boreal peatlands store roughly one third of the world soil carbon, indicating a critical role for these ecosystems in the global carbon cycle. Understanding organisms involved in methane cycling is an important step toward understanding the response of boreal peat ecosystems to changing climate conditions. Methanotrophic bacterial communities were studied in the sediments of the S1 bog, Marcell Experimental Forest, Grand Rapids, Minnesota. Based on analysis of metagenome and SSU rRNA amplicon sequences in field samples, we hypothesized that Type I and Type II methanotrophs would be active in the surface layers of the peat bog. Rates of methane consumption were quantified in microcosm incubations and the metabolically active methanotrophs were revealed through the use of DNA stable isotope probing (SIP). SIP fractions were screened using DNA fingerprinting with ARISA, and the abundance of methanotrophs was estimated using qPCR of pmoA genes. Methane was oxidized at a rate of 625.66 ± 68.51 nmol*g-1*d-1. The relative abundance of methanotrophs was 0.465 in the most enriched fraction. The active methane-consuming populations in the bog were determined to be Type I methanotrophs, and in particular Methylomonas, with a lesser contribution from Type II methanotrophs.

A high-throughput sequencing pipeline for characterization of nitrogen-fixing communities

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Fixed forms of nitrogen often limit primary production in natural and agricultural ecosystems. Biological nitrogen fixation is the enzymatic conversion of dinitrogen gas to the biologically available form of ammonia. The genetic capability to carry out this ecologically important process is possessed solely by microorganisms of the domains Bacteria and Archaea. We have developed a new high-throughput gene sequencing pipeline for characterization of the diversity of nitrogen-fixing bacteria in a range of ecosystems including sugarcane fields, peatlands, and an oil-contaminated marine environment. The pipeline was employed to examine the distribution, abundance, composition, and diversity of nitrogen-fixers in these ecosystems. Through coupling of next-generation sequencing and cultivation-based approaches, this study elucidates the physiological ecology of nitrogen-fixing communities. In particular, we observe an increased abundance of a limited diversity of nitrogen-fixers in beach sands impacted by oil from the Deepwater Horizon spill, indicating selection for hydrocarbon-degrading bacteria that also fix nitrogen. In addition, we have successfully cultivated representative strains of *Klebsiella*, a genus of nitrogen-fixers that is detected in high abundance in the endophyte community of sugarcane.

North Pacific virus dynamics

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Although viruses are the most abundant biological entity on this planet, factors shaping virus abundance and activity across large spatial scales remain poorly understood. Clarification of the constraints on virus activity is highly relevant as viruses are major players in marine biogeochemical cycles. Previous studies of environmental variables (biotic and abiotic) that influence viral distribution and production rates have indicated however that interactions are complex. To begin to addres this we completed series of three research cruises completed between spring 2012 and summer 2013 crossed large regional temperature gradients in the North Pacific and allowed for a closer investigation of the role temperature plays in virus dynamics. Data from these cruises suggest temperature is a key factor regulating virus production rates as well as virus abundance in marine surface waters. Furthermore, our data indicate that virus particle abundance is also be depth dependent. This information will be presented within the context of a larger survey of microbial activity and function in the North Pacific Ocean.

Interrelationships between fire, soil organic matter, and nutrient bioavailability in Amazonian smallholdings

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Fire residues, including black carbon compounds and unburned organic matter, are an under-examined component of many ecosystems. This study examined the impact of burning and other land management practices on soil organic matter and soil chemistry across a range of recently burned agricultural fields in the Peruvian Amazon. I recorded management histories, observed farming practices, and analyzed soil samples from upland and floodplain sites. To determine the nature and quantity of organic residues, soil samples were analyzed for total soil carbon (TC) and black carbon (BC) content. These data were then compared with indicators of soil nutrient availability, including extractable phosphorus (Psol), cation exchange capacity (ECEC), and pH. Multivariate statistical analyses of upland site soil data show tight links among TC, BD, soluble P, and total N. Similar analyses on floodplain data indicated that clay particle-size content drove much of the variation with tight linkages among other variables. These results suggest that the burns left enough charcoal and unburned material to form a substantial pool of plant-available nutrients, increase nutrient retention via expanded exchange capacity, and increase phosphorus bioavailability by raising the pH. In the case of upland fields, these residues may be the prime source of soil nutrients.

The Deepwater Horizon oil spill and methyl mercury concentrations of northwest Florida Reef fishes

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The Florida Panhandle Bight is characterized by a gently sloping continental shelf spotted with patchy “hard bottom” reef habitat. The Deepwater Horizon oil spill resulted in areas of reduced oxygen concentration and an influx of organic carbon to the sediment. Methyl mercury is primarily produced in anoxic coastal marine sediments by sulfate-reducing bacteria. This study aims to determine whether more reducing conditions caused by the oil spill led to higher levels of mercury in commercially important reef associated organisms. We compared pre-spill (collected 2007-09) and post-spill (collected 2012-13) fish species of similar lengths (pre-spill mean standard length = 53.2 ± 28.6 cm; post-spill mean standard length = 43.9 ± 25.7) and $\delta^{15}N$ signatures (pre-spill $\delta^{15}N = 14.1 \pm 1.3$; post-spill δ15N = 14.5 ± 1.6) from hard-bottom reefs on the West Florida Shelf (pre-spill = N 26.85485-30.19833, W 85.16200-86.30200; post-spill = 26.85485-29.55304, W 84.74103-89.02770). Results indicate that some post-spill reef associated species exhibit significantly higher methyl mercury (MeHg) loads (mean MeHg = 1.45 ± 1.34 ug/g dry weight) than their pre-spill counterparts (mean MeHg = 1.76 ± 1.36 ug/g dry weight). Jacks (*Seriola rivolinia* and *S. dumerili*) exhibit the greatest increase in MeHg concentrations (mean pre-spill Hg = 0.82 ± 0.25 ug/g dry weight; mean post-spill THg = 3.12 ± 1.60 ug/g dry weight) but represent the greatest increase in $\delta^{15}N$ signatures between the two sample sets. Porgy (*Pagrus pagrus*, *Stenotomus caprinus*, and *Calamus leucosteus*), Pinfish (*Lagodon rhomboides*) and Cubbyu (*Pareques umbrosus*) also exhibit significantly higher MeHg concentrations after DWH. Seabass (*Centropristis ocyurus* and *C. philadelphica*), groupers (*Mycteroperca phenax*, *Hyporthodus flavolimbatus*, and H. niveatus) and snapper (*Lutjanus campechanus*, *L. griseus*, and *Rhomboplites aurorubens*) MeHg loads remained roughly the same. We also determined that pinfish alone are responsible to transporting approximately 684 g of MeHg offshore during their annual fall egress and represent an important component of a dynamic system contributing to the toxicity of GOM commercial fishes.

Elucidating mechanisms of chromate complexation on iron oxides surfaces using flow calorimetry and infrared spectroscopy

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Chromium has been identified in 49% of the 1270 hazardous waste sites currently on the National Priorities List under the federal Superfund program. Predicting chromium mobility is a critical element in remediating such sites; yet our predictive ability is still limited by our incomplete understanding of all the chemisorption processes that control its mobility. This study investigated hexavalent chromium (Cr(VI)) sorption on two important oxyhydroxides, ferrihydrite and hematite, using a combination of flow adsorption microcalorimetry (FAMC) and attenuated total reflectance (ATR) Fourier transport infrared (FTIR) spectroscopy. Cr(VI) sorption was found strongly exothermic, with molar heats of sorption of - 82 kJ/mol for ferrihydrite and -20 kJ/mol for hematite indicating a potentially stronger surface complexation on ferrihydrite. The ATR experiments show that under the experimental conditions, monodentate species prevail on ferrihydrite and bidentate species prevail on hematite. While no outer-sphere species was observed using spectroscopy, calorimetric results seem to indicate the presence of a small reversible component on FH, potentially attributable to monodentate species. Combining both techniques to collect experimental data from the same samples, an approach yet untested, proved to be powerful in discerning various Cr(VI) surface species and will aid in developing accurate surface complexation models for chromium.

Tuning daily rhythms: Parameter optimization for an individual-based model of Diel cycles in *Prochlorococcus*

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Prochlorococcus spp. are the smallest and most numerous phytoplankton in the ocean. The tightly-phased diel dynamics of cellular growth and division can be used to estimate population growth and mortality rates of Prochlorococcus. However, deconvolving cell cycle phases from DNA distributions in the field is a potential source of error in these growth estimations. In this study, we used an individual-based model (IBM) to capture the cell size patterns, DNA content, and cell cycle phase distributions of *Prochlorococcus*. Model parameters were estimated using cell cycle data from field populations in the North Atlantic Ocean and then optimized using the Nelder-Mead algorithm. This model optimization can be used to derive population growth rates and other cell cycle parameters directly from cellular DNA data, independent of cell cycle phase deconvolution.

Microbial community shifts as an effect of 1-year of experimental warming in permafrost and temperate soils, revealed by metagenomics

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We have begun investigations on microbial communities from Alaskan (AK) permafrost and Oklahoma (OK) grassland soils, which have been experimentally warmed ~2°C for one year above ambient temperatures in-situ. Analysis of rRNA genes recovered from shotgun-metagenomic data revealed that the ratio of fungal to bacterial organisms decreased with warming. The most pronounced bacterial taxonomic shifts observed at both sites were an increase in abundance of Actinobacteria and decrease in Planctomycetes, both representing major phyla in soils. Further, OK warmed communities were enriched in genes involved in heat shock response and cellular surface structures, particularly, trans-membrane transporters for glucosides and ferrous iron. At the AK site, warmed plots were enriched in metabolic pathways related to labile carbon mobilization and oxidation, indicating that soil C is more vulnerable to microbial respiration relative to OK site. These results, which were consistent with independent physicochemical measurements and process rates determined in-situ, were linked with higher primary productivity of aboveground plant communities stimulated by warming. Collectively, our findings suggest that microbial communities of grassland soils play important roles in mediating feedback responses of the soil ecosystem to climate change and that even short periods of warming induce significant changes in microbial community function and composition.

Transcriptional regulation of toluene oxidation genes in *Geobacter daltonii*

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Sediments and water sources contaminated with petroleum must be cleaned for the benefit of both ecosystems and human well-being. It is known that components of petroleum can be degraded anaerobically by microbes. The mechanisms involved and their regulation have not been clearly demonstrated. *Geobacter daltonii* is a strict anaerobic bacterium capable of oxidizing various aromatics while it reduces electron acceptors such as fumarate, nitrate and Fe(III). The *bss* operon in *G. daltonii* is preceded by a gene annotated as "sigma-54 type transcriptional regulator". Analysis of the upstream region of bss fails to identify the classical -35/-10 sequence observed in promoters regulated by sigma 70. Sigma 54 has been demonstrated to regulate expression of toluene oxidation in other anaerobes. The region upstream of *bss* was predicted to contain the sigma 54 consensus sequence using PromScan (http://molbiol-tools.ca/promscan/). This prediction was confirmed using 5'RACE. *E. coli* were transformed with bssABCD and Geob_2440 and grown in the presence of toluene. These cells grew, indicating conversion of toluene to benzylsuccinate, whereas E. coli without this amplicon did not. Sigma 54 deletion mutants failed to grow in the presence of toluene. In *G. metallireducens* the genes bamVW were identified as a sigma 54-dependent two component system previously. These genes were investiaged in *G. daltonii* using qPCR. Both were highly expressed in the presence of toluene. These data indicate that toluene oxidation and bss are regulated via sigma 54-dependent mechanisms in *G. daltonii*.

