2nd Annual
Southeastern Biogeochemistry Symposium

March 28-29, 2015

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Lincoln Memorial University • Louisiana State University
Skidaway Institute of Oceanography • University of Alabama Birmingham
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Keynote Speaker

Professor Ann Pearson, Harvard University

Keynote: *“Do microbial ecosystems have trophic structure?”*

Ann Pearson is the Murray and Martha Ross Professor of Environmental Sciences at Harvard University. Her research focuses on applications of analytical chemistry, isotope geochemistry, and molecular biology to biochemical oceanography and Earth history. Through study of the “how, when, and why” of microbial processes, her work yields insight about environmental conditions on Earth today, in the past, and about potential human impacts on our future. Recent projects have focused on the carbon and nitrogen cycles and on pathways of lipid biosynthesis.

Pearson received a Fellowship for Science and Engineering from the David and Lucille Packard Foundation in 2004, a Radcliffe Institute Fellowship in 2009, and was named a Marine Microbiology Initiative Investigator of the Gordon and Betty Moore Foundation in 2012. She holds a Ph.D. in Chemical Oceanography from the MIT/WHOI Joint Program in Oceanography, where she was awarded the C. G. Rossby Award for Best Dissertation in the Program in Atmospheres, Oceans, and Climate; and a B.A. in Chemistry from Oberlin College.

Schedule

Friday March 27, 2015

Time	Event	Location
6:00 PM - 8:00 PM	Welcome Reception	CULC Rooftop

Saturday March 28, 2015

Time	Event	Location
9:00 AM - 10:00 AM	Check In	CULC Atrium
10:