Geochemical control of methanogenesis in Cape Lookout Bight

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Methane, the most abundant hydrocarbon in Earth's atmosphere, is produced in large quantities in sediments underlying the world's oceans. Very little of this methane makes it to surface sediments as it is believed to be consumed by Anaerobic Methanotrophs (ANME) in consortia with Sulfate Reducing Bacteria (SRB). Less is known about which organisms are responsible for methane production in marine sediments, and whether that production is under thermodynamic control based on hydrogen concentrations. We demonstrated with a bottle incubation of methane seep sediment taken from Cape Lookout Bight, NC that hydrogen is the controlling substrate in methanogenic sediments. While sulfate was present the hydrogen concentration was maintained at below 2 nM. Only after the depletion of sulfate allowed hydrogen concentrations to rise above 5 nM did we see production of methane. Preliminary CARD-FISH cell counts suggest that ANME-2 and other Methanosarcinales increase when sulfate is depleted, which corresponds with a decrease in SRB. Total cell counts demonstrate a decline in cells with the decrease of sulfate until a recovery corresponding with production of methane. Our results strongly suggest that hydrogen concentrations influence what metabolic processes can occur in marine sediments.

Possible coupling between nitrogen and iron redox processes in anaerobic sediments

Nicole Kiriazis*, Jordon Beckler, and Martial Taillefert

Georgia Institute of Technology

Fixed nitrogen is essential for organisms, yet scarce on Earth. Ammonium is produced by decomposition of organic matter and removed by aerobic nitrification. In anaerobic conditions, nitrite and nitrate (NO_x^-) are reduced back to N2 by denitrification and anammox or to ammonium by dissimilatory reduction (DNRA). As NOx- is rapidly produced and consumed by microbes, it does not typically build up in marine sediments. During a recent research cruise on the Congo deep-sea fan, 800 km from the mouth of the Congo River in western Africa, a peak in NOx- with maximum concentrations exceeding overlying water concentrations was found in several sediment cores, suggesting that NOx- was produced anaerobically in these sediments. Mn2+ and dissolved sulfides were not detected, while the maximum in NOx- generally coincided with the onset of Fe2+ production in pore waters, suggesting that iron reduction is coupled to the anaerobic production of NOx . In this study, evidence for the coupling of iron reduction and anaerobic nitrification in these sediments is explored using depth profiles of the main redox species involved, thermodynamic calculations, and sediment incubations. Evidence has emerged for a catalytic cycle in which nitrate may be produced during iron reduction and consumed during iron oxidation.

Biodegradation of microcystin in freshwater lakes

Lauren Krausfeldt*, Robbie Martin, Justine Schmidt, Gary LeCleir, Gregory Boyer, and Steven Wilhelm

University of Tennessee, Knoxville

Microcystin is a potent cyanotoxin produced by the cyanobacteria *Microcystis aeruginosa* and several other cyanobacterial species. This compound is an increasing threat to public health and local economies due to recurring harmful cyanobacterial blooms worldwide, in which *Microcystis* spp. is typically dominant. It also serves as a common component of freshwater microbial communities, serving not only as a potent toxin but also as a potential carbon source. By itself, microcystin is highly stable in natural water for months, however it disappears after about three weeks. Several co-occurring heterotrophic bacteria have been found capable of degrading microcystin in Lake Erie (USA) and Lake Tai (China): both lakes have a history of recurring cyanobacterial blooms. To begin to quantify the process of biodegradation of this compound, bacterial isolates were subjected to a seven day biodegradation assay in which microcystin-LR was the sole carbon source. Microcystin concentrations were measured by High Performance Liquid Chromatography and degradation rates of MCLR were calculated. Our results suggest that in the presence of some bacteria the half-life of microcystin is on the order of days. Ongoing experiments continue to investigate the potential priming effect on the degradation of microcystin as well as other abiotic factors.

Temporal and spatial variations in genome content of *Synechococcus* populations in the Western North Atlantic

Cecilia Batmalle Kretz*, Sam Chiang, Michael W Lomas, Kun Zhang, and Adam C. Martiny

Georgia Institute of Technology

Marine cyanobacteria *Synechococcus* are ubiquitous and important contributors to oceanic primary production. Extensive genome diversity within this group has been observed, but we currently know little about the genomic variation between field populations. To address this, we used a combination of cell sorting and targeted metagenomics to identify the genetic composition of Synechococcus field populations in the Western North Atlantic Ocean. We compared the phylogenetic distribution and analyzed the specific metagenomic datasets for variations in whole genome content as well and the distribution of nitrogen and phosphate genes. We also estimated the role of environmental variables on the clade and whole genome distribution. We found that there is a vertical and seasonal variation in the distribution of *Synechococcus* clades and that nutrients primarily shape *Synechococcus*'s distribution. Moreover, from field populations as well as fully sequenced genomes, phylogenetic structure tends to drive genome content. In our samples, nitrogen appears as a major driver of genome content variations in N and P genes with more N genes at low N concentrations. From this study, we determine that there is a temporal and spatial distribution of *Synechococcus* populations based on clades and whole genome content distribution that is correlated to environmental conditions.

Mercury deposition into the Pensacola Bay watershed

Nishanth Krishnamurthy*, William Landing, Jane Caffrey, and Alexander Maestre

Florida State University

Event-based rainfall deposition of mercury, trace metals, and major ions were monitored from 2005-2011 at multiple sites in the Pensacola Bay watershed to evaluate their temporal and spatial patterns in atmospheric wet deposition. Mercury deposition during the summer months was higher due to higher Hg concentrations in the rainfall and higher summer-time rainfall rates throughout the region. Another goal was to quantify the contribution of local emission sources to atmospheric deposition of mercury using a multiple-tracers approach. Multivariate statistical analysis was used to sort the Hg, trace element, and major ion fluxes into factors that represent potential sources that contribute to the rainfall chemistry. Previously, we estimated that 26-51% of the rainfall mercury fluxes resulted from emissions due to coal combustion. We are refining our estimates by including storm classification type for each individual rain event to distinguish between "global background" Hg and that from local and regional sources. We will also quantify the changes in rainfall chemistry following the December 2009 installation of a high-efficiency wet scrubber on a coal-fired power plant in Pensacola.

Biodegradation of the allelopathic chemical, resveratrol by an *Acinetobacter* from the peanut rhizosphere

Zohre Kurt*, Marco Minoia, Shirley F. Nishino, and Jim C. Spain

Georgia Institute of Technology

Resveratrol is an important allelopathic compound in grapes and peanuts because of its role in protection of plants from fungi. The ecological role of resveratrol in the field is difficult to establish rigorously because it does not seem to accumulate. It is likely that bacterial degradation plays a key role in determining the persistence, and thus the ecological role, of resveratrol in soil. Here we report an Acinetobacter strain isolated from the rihizosphere of peanut plants that can use resveratrol as the sole carbon source. Resveratrol disappearance and transient appearance of the metabolites in the pathway were measured via HPLC during growth of the isolate on resveratrol. Stoichiometric conversion resveratrol to 3,5-dihydroxybenzaldehyde and 4-hydroxybenzaldehyde by dialyzed cell extracts indicated that an carotenoid cleaving dioxygenase enzyme with properties similar to lignostilbene dioxygenase could be responsable for the initial reaction. The gene that encodes the enzyme responsible for the oxidative cleavage of resveratrol was obtained from the Acinetobacter strain JS 678 genome sequence and overexpressed it in E. coli. Assays with dialyzed cell extracts, and oxygen uptake measurements supported by the information obtained from the genome sequence indicated that the aldehydes are oxidized to substituted benzoic acids that subsequently enter central metabolism. The results establish the close proximity of specific resveratrol degrading bacteria to the roots of the plants that produce resveratrol and set the stage for studies to evaluate the ecological role of the bacteria in plant allelopathy.

Re-examination of methodologies to determine biogenic silica content in northern Gulf of Mexico continental-shelf sediments

Ashley M. Larson*, Elizabeth S. Darrow, Ruth H. Carmichael, and Jeffrey W. Krause

Dauphin Island Sea Lab

The delivery and sequestration rates of silicon at the land-sea interface are among the most poorly constrained in the global Si budget. These environments are particularly important areas of Si exchange as biogenic silica (bSi) delivered-to and created within these systems can be buried in the sediments. This sequestration reduces the Si input into the rest of the ocean, and affects global primary production through potential Si limitation of diatom growth. Previous measurements of sediment bSi in the northern Gulf of Mexico (nGoM) shelf report low amounts, but a 2-3 fold increase over the last half century. Recent evidence suggests methodological bias may underestimate sediment bSi by the abiotic formation of authigenic clays, as the incorporation of metal hydroxides on bSi matrix suppresses the ability to distinguish it from mineral silica when using traditional alkaline digestions. We adapted a method used in Amazon River sediments which lessens the interference of metal hydroxides and show that an initial acid leach increases the measured bSi by 2-6 fold above quantities detected using traditional digestion methods. These findings suggest that within-core differences in bSi content reported by other studies for this region, and the interpretation of the temporal trends, may require re-examination.

Assessing the role of the rare biosphere in microbial community response to environmental perturbation

Gina M. Maresca*, Michael R. Weigand, Rajkumar Krishnan, Jim C. Spain, and Konstantinos T. Konstantinidis

Georgia Institute of Technology

A major source of drinking water for North Georgia, Lake Lanier is impacted by varied land-use within its watershed, which influences chemical cycling within its ecosystem. Freshwater communities like those found in Lake Lanier can include thousands of low abundance, ‘rare’ organisms. The contribution of this ‘rare biosphere’ to ecosystem function and microbial community response to environmental perturbations remains poorly understood. In this study we incubated lake water mesocosms supplemented individually with organic compounds that included 2,4-dichlorophenoxyacetic acid (2,4-D), a synthetic herbicide; 3-nitrotyrosine (3-Nty), a natural nitro compound produced by many organisms; and caffeine in order to isolate and characterize rare microbes capable of their degradation. Disappearance of each compound was monitored by HPLC and enriched microbes able to degrade them were isolated. Isolate characterization by 16S rRNA amplicon and whole genome sequencing revealed the identity of the degraders and the presence of known degradation pathways, respectively. For example, mesocosms supplemented with 2,4-D selected for a *Novosphingobium* sp., which encoded homologs to the previously characterized cadRABKC system and was able to degrade 2,4-D in pure culture. Our results suggest that rare organisms capable of metabolizing a varied of compounds are present within the microbial community of Lake Lanier below the detection limit of standard metagenomic sequencing efforts and contribute to ecosystem chemical balance in response to nutrient perturbation.

Impacts of Corexit® EC9500A on oil biodegradation potential and toxicity to marine rotifer *Brachionus manjavacas*

Kala P. Marks*, Terry W. Snell, and Joel E. Kostka

Georgia Institute of Technology

In response to the Deepwater Horizon oil spill, approximately 1.8 million gallons of the chemical dispersants Corexit® EC9500A and Corexit® EC9527A were applied to the Gulf of Mexico in an attempt to disperse and prevent oil from reaching shorelines. Since this was the first large-scale application of dispersants, the total ecological impacts are unknown. Two oil-degrading isolates, *Alcanivorax* sp. and *Acinetobacter* sp., were studied to elucidate the effects of dispersants on microbial degradation and to understand how biodegradation affects the toxicity of dispersed oil. The strains were grown on either 0.5% Macondo oil or a 1:100 Corexit® EC9500A:Macondo oil mixture. Biodegradation potential was quantified by the depletion of total petroleum hydrocarbons using GC-FID, and acute toxicity was tested using the marine rotifer *Brachionus manjavacas*. Surprisingly, the addition of Corexit® EC9500A resulted in either no significant difference (*Acinetobacter*) or a 20% reduction (*Alcanivorax*) in biodegradation potential between oil only and dispersed oil treatments. After 24-hour acute toxicity tests, *Alcanivorax* slightly reduced toxicity of dispersed oil compared to uninoculated controls, whereas *Acinetobacter* significantly increased its toxicity. *Alcanivorax* is hypothesized to preferentially degrade components of Corexit® EC9500A, thus explaining the reduction in oil-degradation potential and decrease in toxicity to *B. manjavacas*.

Mesopelagic carbon flux attenuation in the North Atlantic

Chris Marsay*, Richard Sanders, Katsia Pabortsava, Stephanie Henson, Kevin Saw, and Eric Achterberg

University of South Carolina

The biological carbon pump transfers carbon to the ocean interior by gravitational settling of organic material from the surface ocean. Though an important control of air-sea CO_2 partitioning, we have limited understanding of what regulates the attenuation of this organic matter flux with depth, with models either using a simple formulation based on the observed depth-related change in flux or a parameterisation based on ballast biominerals. Using flux measurements from 8 locations derived from neutrally buoyant sediment traps, we propose that variability in mesopelagic flux attenuation can be explained by temperature, with warm settings having shallower attenuation than cold settings. This pattern is seemingly inconsistent with that diagnosed from analyses of deep sediment trap and satellite data, which suggest that transfer efficiency (deep flux/export flux) is highest in warm waters, and linked to the aggregates exported in those regions being tightly packaged due to intensive recycling in the photic zone. The two results can however be reconciled by consideration of the depth range over which the analyses are conducted, with intense mineralisation of a labile pool followed by efficient sinking of the remaining fraction occurring in warm regions and the converse being the case in cold environments.

The consequences of mesoscale eddy type on the coupling of Si and organic matter export in the Sargasso Sea

Israel A. Marquez*, Michael W. Lomas, and Jeffrey W. Krause

University of South Alabama

The Bermuda Atlantic Time Series (BATS) is an ongoing 25-year biogeochemical record in the Sargasso Sea. But contemporaneous data on the particulate phases of four major bioreactive elements (C, N, P, Si) only exist for two years and also for a companion project (Trophic BATS, i.e. TBATS). Diatoms, the major phytoplankton group to use Si, typically have low regional abundances. Their abundance can be enhanced in mesoscale eddies, but the resulting biogeochemical consequences are not well understood. The lack of concomitant measurements has left a knowledge gap regarding the coupling of the Si cycle with those of C, N, P. Data from BATS and TBATS provide an opportunity to improve our understanding about the coupling of these elements and Si in the water-column and exported material, and the biogeochemical effects of increased diatom abundance in eddies. Preliminary results suggest the coupling of Si to organic matter export is variable: the sampled cyclones and non-eddy conditions appear to operate similar, but the anticyclones have slightly higher siliceous biomass and a lower diatom contribution to export. This suggests the hydrography and age of the anticyclone promoted euphotic-zone retention of diatom organic matter, thereby lowering their contribution to the biological pump.

Biogenic ethane production in hypersaline environments

Tyler Mauney*, Jeff Chanton, Brad Bebout, Cheryl Kelley, Angela Detweiler, Amanda Tazaz, and Claire Beaudoin

Florida State University

Trace gas analysis in Earth systems play an important role in planetary research. Whiticar (1999) proposed that a differentiation could be made between biologically produced methane and thermogenically or geologically produced methane in marine environments through isotopic analysis coupled with methane to higher alkane concentration ratios. This topic is of the upmost importance to the study of exobiology. The ability to determine the source of production through isotopic and/or concentration analysis would prove critical to the search for a “second genesis” within our solar system, greatly increasing the probability of life throughout the rest of the universe. Given the significance of such findings, it is essential to examine extreme Earth environments that could be analogous to other planetary systems in order to better understand the bio markers in trace gas analysis. This project is concerned with looking at the biological production of ethane in relation to methane which could alter the previously proposed ratio boundaries of biogenic vs. thermogenic methane production. This work is an expansion of previous research done on expanding the isotopic boundaries of biogenic methane by Tazaz et al., 2012.

Trophic structure, feeding ecology and the bioaccumulation of mercury (Hg) in Gulf of Mexico hagfishes: An elemental analysis approach

Alejandra Mickle*, Dean R. Grubbs, and Jeffrey P. Chanton

Florida State University

Hagfish are common in deep waters of the Gulf of Mexico (GOM). Two out of the three species found in the GOM are endemic and yet, very little is known about their life histories. To date, there is no hagfish fishery in the area, but a fishery may develop soon, as Pacific and Atlantic stocks are rapidly declining. This research aims to create an information base on hagfishes from the GOM which could provide information on basic life history traits, and could be useful for the creation of a fisheries management plan. We will study the trophic structure, feeding ecology and bioaccumulation of Hg on the three species found in the region (*Paramyxine springeri*, *Eptatretus minor*, *Myxine mcmillanae*). The trophic structure and feeding ecology will be examined using $\delta^{13}C$, $\delta^{15}N$ and $\delta^{34}S$ stable isotope analysis and by examining stomach contents using molecular genetic analysis. Muscle samples will be analyzed for total Hg and Methyl-mercury (MeHg) content and compared for potential variations in bioaccumulation rates caused by the changing conditions that originated after the Deepwater Horizon oil spill. Preliminary data on the effects of treatments on isotopic ratios suggest that samples should be treated and analyzed individually for each element.

Will severe droughts exceed the tolerance threshold of symbiotic dinitrogen fixation and impair ecosystem resilience?

Jeffrey M. Minucci*, Chelcy Ford Miniat, and Nina Wurzburger

University of Georgia

In the eastern United States, global climate models predict reductions in summer precipitation resulting in more severe drought events. One key way in which drought may alter ecosystem dynamics is through its influence on the nitrogen (N) cycle. N limits primary production in terrestrial ecosystems of the temperate zone, making a consideration of symbiotic N_2-fixation (SNF), the main natural source of new N, crucial for these ecosystems. N_2-fixing plants are abundant during early stages of succession, acting to replace N lost during disturbance events. Therefore, SNF is a recovery mechanism that supplies new N to ecosystems, facilitating resilience in the context of disturbance. To examine how drought affects this process, we are diverting 0%, 20% and 40% of growing season precipitation from 18 9 m^2 plots in a regenerating forest. Tree census data from the first summer of treatment revealed that growth of *Robinia pseudoacacia*, the system's dominant N_2-fixing species, was more affected by drought than its competitors. This upcoming summer I will measure N_2-fixation rate of *R. pseudoacacia* through acetylene reduction assay and foliar $\delta^{15}N$ isotopic analysis. These data will allow me to assess whether drought can constrain the symbiotic N_2-fixation and thus potentially impair ecosystem resilience.

Challenges of working with deep-water organisms: Case study of *Verdigellas peltata*

April C. Mitchell*, Ana Tronholm, and Juan Lopez-Bautista

University of Alabama

Current hypotheses on the evolution of Virdiplantae assume the early divergence of two clades, Streptophyta and Chlorophyta, from an ancestral green flagellate unicellular organism. Few photosynthetic organisms thrive in deep marine habitats, but among those that do is *Verdigellas peltata*. Understanding the phylogenic relationship of this genus is important to understanding early divergences and making inferences about that nature of the common ancestor of the green plant lineage. This study primarily tested for ribosomal small subunit 18S and rbcl genes in *Verdigellas peltata* using several different extraction methods, polymerase chain reaction (PCR) protocols, DNA concentrations, primer lengths, and PCR thermocycler parameters. Sequences obtained from amplified and purified DNA were unquantifiable. A possible explanation for our obtained results is improper preservation methods at the time of collection. We recommend *Verdigellas peltata* be frozen immediately upon collection of the species.

Oxygen isotopes in Borneo cave dripwater resolve the 2009-2012 ENSO cycle

Jessica W. Moerman*, Jess F. Adkins, Judson W. Partin, Brian Clark, Syria Lejau, Jenny Malang, Andrew A. Tuen, and Kim M. Cobb

Georgia Institute of Technology

The extent to which changes in El Niño-Southern Oscillation (ENSO) variability have contributed to hydrological changes throughout earth's climate history is poorly constrained by available paleoclimate data. Stalagmite oxygen isotope ($\delta^{18}O$) records from Borneo - a region where ENSO has a profound impact on precipitation amount and rainfall $\delta^{18}O$ - hold immense potential as archives of paleo-ENSO, provided that the large-scale ENSO phenomenon is faithfully translated into dripwater geochemical variations. Here we present the results of a 5-year modern monitoring study of cave dripwater $\delta^{18}O$ collected biweekly from three distinct drip sites in northern Borneo caves. All three dripwater $\delta^{18}O$ timeseries largely preserve the interannual variability observed in rainfall $\delta^{18}O$, with relatively high $\delta^{18}O$ values during the 2009/2010 El Niño event and relatively low $\delta^{18}O$ values during the 2010/2011 and 2011/2012 La Niña events. ENSO-related dripwater $\delta^{18}O$ variations of up to 5‰ reflect amount-weighted Borneo rainfall $\delta^{18}O$ averaged over the preceding 3-9 months. We demonstrate that changes in ENSO characteristics can drive stalagmite $\delta^{18}O$ changes of up to 3‰ on interannual timescales and 0.6‰ on multi-decadal timescales. Overall, this study illustrates the value of monitoring modern water isotope systems to refine and improve interpretations of hydroclimate paleo-proxies.

Development of a molecular indicator for iron nutritional status in a polar diatom

Carly Moreno* and Adrian Marchetti

University of North Carolina at Chapel Hill

The polar pennate diatom, *Fragilariopsis kerguelensis*, is ubiquitously found in the Southern Ocean and has large responses to iron fertilization. We are developing a molecular-based approach to assess the iron nutritional status of *F. kerguelensis* in natural diatom assemblages. To identify target genes responsive to iron, we performed a comparative transcriptomic analysis of *F. kerguelensis* grown under varying iron conditions. We have identified two protein-encoding genes that are affected by iron status. The first gene, FTN, encodes for the iron storage protein ferritin and is up-regulated in iron-replete conditions. The second gene, ISIP2A, encodes for an iron-starved induced protein of unknown function that is up-regulated under iron-limiting conditions. The transcript ratio of ISIP2A:FTN is indicative of the iron status of the cell. The expression patterns of these genes in cultures of F. kerguelensis were measured under various growth conditions to verify that the ISIP2A:FTN transcript ratio is specific to iron limitation. The molecular indicator was then used with environmental samples collected during Palmer LTER time series cruises to elucidate the iron status of *F. kerguelensis* along natural iron gradients.

Osmoprotective role of dimethylsulfoniopropionate (Dmsp) for estuarine bacterioplankton

Jessie Motard-Côté* and Ronald P. Kiene

University of South Alabama /Dauphin Island Sea Lab

Dimethylsulfoniopropionate (DMSP) is synthesized and used by phytoplankton as an osmolyte. Previous studies showed that some of the dissolved DMSP in seawater is taken up by bacterioplankton and not degraded.

Here, we show that DMSP can be used by natural bacterioplankton to alleviate inhibition of bacterial production (BP) under osmotic stress. Coastal water (10ppt) was filtered through GF/F and incubated for days to allow depletion of endogenous DMSP. Three salinity treatments were prepared by adding NaCl (Control, + 5ppt and +10ppt). Half of each treatment received 20 nM DMSPd, whereas the other half remained DMSP-free. Two hours after NaCl addition, BP was significantly lower (-43%; ANOVA, $p < 0.005$) in the +10ppt treatment compared to the control (ambient salinity). When DMSP was added, BP increased by 55% (t-test, $p < 0.01$), decreasing the inhibition of BP to -11% of the control. After 6 hours, the inhibition of BP was significant for both the +5 and +10ppt treatments (-32 and -34%, respectively; ANOVA, $p < 0.01$). A significant effect of DMSP on BP was only observed at +5ppt (+32%; t-test, $p < 0.01$), decreasing the BP inhibition to -9%. These results suggest an osmoprotective role of DMSP for marine bacterioplankton.

Oral Session III
9:00-10:30AM
Sunday April 6

9:00 AM
How metal stress influences viral infection: Effects of Syn9 viral infection on iron-stressed *Synechoccoccus* strain DC2

Brady R Cunningham* and Seth G John

University of South Carolina

The cyanobacterium *Synechococcus* is one of the most abundant phytoplankton in the open ocean, where its growth is constrained by both nutrient-limitation and viral infection. One of the most important growth-limiting nutrients in the open ocean is iron (Fe), however the interactions between Fe-limitation and viral infection of *Synechococcus* have not been previously studied. We present data on growth rates and burst size of DC2 infected with cyanophage Syn9 under a variety of Fe-limitation conditions. Growth was measured by bulk fluorescence and flow cytometry, while burst size and viral latency period were determined by plaque assay. Infected Fe-limited cultures of DC2 revealed a decline in growth and lysis rate compared to cultures grown in replete media. Plaque assays will clarify whether this difference is due to a change in host burst size or viral latency period. Experiments so far have shown that reducing media concentrations of zinc, cobalt, and vitamin B_{12} have no effect on the population dynamics of the host-phage system. Fe-limitation affects the *in vitro* population dynamics of DC2, suggesting a possible role for Fe in phytoplankton bloom termination and the marine carbon cycle.

9:15 AM
Variations in vitamin B_{12} requirements among bloom-forming diatoms

Kelsey Ellis*, Natalie Cohen, and Adrian Marchetti

University of North Carolina, Chapel Hill

The requirement for cobalamin (vitamin B_{12}) in microalgae is primarily a function of the type of methionine synthase present within their gene repertoires. Diatoms with an obligate requirement for vitamin B12 possess a cobalamin-dependent methionine synthase (MetH), whereas those with a facultative requirement possess both MetH and cobalamin-independent methionine synthase (MetE). *Pseudo-nitzschia* and *Fragilariopsis* are two ecologically important diatom genera that often dominate diatom assemblages. *Pseudo-nitzschia* possess MetH whereas *Fragilariopsis* possess both MetH and MetE, suggesting a fundamental difference in B12 requirements between the two closely-related genera. *P. granii* cells ceased growth without vitamin B12 and MetH was down-regulated upon resupply of vitamin B_{12} to cobalamin-deficient cells. In *F. cylindrus* cultures, MetH was constitutively expressed and no difference in cell growth was observed between both treatments. In contrast, MetE was highly expressed when *F. cylindrus* cells were grown without vitamin B_{12} and expression decreased 103-fold upon vitamin resupply. Similarly, other examined diatoms exhibited growth responses to B_{12} availability consistent with sporadic patterns of MetE distribution. This further substantiates a lack of obvious phylogenetic trends underlying obligate diatom vitamin B_{12} requirements. Our findings demonstrate the important role vitamins can play in diatom community dynamics within areas where vitamin supply may be limiting.

9:30 AM
Too much cadmium in the western North Pacific: sources, sinks and the biological response

Peter Morton*, Cheryl Zurbrick, Clifton Buck, Celine Gallon, John Donat, William Landing, Alan Shiller, and A. Russell Flegal

Florida State University

To explore the influence of atmospheric deposition on the biogeochemistry of Cd in the western and central North Pacific Ocean, dissolved, total dissolvable, marine particulate and soluble aerosol Cd concentrations were measured in samples collected during the fourth Intergovernmental Oceanographic Commission (IOC-4) Global Investigation of Pollution in the Marine Environment (GIPME) cruise. Aerosols and surface waters of the oligotrophic subtropical gyre were depleted in Cd, indicating that aerosol inputs of Cd are relatively inconsequential for these surface waters. In the Western Subarctic Gyre, high dissolved Cd concentrations persist due to physical processes. In addition, waters near the Aleutian Margin are enriched in Cd relative to PO_4^{3-}, and the Cd/PO_4^{3-} gradually decreases during lateral transport from the Western Subarctic Gyre into the central North Pacific. Excess Cd, combined with the high nutrient/low Fe conditions of the Western Subarctic Gyre, induces high particulate Cd/P ratios in the surface waters, as biological uptake of Cd is increased through survival mechanisms designed to sequester Fe. The intense vertical flux of Cd into the Western Subarctic Gyre is relieved through lateral transport into the central subtropical gyre.

9:45 AM

Speciation of uranium controls its reduction by metal-reducing bacteria

Keaton M Belli*, Thomas J DiChristina, Philippe Van Cappellen, and Martial Taillefert

Georgia Institute of Technology

Uranium bioreduction, the microbial reduction of soluble U(VI) to highly insoluble U(IV), is considered a promising in situ bioremediation strategy to immobilize uranium in the subsurface. Our ability to predict the success of uranium bioreduction is complicated by the wide range of geochemical conditions at contaminated sites and the strong influence of uranyl speciation on the bioavailability and toxicity of U(VI) to metal-reducing bacteria. To deconvolute the effects of uranyl speciation on uranium bioreduction kinetics, viability assays and bioreduction incubations with Shewanella putrefaciens strain 200 were conducted over a range of pH and DIC, Ca^{2+}, and Mg^{2+} concentrations. Results from these incubations were incorporated into a speciation-dependent biogeochemical model able to reproduce the rate of uranium bioreduction over a wide range of geochemical conditions. DIC, Ca^{2+}, and Mg^{2+} led to the formation of less bioavailable carbonate uranyl species and retarded uranium bioreduction by decreasing the concentration of more bioavailable non-carbonate uranyl species. At high concentrations of bioavailable uranyl species, however, uranium toxicity inhibits bioreduction due to elevated concentrations of the 'free' hydrated uranyl ion. Our results highlight the complex influence of speciation on uranium bioreduction kinetics and identify geochemical constraints that will determine the feasibility of uranium bioreduction at contaminated sites.

10:00 AM

Combining single cell and metagenomic sequencing: The first look at three members of the widely distributed, uncultured archaeal clade, SM1

Jordan T. Bird*, Brett Baker, Cassandre Lazar, Mircea Podar, Andreas Teske, and Karen G. Lloyd

University of Tennessee, Knoxville

SM1 is an uncultured archaeal clade that branches deeply within the Euryarchaeota in 16S rRNA gene phylogenies. After this archaeal lineage was first observed in a monoarchaeal biofilm in Sippenauer Moor near Regensburg, Germany, further 16S amplicon surveys suggested the presence of members of the clade in a variety of marine, estuarial, and terrestrial sediments. We sequenced a single amplified genome (SAG) from SM1 isolated from marine sediment in the White Oak River estuary, North Carolina. This SAG represents the first draft genome from the SM1 clade. Assembly of quality trimmed paired reads using CLC Genomic Workbench yielded scaffolds >2.5 Mbp and encoding 2358 predicted coding sequences. Estimates of genome completeness range from 68% to 87% and the GC content is 37.1%. The single 16S rRNA sequence found within the SAG shares 100% sequence identity to full-length 16S rRNA gene sequences assembled from metagenomics reads recovered from the sulfate-methane transition and methanogenic zones in White Oak River estuarial sediments. Two separate genome sequence assembly bins recovered from the metagenomes contain phylogenetic marker genes aligning within the SM1 clade and were estimated to be 68.8% and 90.6% complete. Here we will discuss the genomic evidence for energy metabolism and environmental interactions of the SM1 clade.

10:15 AM

A high-resolution investigation of the relationship between the Steptoean Positive Carbon Isotope Excursion and the end-Marjuman extinction within the Nolichucky Formation of the southern Appalachians

Angela M. Gerhardt*, Benjamin C. Gill, Theodore R. Them II

Virginia Tech

The Cambro-Ordovician transition contains several enigmatic marine extinction events followed by rapid diversifications. The first of these extinctions (the end-Marjuman) is thought to coincide with the beginning of the Steptoean Positive Carbon Isotope Excursion or SPICE, a large and rapid excursion in the marine carbon isotope record. This excursion, which is expressed in sedimentary successions globally, is thought to represent a large perturbation to the carbon cycle during this time. Additionally, a limited amount of carbon isotope data from the Black Hills of South Dakota suggests the possibility of a small negative $\delta^{13}C$ excursion at the extinction boundary preceding the SPICE. Previous high-resolution biostratigraphy has identified an expanded record of extinction event within the Nolichucky Formation of the Southern Appalachians making it an excellent candidate for the study of the precise relationship between the extinction and changes in the carbon cycle. This investigation confirms the onset of the SPICE occurs at the extinction boundary however no negative $\delta^{13}C$ excursion occurs at the extinction boundary. Further there is no systematic relationship between local facies changes and $\delta^{13}C$ or the extinction interval across the basin. This suggested that global environmental changes are responsible for both the $\delta^{13}C$ record and the extinction event.

Poster Session II
(First author last names N-Z)
10:30AM-12:30PM
Sunday April 6

Microbial diversity in a Gulf of Mexico deep sea hypersaline basin

Lisa M. Nigro*, Felix Elling, Samantha B. Joye, and Andreas Teske

University of North Carolina at Chapel Hill

Orca Basin is a deepwater (2400 m) depression on the northern Gulf of Mexico slope containing a ~200 m deep anoxic, high-salinity (~26%) brine lake. Since its discovery 39 years ago, there have been many studies investigating its unique geology and chemistry. The brine is formed by dissolution of Jurassic-derived halite exposed at the upper portions of the basin. The strong density gradient across the brine/seawater interface prevents solute exchange and acts as a particle trap and a microbial activity hot spot. Below the interface, the brine is nearly saturated with sodium and chloride, and elevated in potassium, calcium, sulfate, iron, manganese, organic carbon and methane, but depleted in nitrate and oxygen. Few studies have investigated the potential microbial diversity and community composition of this unique hypersaline system. Preliminary results from 16S rDNA analyses indicate that the brine contains specialized bacteria that belong to diverse taxonomic groups, including Gamma- and Deltaproteobacteria, Bacteroidetes, and Candidate Divisions OP11, SR1, JS1 and KB1. The potential metabolic and biogeochemical roles of the Orca Basin microbial community will be discussed, including the challenges in determining these functions due to biases in molecular techniques and difficulties in microbial cultivation.

Ironing out the RNA world

C. Denise Okafor*, Chiaolong Hsiao, Shreyas Athavale, I-Chun Chou, Anton Petrov, Jared Gossett, Lively Lie, Eric O'Neill, Jessica Bowman, Nicholas V. Hud, Roger Wartell, Steve Harvey, and Loren Dean Williams

Georgia Institute of Technology

In folded RNAs in vitro, Mg(II) can be replaced by Fe(II) in anoxic conditions. We have recently shown that Fe(II) can substitute for Mg(II) in RNA folding and catalytic function. We tested the hypothesis that the substitution of Fe(II) for Mg(II) can add new catalytic functionalities to RNA. Since Fe(II) can readily change oxidation state while Mg(II) cannot, we have explored the possibility that association with Fe(II) can confer on RNA the ability to catalyze electron transfer. We performed a metal swap, Mg(II) to Fe(II), with a variety of RNAs, while excluding oxygen. The results demonstrate that several large RNAs, including a bacterial 23S rRNA, in association with Fe(II), can efficiently catalyze electron transfer. Our experiments may be extending the catalytic functionalities of certain RNAs, or alternatively, are reviving latent functionalities that were extinguished by free oxygen and the catalytic superiority of proteins. We have found that the effectiveness of electron transfer catalysis is dependent on the RNA structure.

Development of a rate law for arsenic oxidation by manganese oxides over a range of pH conditions

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Arsenic concentrations above natural levels have been detected in the Chattahoochee River (GA). Experiments conducted with these sediments show that addition of small concentrations of arsenic (< 1 μM) increased the rate of iron oxidation by four fold. Iron-reducing bacteria likely increase their rates of respiration to offset the energy cost of detoxification. In this system manganese oxides are found in high concentrations. Arsenite (As(III)), is adsorbed to the surface of manganese oxides and chemically oxidized to arsenate (As(V)) over a wide range of pH values. The increase in iron reduction rate is proposed to be resulting from a catalytic cycle: As(III) produced biogenically is continuously reoxidized by manganese oxides, and recycled As(V) is continuously reduced by detoxification. The objective of this study is to develop a kinetic rate law for the reduction of arsenate by manganese oxides across a range of pH conditions. Analytical techniques including spectrophotometry, voltammetry, and ICP-MS are used to monitor concentrations of MnO_2, Mn(II), Mn(III), As(III), and As(V) during the experiments. The rate law will be used to determine whether the recycling of As(V) is fast enough to sustain a toxicity effect on iron-reducing bacteria in a variety of geochemical conditions.

Extended alkaline incubation times to quantify protein content in karstic aquifers and other oligotrophic groundwater systems

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Our group uses a multi-pronged approach to characterize relationships between seasonal recharge, dissolved organic matter (DOM) composition, and microbial community structure in oligotrophic aquatic systems. However, there are few methods to quantify and monitor DOM macromolecules, such as proteins, in such systems. In this study, we tested the Modified Lowry Protein Assay Kit (Pierce Biotechnology) as a rapid, high-throughput tool to measure DOM-associated proteins in raw waters and 0.2 μm PVDF filter extracts from karst water. The manufacturer recommends a 10 minute incubation period for the Biuret reaction, when the CuSO4–tartrate reagent is reduced to form protein-copper complexes. These complexes are subsequently reduced by Folin Ciocaltue to produce a blue color that can be quantified at 750 nm absorbance via UV-Vis spectrophotometry. With bovine serum albumen as the standard, the Biuret reaction continues at room temperature beyond the recommended time limit, and this yields highly variable results. We tested incubation times from 2-4 hours with the standard and samples. Results varied by site, whereby protein content from the most organic carbon-poor site underwent degradation after 2 hours, possibly due to alkaline hydrolysis or to the presence of different protein structures in the DOM.

Enhanced anaerobic petroleum hydrocarbon degradation with the addition of clay and seasonal variation of microbial activity in Deepwater Horizon oil spill-impacted salt marsh sediments

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Sulfate- and Fe(III)-reducing, and methanogenic prokaryotes (SRP, FRP, MGP) are key players in metabolic pathways involved in crude oil degradation by coupling anaerobic petroleum hydrocarbon (PHC) oxidation to anaerobic respiration. Understanding the metabolic activity of these microbes in contaminated environments will enhance oil spill bioremediation. In this study, metabolic activity of these prokaryotes were monitored seasonally and metabolically-active communities were identified in oil-impacted salt marsh sediments using quantitative real time RT-PCR and clone library analysis of key functional genes: Dissimilatory (bi)sulfite reductase (*dsrAB*), Geobactereceae-specific citrate synthase (*gltA*), methyl coenzyme M reductase (*mcrA*), and benzyl succinate synthase (*bssA*). In situ application of montmorillonite clay was assessed for its potential to accelerate PHC degradation by stimulating microbial activities. Levels of *dsrA*, *gltA* and *bssA* gene transcripts suggested that PHC-oxidizing SRP are more active in summer while FRP are more active in winter, indicating their activities' link to the seasonal growth cycle of *Spartina* sp. *bssA* gene expression peaked in winter, and was highest at more highly oil-impacted sites. Expression of all genes was higher in clay-amended sites. PHC analyses suggest that alkane degradation was significantly ($p>0.05$) enhanced by in situ clay amendment. BssA transcript levels and Fe(II) production were highest in clay-amended microcosm.

Biogeochemical consequences of arctic shrub expansion: a plant soil feedback perspective

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Arctic tundra is experiencing an unprecedented rise in temperature. One consequence of warming is the proliferation of woody shrubs across previously grassy tundra. The fate of arctic soil carbon has major implications for global climate change as tundra soils store more than twice as much carbon as is currently in the atmosphere. Models and ecosystem-scale observations suggest that areas of shrubs are a net source of carbon to the atmosphere, however the mechanism driving this imbalance is unknown. My research begins to address this by investigating the soil impact of three shrub species (*Betula nana*, *Salix pulchra*, and *Alnus fruticosa*). Using soils collected on the North Slope of the Brooks Range in Alaska, I incubated shrub-conditioned and non shrub-conditioned soils (organic and mineral layers) from each species with corresponding root and leaf litter, and measured rates of CO_2 efflux. I found strong evidence of plant-soil conditioning in the organic layer of each species, but no response in the mineral layer except for B. nana, which could indicate selection for microbial species that can better breakdown shrub material. This research has led to new questions about nutrient co-limitation and shrub root symbionts that I will explore in my continuing dissertation research.

Tri-octahedral domains and crystallinity in synthetic clays: Implication for lacustrine paleoenvironmental reconstruction

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Pure Mg-silicates precipitate in a number of saline alkaline settings, likely only if Al-rich detritus is absent. We are comparing the behavior of Mg-silicate saturated solutions containing no detrital material with solutions containing Al-rich smectite (Clay Minerals Society Source Clay SWy-2). We replicated Mizutani et al. (1991) to prepare a Mg-silicate gel. Solid phase analyses were performed with WD-XRF and XRD. The molar Si:Mg ratio of the gel was 2.3:1. The Mg-silicate gel was then seeded with sepiolite (Sep-sp-1), sonicated, and heated to 200°C in a Teflon lined Parr bomb for varying lengths of time. This produced a precipitate with no key differences from Sep-sp-1 by oriented XRD, but as time heated increased, a slight shift of the 060 peak commonly associated with clay octahedral sheets was observed. Peak height also increased linearly with heating time, suggesting an increase in crystallinity. When Na-montmorillonite (SWy-2) is used instead of Sep-sp-1, a new 060 peak appeared at ~1.526 Å, contrasting with the original SWy-2 060 peak (1.492 – 1.504 Å). This suggests we synthesized trioctahedral domains in a smectite structure. Investigation is continuing to characterize these newly synthesized phases and determine the compositional and textural relationship to the Al-rich detritus.

Microorganisms in sediments from an Antarctic subglacial lake mediate S-cycling

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Vast networks of liquid water reside beneath the Antarctic ice sheets including approximately 400 subglacial lakes. Accessing subglacial environments is challenging because of thick ice covers, consequently the metabolic function and diversity of resident microbes remains largely unknown. Metabolically active microorganisms in subglacial environments would enhance subglacial mineral weathering, thus influencing global biogeochemical cycles. Subglacial Lake Whillans (SLW) is a shallow, permanently dark and cold (-0.5°C), freshwater lake under the Whillans Ice Stream. SLW is considered an active lake because the residence time of water is short, draining and refilling on a sub-decadal scale. The Whillans Ice Stream Subglacial Access Research Drilling (WISSARD) Project drilled through more than 800m of glacial ice into SLW utilizing clean access strategies to recover water and sediment samples for microbiological and geochemical analysis. Here we report the presence of microbially mediated sulfur transformations in sediments from SLW. Sediments were incubated with 35S-labeled sulfate to measure sulfate reduction. The diversity of key genes that mediate sulfur cycling including adenosine-5-phosphosulfate reductase (*aprA*) and dissimilatory sulfite reductase (*dsrAB*) was analyzed. These results support previous reports of microbially mediated sulfur cycling in subglacial environments and further elucidate the structure and function of these underexplored microbial communities.

A hominin story: Uncovered through X-ray diffraction and analysis of clay Minerals

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Lacustrine sediments provide a wealth of information related to regional paleoclimate, paleoecology, tectonic activity, and paleoenvironmental change. Core samples have been collected from East African paleolakes associated with important hominin fossil sites. Our research is part of three large collaborative projects: the Hominin Site and Paleo-lake Drilling Project (HSPDP) and the Ancient Climate and Authigenic Clay Index of Aridity (ACACIA), both funded by NSF, and the Ologesailie Drilling Project funded by the Smithsonian Institution. We are examining the causes and effects of environmental change in East Africa through Quaternary time, to help understand the evolution of the hominin lineage and vertebrate ecosystems. We use X-ray Diffraction (XRD) to determine the mineralogy and geochemistry of lacustrine sediments collected from the West Turkana, Baringo, Olorgesailie, Olduvai, and Lake Magadi basins. Analyses of bulk mineralogy for West Turkana and Tugen Hills samples are underway, and clay mineralogy analysis of Olorgesailie, Olduvai, and Magadi material will begin later this year. Preliminary analyses show the presence of authigenic phases such as zeolites (analcime, phillipsite, chabazite), Mg-calcite, and trioctahedral smectite. In concert with biotic and other proxies, these data will inform our understanding of environmental change over the past several million years.

Anaerobic methane oxidation coupled to iron reduction in an Archaean ocean analogue

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Anaerobic oxidation of methane (AOM), regarded as one of the earliest forms of metabolism on Earth, is widespread in modern anoxic ecosystems, with significant implications for global carbon cycling. Microorganisms that couple AOM to reduction of nitrate and sulfate have been discovered, and geochemical data suggests that AOM coupled to Fe(III) reduction (Fe-AOM) is also occurring in marine and freshwater environments. Nitrate and sulfate were largely unavailable in Archaean Earth, while Fe(III) and methane were abundant, suggesting that Fe-AOM may have been an important primitive microbial metabolism. Lake Matano, Indonesia is an Archaean ocean analogue with abundant Fe and methane, and extremely low sulfate and nitrate. Fe-AOM is likely a thermodynamically favorable microbial metabolism in Lake Matano's anoxic, Fe(III)-rich sediments. This work aims to isolate the microbes mediating Fe-AOM from Lake Matano sediments through serial enrichment cultures in minimal media lacking nitrate and sulfate with added methane and Fe(III). After 90 days, three layers of Lake Matano sediments each showed high levels of Fe(III) reduction in the presence of methane compared to no methane and heat killed controls. This research will explore alternative microbial pathways for carbon and iron cycling under energy-limiting conditions, present on ancient Earth and other planets.

Phaeocystis antarctica maintains cellular DMSP and other cellular constituents but loses DMSO in prolonged darkness

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The prymnesiophyte *Phaeocystis antarctica* is an important primary producer in areas such as the Ross Sea, Antarctica and must survive over 4 months of darkness during the austral winter. *Phaeocystis* is one of the largest producers of the sulfur metabolite DMSP (dimethylsulfoniopropionate) and we therefore investigated the effects of prolonged darkness on DMSP and other biogeochemically-relevant constituents of *P. antarctica* (CCMP 1374). Replicate exponential phase cultures of *P. antarctica* were placed in darkness at 1°C and sacrificed for analysis over 144 days. Intracellular DMSP, chlorophyll *a* and cell numbers all declined over the first few days but remained fairly constant for the remainder of the experiment at 38-54%, 64-83% and 59-71% of the initial values, respectively. Additionally, POC and PON followed similar patterns indicating that *P. antarctica* maintains a large proportion of its initial biogeochemical makeup. In contrast, particulate dimethylsulfoxide (DMSO) declined to nearly undetectable levels presumably because its production is light dependent and unlike DMSP, the remaining intracellular pool can readily cross cell membranes into the surrounding medium. Measurable DMSO in the cells may be a useful indicator of length of time in dark since it was only measurable for the first month in darkness.

Dispersal and habitat limitations detected in a bacterial metacommunity from connected freshwater ecosystems

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Environmental factors limit diversity in a given habitat, while dispersal constraints limit it geographically. The former are explicitly incorporated into biogeochemical models; but the effects of dispersal as ecologic constraint in bacterial communities are often neglected. To provide new insights into the latter issue, we sequenced and compared the metagenomes of planktonic communities from five connected lakes along the Chattahoochee River (Southeast USA) and time-series samples from one of the lakes (Lake Lanier, GA). We found anticipated shifts in functional composition along the freshwater-to-marine gradient, reflecting the influence of habitat factors in the composition of the communities. More notably, we detected dispersal constraints, reflecting historical influence in the regional pool. Abundant populations decreased in abundance downstream in the connected lakes, documenting dispersal constrains in population dispersion. For instance, the most abundant population upstream (Burkholderiaceae) monotonously decreased in abundance from >10% in upstream lakes to <0.1% in the estuary, while accumulating genomic variations. Spatial variation in abundant populations exceeded seasonal variation, highlighting the effect of dispersal constrains. Altogether, our results show that both dispersal and habitat constraints shape functional diversity, distribution of populations and presumably the assembly of bacterial communities in freshwater environments.

A spatial and temporal investigation of carbon isotopes in POC in the Gulf of Mexico

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The Deepwater Horizon blowout released 500,000t of gaseous hydrocarbon into the water column, but >0.01% of this reached the sea surface. Metabolically efficient methanotrophs consumed the gasses, converting them into biomass that was then consumed by other organisms. By analyzing POC samples, carbon isotopes can trace the original gas up the food chain. POC samples were collected from Desoto Canyon and other seep sites across the Northern GOM. Seawater was filtered, collecting the POC on glass microfiber filters, which were then acid fumed, dried and processed for $\delta^{13}C$ and $\Delta^{14}C$. The range of $\delta^{13}C$ signatures of POC was from -20.99‰ to -34.55‰. The more depleted $\delta^{13}C$ signatures were from greater depths in the water column. Preliminary results for $\Delta^{14}C$ range from modern 8‰ to -500‰. One trend in the data shows that samples with highly depleted $\delta^{13}C$ signatures also have highly depleted $\Delta^{14}C$ values. For instance, one sample from a depth of 1040m has $\delta^{13}C$ and $\Delta^{14}C$ signatures of -30.29‰ and -519‰, respectively.

Mineralogical constraint of reverse weathering reactions

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The role of marine sediments in ocean acidification is poorly constrained, but may represent an integral feedback through reverse weathering reactions. The objective of this study is to characterize the (bio)geochemical reactions involved in the formation of clay minerals during reverse weathering, specifically as influenced by iron reduction. Synthetic amorphous Al oxides and either ferrihydrite or organic ligand bound Fe(III) were reacted with either glass beads or biogenic silica from the marine diatom, *Thalassiosira pseudonana*, in order to investigate the mineral transformations that occur in typical coastal sediment conditions. The effects of pH, Fe(II) concentration, and Fe(III) source were examined. Aqueous concentrations of Fe(II), Fe(III), Al, and Si were measured to indicate the rate and extent of mineral dissolution. Morphological changes of the minerals during the reaction were also characterized. This study provides further constraint of diagenetic processes that influence the buffering capacity of marine sediments, especially the balance between reverse weathering and iron reduction.

Enrichment and characterization of petroleum hydrocarbon-oxidizing, Fe(III)- and sulfate-reducing prokaryotes from salt marsh sediments impacted by the Deepwater Horizon oil spill

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Fe(III)-reducing (FeRP) and sulfate-reducing prokaryotes (SRP) play a key role in bioremediation of crude oil in anoxic environments by coupling oxidation of aromatic compounds with reduction of Fe(III) and sulfate. In this study, we enriched FeRP and SRP with crude oil, naphthalene and phenanthrene as electron donors from oil-contaminated Louisiana salt marsh sediments. In the enrichments demonstrating active Fe(III)- and sulfate-reduction, expression of benzyl succinate synthase (bssA), naphthylmethylsuccinate synthase (nmsA), Geobacteraceae-specific citrate synthase (gltA), and dissimilatory (bi)sulfite reductase (dsrAB) genes were analyzed as molecular proxies for metabolically-active aromatic-oxidizing FeRP and SRP. Phylogenetic analyses of Fe(III)-reducing enrichment cultures were performed by pyrosequencing of 16S rRNA cDNA. The results suggest that the Geobacteraceae family consist of approximately 60% of active prokaryotes in the cultures. Isolation of novel anaerobic petroleum hydrocarbon (PHC)-oxidizing prokaryotes is underway using a polyphasic approach including diffusion chamber and agar-shake dilution methods. Ongoing PCR analysis and microscopy of isolated colonies from agar-shake dilution series indicate active growth of FeRP and SRP. The findings obtained from this study will contribute to our understanding of the complex microbial communities that are involved in PHC degradation and potentially facilitate oil spill remediation.

Microbial platform for biogeochemical transformation of lignocellulosic biomass to biodegradable plastic

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Environmental concern over non-biodegradable plastic has stimulated development of alternative clean technologies for production of biodegradable plastic. Alternative clean technologies include biosynthesis of biodegradable polymers by recombinant microorganisms genetically engineered to produce biodegradable plastic from renewable resources. The plastic industry primarily produces polymers from petroleum-based sources. Second generation biodegradable plastics include polyhydroxybutyrate (PHB) that is produced from renewable sources such as lignocellulosic biomass. PHB therefore provides an attractive alternative to conventional plastics. The proposed biogeochemical platform for production of biodegradable plastics is based on a microbially-driven Fenton reaction that oxidatively degrades cellulose, hemicellulose, and lignin, thus avoiding use of expensive cellulase, hemicellulase, and lignolytic enzymes for lignocellulose degradation. In comparison to traditional Fenton or photo Fenton-based oxidation systems, the microbially-driven Fenton reaction operates at neutral pH and does not require addition of exogenous H2O2 or UV irradiation to regenerate Fe(II). Microbial Fe(III) reduction by Shewanella oneidensis replaces the requirement of UV irradiation to regenerate Fe(II) as a Fenton reagent, while the aerobic electron transport system produces H2O2 as a byproduct of aerobic respiration. Simple reducing sugars are the predicted primary degradation products of lignocellulose degradation from the Fenton reaction. The consolidated biogeochemical process consists of S. oneidensis-driven Fenton degradation of lignocellulosic biomass coupled to PHB production using the PHB biosynthetic cassette phaCAB of Ralstonia eutropha cloned into a recombinant, sugar-adapted S. oneidensis strain.

Spectroscopic analysis and role of iron minerals in geocatalytic formation of biomolecules on early earth

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Heterogeneous catalysis at mineral surfaces was a major pathway to the abiotic formation of biomolecules on early earth. The hypothesis is that an enhanced rate of formation could have led to the accumulation of the biomolecules. The current challenges are in finding simulation experiments that mimic the geochemical environment on early Earth. Pyrite, an iron sulfide mineral, is found in coal and was used in the current study to enhance the yield of glycine and nucleobases in an aqueous pond scenario. Formamide, water, and pyrite mixture was irradiated with ultraviolet light at 254 nm and heated at 100°C for 48 hours. The reaction was performed under argon. The results showed an enhanced yield of glycine when pyrite was used. However, nucleobases were not formed. The formation of glycine is consistent with our recent theoretical predication that formamide is a precursor of glycine. The results suggest that pyrite mineral may have played an important abiotic catalytic role leading to the accumulation of glycine. ^{57}Fe Mössbauer data of the pyrite mineral was recorded before and after the reaction. These data will provide additional information whether or not electron transfer processes, if any, are taking place in these reactions.

Metagenomic analysis of endosymbionts of the deep-sea tubeworm *Ridgeia piscesae*

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Symbioses between Vestimentiferan tubeworms and intracellular sulfur-oxidizing bacteria are important sources of primary production and habitat structuring at deep-sea hydrothermal vents and cold seeps. These symbioses involve multiple host genera occupying distinct physiochemical niches. However, the extent to which tubeworm symbionts differ functionally between host species, or between ecotypes of the same host species, is unknown. We present a preliminary metagenomic analysis of functional gene content in the endosymbiont of the vent tubeworm *Ridgeia piscesae*. Total DNA, representing both host and symbiont cells, was extracted from the endosymbiont-bearing trophosome of a single host individual collected from the Juan de Fuca Ridge and shotgun sequenced (Illumina). Reads were separated into putative “symbiont” and “host” fractions and assembled separately. Predicted symbiont genes were annotated according to function and taxonomy. Mapping of reads onto a set of core genes and to the internal transcribed spacer of the rRNA operon revealed a clonal symbiont population, likely due to limited genetic diversity in the founding symbiont population acquired during host development. Comparisons of genome content between the *R. piscesae* symbiont and the symbionts of two other deep-sea vestimentiferans (*Riftia pachyptila* and *Tevnia jerichonana*) suggest functional differences potentially reflective of varying ecological niches in the deep-sea vent environment.

Characterization and stability of organic carbon in sediments/soils of a young prograding delta: the Wax Lake Delta, Louisiana

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Wax Lake Delta, Louisiana formed as a result of the construction of the Wax Lake Outlet in 1941 and now serves as a “model” delta for delta restoration projects. This delta, which has been building subaerially since 1973, offers an ideal opportunity to examine how decadal changes in the vegetation and elevation affect the composition, partitioning, and stability of organic carbon in soils/sediments. This chronosequence work will also be linked with recent modeling studies that have now included organic carbon in long-term delta formation dynamics. We analyzed bulk stable isotopes, chemical biomarkers, and compound-specific stable isotopes to uncover the sources and characteristics of organic carbon (OC) in soils/sediments along a chronosequence (38, 26, and 13 year old sites) of the Wax Lake Delta. Here, we posit that the burial efficiency of OC deposited in Wax Lake Delta sediments/soils will increase with time due to greater trapping of fines, enhanced organo-mineral aggregate associations, higher inputs of vascular plant versus algal sources, and changing redox.

Anaerobic hydrocarbon-degradation by microorganisms isolated from the Gulf of Mexico after the Deepwater Horizon oil spill

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Georgia Institute of Technology

In April 2010, approximately 584.28 million liters of petroleum were discharged into the Gulf of Mexico from the Deepwater Horizon oil spill. It was estimated that 78% of the discharged oil were removed, but the fate of remaining 22% is still poorly understood. Discharged crude oil persists in the deep sea of the Gulf of Mexico, but remaining oil can be decomposed by microorganisms aerobically or anaerobically. Although aerobic oil-degradation by microorganisms is much more rapid, anaerobic hydrocarbon degradation pathways may predominate in sediments over the long-term approach because oxygen supply is limited in muddy sediments found in the deep sea. Thus, the objectives of this study are to (i) quantify and determine the rates and pathways of anaerobic hydrocarbon degradation, (ii) enrich and isolate microbes that are capable of anaerobic hydrocarbon-mineralization, and (iii) use pure cultures to characterize the biochemical pathways. Sediment samples were collected on research cruises in the Gulf of Mexico during 2012 and 2013. Enrichment cultures were initiated using sediment samples from deep or shallow sedimentary environments, and microbial activity in the enrichment cultures was confirmed by quantification of transformation of electron acceptors. Several strains were isolated through successive transfers of enrichment cultures followed by plating on solid media.

Tracking the fate of incorporated carbon and nitrogen of leucine in marine heterotrophs

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In the ocean, bacteria dominate numerically and drive much of nutrient cycling. Their activity in the microbial loop makes dissolved organic matter accessible to higher trophic levels. The incorporation of leucine into bacteria has traditionally been used as a proxy for this activity in aquatic systems. While leucine is primarily incorporated into proteins within these cells, it can also be catabolized and respired; however, these specific catabolic processes have been less well studied, particularly the role of leucine as a source of nitrogen. To investigate the eventual fate of leucine within cells, we used traditional methods consisting of ^{3}H-leucine uptake measurements alongside an untargeted metabolomics approach to track the incorporation of C and N of leucine into small metabolites other than bulk protein in a natural marine community. This was performed via the addition of fully labeled ^{13}C- or ^{15}N-leucine. We additionally followed label incorporation from alternate C and/or N sources acetate, ammonium, and urea. While most leucine was used for protein synthesis, we observed incorporation of C into UDP-d-glucose and N into glutamate, suggesting that leucine may be used a source of C or N, though not in the same manner that urea, acetate, and ammonium were utilized.

Temperature sensitivity of recalcitrant soil organic carbon decomposition

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Soil has the largest carbon storage in terrestrial ecosystems. How soil organic carbon decomposition responds to climate changes will have significant influences on global carbon cycle. Kinetic theory predicts that recalcitrant organic carbon has relatively higher response to rising temperature. Therefore, understanding how the recalcitrant organic carbon decomposition responds to global warming is key to predict global carbon cycle in the future. In addition, most soil warming experiments are carried out in northern latitude. Few studies focus on the highly weathered tropic and subtropical soils. In this study, we incubated highly weathered ultisols sampled from a temperate forest in Georgia with temperature and moisture treatments to investigate their influences on the temperature sensitivity of recalcitrant organic carbon decomposition. Our results show that temperature and moisture both influence the decomposition rate of recalcitrant organic carbon but the temperature sensitivity is not significantly altered.

Aerobic hydrocarbon degradation in deep sea sediments of northeastern Gulf of Mexico

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Georgia Institute of Technology

Benthic microbial communities provide key ecosystem services such as organic matter decomposition and nutrient regeneration in the Gulf. Main objectives of this research are to: 1) elucidate the rates, pathways, and controls of biodegradation of oil hydrocarbons, and 2) quantify the effects or impacts of hydrocarbon discharge on the functional diversity of sedimentary microbes. Degradation rates of Macondo oil were quantified at close to ambient (4°C) and room temperatures (20°C) by measuring both hydrocarbon degradation and mineralization. Degradation rates under cold conditions rivaled those of warmer conditions. Thirty strains of oil-degrading bacteria from two groups (*Rhodococcus* and *Halomonas*) were isolated from deep sea sediments. Gene sequences retrieved from deep sea sediments showed high sequence identity to those of the cultivated strains. Highly diverse microbial communities were observed in all samples and community composition correlated with both core depth and water column depth. This research elucidates model bacterial strains that may be used as microbial indicators of hydrocarbon degradation as well as for understanding the ecophysiology of hydrocarbon metabolism in the deep sea.

Metabolomic assessment of inorganic carbon assimilation by phytoplankton in the N. Pacific Ocean

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In the euphotic zone of the oligotrophic North Pacific Ocean, research suggests phytoplankton growth is constrained through nutrient limitation. To investigate the effects of nutrient availability on phytoplankton metabolism, we traced inorganic carbon incorporation into metabolites of cells in size-fractionated and nutrient-amended natural seawater microcosms. The rate of carbon incorporation from stable isotope labeled carbon dioxide-supplied as ^{13}C-bicarbonate- into intercellular metabolites of our microcosms was quantified using ultra performance liquid chromatography—mass spectrometry based metabolomics on an Exactive Plus Orbitrap mass spectrometer. Observed rates of labeling in the key metabolites glutamine and glutamate suggest that different size classes of phytoplankton utilize different metabolic strategies for assimilating nitrogen during periods of nitrogen influx.

How could future climate change impact ocean deoxygenation?

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In a warming climate, dissolved oxygen is hypothesized to decline due to the temperature dependence of solubility and weakening ventilation which may be associated with increased stratification. Simulations using coupled carbon-climate models generally support this hypothesis, however, it is challenging to investigate what aspect of climate forcing could impact on dissolved oxygen in global to regional scale. In this study, we used an idealized global ocean biogeochemistry model as a tool to evaluate how climate changes impact on dissolved oxygen in the ocean. We have conducted sensitivity experiments imposing, 1) a uniform, global warming of SST, 2) an intensifying freshwater flux, 3) an increase in Southern Ocean zonal wind, and 4) a decreasing trade wind in the tropical Pacific Ocean. The results show that global warming and enhancement of freshwater flux tend to decrease global oxygen due to the changes in solubility and stratification. However, increase in Southern Ocean zonal wind tends to compensate the decrease in dissolved oxygen due to increasing ventilation. Decrease in trade wind tends to change regional export production which results in increasing dissolved oxygen in the tropical Pacific Ocean. In this presentation, we will compare changes in global and regional patterns of dissolved oxygen.

Environmental lead contamination: Heavy metals and cerussite in Nigerian gold ores

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Artisanal gold mining has contaminated many villages in northwest Nigeria, killed >400 children, and affected thousands. Ore is processed in living areas followed by mercury amalgamation to recover gold using home cooking pots. Processed ore and dust samples were collected from 54 villages by the USCDC and Nigerian colleagues. Our team at Georgia State University analyzed the samples using XRD, ICP-AES, and SEM. Processed ore samples contained high levels of lead, mercury, arsenic, antimony, and copper. Pb concentrations exceed the US EPA Residential Soil Screening Level in children's sleeping areas (as high as 1,400 mg/kg), but not in play areas. XRD analyses identified cerussite (PbCO3), a secondary weathering product of galena (PbS), in the processed ore. No Pb-bearing crystalline phases have yet been found in dust samples, suggesting likely abundances of <0.5 wt% cerussite (as expected with Pb <2000 mg/kg). The presence of cerussite, a high bioavailable carbonate mineral, provides a probable explanation for the Pb poisoning through inhalation and/or ingestion of dust brought into the home. These results provide a key step in understanding the risks associated with gold ore processing. Further work will determine concentrations and partitioning of heavy metals in relation to cerussite and other minerals present.

A global perturbation to the carbon cycle during the Early Jurassic

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The Toarcian Stage of the Jurassic is thought be a time of large-scale changes to the carbon cycle and an interval of widespread marine anoxia: the Toarcian Oceanic Anoxic Event (T-OAE). It is believed that these environmental changes were triggered by a sudden injection of greenhouse gases to the atmosphere through volcanism, analogous to the anthropogenic flux observed today. However, it has also been posited that the T-OAE was not of global extent and instead was a regional phenomenon whose geochemical signatures, particularly the carbon isotope record was the result of local oceanographic processes. One of the key issues fueling this debate is the overwhelming majority of Toarcian studies have focused on sedimentary successions confined to Europe. We have conducted a high-resolution chemostratigraphic study of the Jurassic Fernie Formation from the Western Canadian Sedimentary Basin (WCSB) in western Alberta. The independent identification of the Toarcian interval in this succession has been constrained by previous biostratigraphic studies of ammonite fauna within each section. Importantly, a negative 3.5‰ shift recorded in $\delta^{13}C$ at all the study sites during the Early Toarcian is consistent with the European geochemical datasets that suggest the changes in the carbon cycle surrounding the T-OAE were global.

Interactions between viruses and their hosts as captured by time-series metagenomes in a temperate freshwater ecosystem

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Despite the increasing appreciation of the importance of viruses in the ecology of natural microbial populations and their implications in biogeochemical processes, little is known about the population dynamics of viruses in the environment, especially in temperate freshwater ecosystems. Here, we report the analysis of seven viral metagenomes from Lake Lanier (Atlanta, GA), collected over the span of three years. Despite the low portion of sequences with matches against public databases (10-20% of reads; 25-35% of assembled contigs), assembly and de novo clustering of the time-series libraries enabled us to identify several complete genome sequences representing individual viral populations. The identified viral populations displayed short-term stable abundance profiles, while the overall taxonomic composition was more similar to other freshwater viromes than to marine or hypersaline viral communities. Fifteen microbial metagenomes collected during the same time period (collecting filter size 0.22μm), allowed us to identify over a hundred nearly complete microbial genomes from the same environment. Correlating the abundance of microbial and viral populations over time allowed us to detect potential viral-host pairs and evaluate the degree of host specificity of individual viruses. Additionally, the deeply sequenced and highly resolved microbial genomes allowed the identification of several CRISPR loci, which showed increasing diversity and abundance during the summer time relative to winter. For several of those loci, proto-spacers were identified in the companion viromes, with varying abundance profiles though time. Therefore, these results offered snapshots of ongoing viral-host associations under natural settings and provided new insights into the dynamics of phage-host interactions.

The paradox of iron demand due to diatom productivity in the Southern Ocean

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Iron plays an important role in the regulation of biological productivity and the carbon cycle in the Southern Ocean. Recently, X-ray spectromicroscopic techniques revealed high molar Fe:Si ratios in Antarctic biogenic silica from living phytoplankton samples (Ingall et al., 2013). The export and burial of biogenic silica can be a major removal pathway of iron from the Southern Ocean. Based on this new data, we estimate the iron removal rate in the pelagic Southern Ocean using a simple inverse box model. Combining the existing dissolved iron and silicic acid datasets we reveal that, even with the most conservative estimates of the Fe:Si ratio, the upwelling of subsurface waters cannot supply enough iron to balance the loss due to diatom production.

Evaluating the effects of disturbance on microbial diversity from marsh sediment and water at Grand Isle, Louisiana

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The diversity of marsh sediment microbial communities can be affected by changes in salinity, pH, temperature, sediment input, and other environmental factors that correspond to tidal cycles, storms, or seasonal processes. Sediment and water samples were collected in 2012 from five marshes near Grand Isle, Louisiana, to examine microbial diversity relationships between sediment 1 m offshore (at 0-1 cm and 1-2 cm depth) from the marsh edge and from the water column. These marshes were previously affected by the BP-Deepwater Horizon oil spill, and were also affected by Hurricane Isaac (i.e. marshes were completely inundated). All of the sites had similar water temperature (28-33 oC) and salinity (22-25 ppt) over time. Bacterial diversity from the sediments, examined from 16S rRNA gene sequences, differed from marsh to marsh. Although Proteobacteria dominated the benthic sediments at all sites, there were differences in the relative abundances of Alphaproteobacteria, Deltaproteobacteria, and Gammaproteobacteria between sites, and with depth, that may possibly indicate differences in sulfur cycling that is specific to each marsh. Ongoing work includes comparing sediment community compositions to those from the water column at each marsh, and to determine whether communities shifted (or became more similar) after Hurricane Isaac**.**

Genetic diversity and expression patterns of diatom Rubisco and CCM genes in the Amazon plume

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My research applies metagenomic and metatranscriptomic approaches to answer the question of how biological response to climate change may affect the rate of oceanic carbon sequestration. Anthropogenic CO2 buildup in the atmosphere drives climate change; therefore, the effects of climate change on processes that remove carbon from the atmosphere are relevant to understanding feedback mechanisms. Rising CO_2 concentrations enhance the solubility pump of CO_2 to depth, compensating to some extent for the increased flux to the atmosphere, but what about enhancing (or damping) the biological pump? POC flux to depth varies significantly both spatially and temporally, with large pulses often associated with blooms of diatoms, which, thanks to silicate frustules, sink quickly and sometimes fully intact. In the mesohaline region of Amazon plume, symbiotic association between diatoms and N_2-fixing bacteria contribute to a significant C flux. I am interested in whether diatom growth rates will change with increasing CO_2 concentrations as a result of changes in expression, or even evolution, of genes responsible for C uptake. Therefore, I am analyzing patterns of expression and genetic diversity of diatom carbon concentrating mechanism and Rubisco genes in metagenomic and metatranscriptomic samples from the Amazon plume.

Sediment denitrification overcome sulfides inhibition under low salinity environment

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Anthropogenic activity is increasing nitrogen (N) inputs to coastal systems, reinforcing the need to understand how the N cycle functions in different environments. Previous studies have detected low rates of nitrification and denitrification in the northern Gulf of Mexico. One of the reasons may be the inhibitory effects of porewater sulfide on these processes. The objective of this study was to identify factors limiting denitrification in coastal sediments. Mud flat sediments under different salinities were collected seasonally. We hypothesized that under lower salinity, due to lower sulfate, the inhibition of HS^- would be lifted and nitrification and denitrification would become higher. Potential nitrification was low (0.06-0.25 nmol N g^{-1} h^{-1}) at both sites throughout different seasons, corresponding with low numbers of bacterial and archaeal *amoA* genes. Although high abundances of sulfate reducers and high sulfide concentrations were detected at both sites, potential denitrification rates were significantly higher at the low salinity site (3.35-10.11 nmol N g^{-1} h^{-1}, compared to 0.14-1.70 nmol N g^{-1} h^{-1} under high salinity) and increased with decreasing temperature. *nirS* gene abundances positively correlated with potential denitrification rates ($R= 0.70$, $P<0.0001$). Other factors besides sulfides may also play a role regulating nitrogen removal processes.

Enrichment, sequencing and ongoing analysis of an ammonia-oxidizing bacterial community from sediments in Jiaozhou Bay, China

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Jiaozhou Bay is a hypernutrified semi-closed water body hosting the metro area of Qingdao, China. The environmental quality of Jiaozhou Bay has dramatically deteriorated in recent decades because of the increasing input of crude oil, industrial pollution, agricultural fertilized water and human wastewater with one of the consequences being the high concentration of fixed nitrogen in the Bay. Given this fact, we were interested in looking at the sediment bacterial community, especially ammonia-oxidizing chemolithotrophic bacteria, in this heavily polluted environment. Sediment samples were collected in September 2008 from 10 stations representative of different water qualities and investigated using PCR for the abundance and distribution 16S rRNA and hao genes to identify the existence of ammonia-oxidizing Gammaproteobacteria (Gamma-AOB). Signal-positive sample D1 was the start for an enrichment culture with the goal to isolate a Gamma-AOB key to the N cycle in Jiaozhou Bay. In November 2013, metagenomic analysis of community DNA was performed using Illumina-based high-throughput sequencing. Preliminary binning of the metagenomic data and use of the finished genome of *Nitrosococcus halophilus* NC4 as an anchor generated the draft genome of a Gamma-AOB isolate (D1) with an average nucleotide identity (ANI) of 90.84% to strain Nc4, likely a representative of a new *Nitrosococcus* species. The metagenomic data revealed the residence of two other genera such as putative PAH-degraders *Marinobacter* and *Sphingomonas* as residents in the enrichment, in which the Gamma-AOB was the sole primary producer. Detailed metagenome sequence binning, statistical and sequence analyses have started with the goal to characterize the enriched bacterial community in silico followed by genome-informed experiments using approaches of ecogenomics, ecophysiology and biogeochemistry.

Influence of temperature on alternative nitrogenase activity: implications for nitrogen cycling in high latitude peatlands

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Nitrogen fixation is thought to be the dominant source of nitrogen to peatlands, which store a third of the world's soil carbon. Previous studies have suggested that the alternative vanadium-containing nitrogenase is more efficient than the canonical molybdenum-nitrogenase at low temperatures typical of high-latitude peatlands. We found that vanadium and molybdenum nitrogenase genes are present and transcribed in Minnesota peatland bogs. The highest percentage of the metagenomic vanadium nitrogenase (*vnf*) hits showed greatest similarity to *Rhodopseudomonas palustris*, a ubiquitous diazotroph. We are currently investigating the effects of temperature on rates of acetylene reduction to ethane, an indicator of vanadium nitrogenase activity, using *R. palustris* CGA wild-type and *vnf*-only mutant strains. This work will shed new light on the effects of warming temperatures on nitrogen fixation in high latitude peatland ecosystems that are on the tipping point of global climate change.

The generation of DOC and POC by marine viruses

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Viral lysis of marine microorganisms influences the carbon cycle by transforming organic carbon among dissolved and particulate reservoirs. Cell disruption due to viral lysis transforms cell biomass into dissolved organic matter, some of which may aggregate into the particulate phase and serve as a carbon source for other organisms. Remnants of lysed cells may also remain in the particulate phase. The goal of this project is to assess the fate of microbial biomass following viral lysis. We report the effects of viral lysis on *Vibrio alginolyticus*, isolate PWH3a. We used an immunological staining technique and microscopy of lysed cells to distinguish cells containing double-stranded DNA, cell-like structures without double-stranded DNA, and amorphous polysaccharide-rich structures. Furthermore, we quantified the abundance of particulate organic carbon, and the quantities of dissolved organic carbon in the size ranges of <3 kDa, 3-10 kDa, and 10-100 kDa, and >100 kDa. The results demonstrate how the activity of viruses generates a continuum of size classes of organic matter. The results will be presented in an effort to further our understanding of how viruses shape the marine carbon cycle.

Genome sequencing of environmental *Enterococcus faecalis* reveals the signature of gut colonization and biomarkers for improved water quality monitoring

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Enterococci are common members of gut microbial communities and their ease of culturing has facilitated worldwide utility as indicators of fecal pollution in the assessment of water quality. However, enterococci also persist in environmental habitats, often in the absence of fecal input, potentially confounding their monitoring for public health protection. We hypothesize that discrete gene signatures facilitating habitat specialization could differentiate environmental and human-associated enterococci. Toward resolving this issue, 11 isolates of *Enterococcus faecalis* recovered from freshwater watersheds (environmental) were sequenced and compared to 59 publically available enteric genomes (both commensal and pathogenic). Phenotypically and phylogenetically (16S rRNA gene and core genome), the environmental *E. faecalis* were indistinguishable from their enteric counterparts. However, analyzing variable genes uncovered discrete environment- and host-specific signatures, encoding accessory nutrient utilization pathways. For instance, it appears that a putative nickel uptake operon was enriched in the environmental genomes and undetectable in human gut metagenomes, suggesting its importance in extra-enteric habitats. The distribution and phylogeny of these identified signatures suggest that certain genotypes of *E. faecalis* preferably reside in extra-enteric habitats, challenging prevailing views of enterococci ecology and their preferred use as fecal indicators in recreational waters.

Temporal and spatial extrapolation using remotely sensed ocean color

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Ocean chlorophyll concentration is a key indicator of ecosystem and biogeochemical conditions. Remotely sensed ocean color provides comprehensive information about the global distribution of chlorophyll. However, consistent estimates have only been available since the late 1990s with the deployment of SeaWiFS. The relatively short history of satellite measurements limits their utility for considering long-term variability (decadal to multidecadal) and trends. Direct in situ estimates of chlorophyll have been made in sporadic locations since the 1950s, but extrapolation of these point measurements requires some understanding of the spatial and temporal scales over which they are representative. Here, we examined autocorrelation in the 10-year SeaWiFS ocean color record to estimate the spatial and temporal scales of chlorophyll variability. Our results are consistent with expectation of low-frequency variability in regions associated with the El Nino Southern Oscillation. Higher latitude regions exhibited less autocorrelation in space and time, characteristic of a significant influence at synoptic scales. Additionally, we found that spatial scales of variability tended to be greater in the zonal direction than in the meridional direction. With this information, a better understanding of chlorophyll sampling can be established in relation to space and time, and more efficient ways of sampling can be implemented.

Biomolecule preservation in hyper-arid desert soils and application to Mars

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The Atacama Desert in Chile is one of the oldest, driest, and organically lean deserts on Earth and is an excellent terrestrial analog for the moisture conditions and soil chemistry occurring on the surface of Mars. Soil samples were collected with depth (0-1 meter) in the hyper-arid core of the Atacama in the Yungay region during the summer of 2013. We have quantified refractory lipids (e.g. isoprenoids) in order to characterize the quality of preservation of organic material that is preserved in these approximately two million year old soils, providing information about the level of degradation and depth distribution/concentration of this class of robust and informative biomarkers in extremely arid environments. Characterization was performed by solvent extraction, GC-MS and pyrolysis-GC-MS while maintaining rigorous protocols to mitigate contamination. Preliminary results indicate the presence of phytane, halogenated aromatics, and greater preservation with increasing soil column depth. Results from this study will help to inform sampling strategies and extraction efficiencies for the SAM experiment as part of the Mars Science Laboratory currently on Mars, as well as determine timescales of preservation of refractory organics in desert environments.

pH Effects on the microbial reductive dechlorination process

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The chlorinated solvents tetrachloroethene (PCE) and trichloroethene (TCE) are common groundwater pollutants. Several bacterial populations dechlorinate PCE and TCE to cis-1,2,-dichloroethenene (cis-DCE); however, further reductive dechlorination to non-toxic ethene is restricted to certain hydrogenotrophic *Dehalococcoides mccartyi* strains. Biostimulation with organic substrates to increase the flux of hydrogen and bioaugmentation (i.e., the addition of *Dehalococcoides*-containing consortia) provide effective means for tackling chlorinated solvent contamination and achieving detoxification. Fermentation processes stimulated by the addition of organic substrates and the release of hydrochloric acid during reductive dechlorination cause pH decrease and associated loss in reductive dechlorination activity. We are 1) investigating the effects of low pH on anaerobic reductive dechlorination and 2) working on enriching or isolating dechlorinators which can perform chlorinated solvents degradation at low pH condition.

Changes of terrestrial organic matter inputs to Colville River Delta sediments over last ~500 years, Beaufort Sea, Alaska

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The Colville River is the largest North American Arctic River, both in terms of freshwater and sediment load, that drains only continuous permafrost environments. It provides a unique signal of historical records of terrestrial organic input to climate change. One core collected from the delta and spanning around 550 years were analyzed for this study. Both bulk organic matter and fatty acids biomarker were investigated to track the provenance of organic matter in sediments and changes of terrestrial inputs over the time period of the core. Total organic carbon (TOC, 0.3~4.1%) and carbon to nitrogen ratio (C/N, 9.7~16.5) both showed an increasing trend over the past 200 years, which maybe caused by climate change. The stable carbon isotopic signatures ($\delta^{13}C$, -26.8~-26.1‰) of bulk TOC were uniformly depleted, indicating the predominant contributions of C3 vascular plant sources. The total concentration of saturated fatty acids and terrestrial-to-aquatic ratios of fatty acids (TARFA) both showed positive correlations compared with Alaska North Slope average temperature profile (unpublished data from Schreiner), suggesting higher terrestrial organic input during warm periods. These data provide a fine-scale history of terrestrial carbon input changes over the last hundreds of years in Arctic region.

Distribution and transport efficiency of domoic acid in the Santa Barbara Basin

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Domoic acid (DA) producing blooms of the diatom *Pseudo-nitzschia* have increased in frequency off the coast of California since the year 2000. Recent work has found that *Pseudo-nitzschia* cells and DA have been found at depths up to 800m in sediment traps in the Santa Barbara Basin, with DA concentrations above the allowable limit in shellfish. In this study, sediment trap samples from 150 and 540 m and water column samples from the upper 150m were collected from 2009-2011 and analyzed for *Pseudo-nitzschia* cell abundance and dissolved and particulate DA concentrations. Although highly variable, on average only 8-9% of *Pseudo-nitzschia* from the overlying 150m of the water column reach the 150 and 540 m sediment traps. An even smaller percentage of the DA in the top 150m of the water column reach the 150 and 540 m sediment traps, <1%. These results suggest that sediment trap DA concentrations, although quite high, a minimum estimate of the DA found in the water column and that DA concentrations below the ocean surface must still be taken into account when considering the long term impacts of *Pseudo-nitzschia* blooms on the ecosystem.

Illumina sequencing of fungi associated with manganese oxide deposits in karst systems

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Fungi have been observed to produce Mn(III/IV) oxides resembling buserite, birnessite, and todorokite. The trigger leading to the production of these minerals is unclear, however, they influence the environment strongly by breaking down recalcitrant carbon sources as well as offering protective barriers to the microbes that produce them. In this study, pristine and anthropogenically impacted microbial communities associated with manganese oxide deposits within two karst systems are compared and contrasted by using next generation sequencing and quantitative molecular techniques. qPCR data of sampled sites indicate that fungi are present in relatively low abundance when compared to bacteria. However, we show that not only does the input of exogenous carbon lead to increased fungal populations compared to bacteria in some cases, but can also visibly increase Mn oxides in situ. Using ultra-deep Illumina sequencing in conjunction with the QIIME pipeline, millions of paired-end fungal ITS amplicons have yielded a plethora of OTUs providing unprecedented insight into phylogenetic assemblages of this unique biome. As well as revealing genera of known cultured or enriched manganese oxidizers, such as *Acremonium*, *Cladosporum, Mortierella, Pleospora*, and *Pyrenchaeta*, a stark difference between top phyla endemic to each cave has been deciphered.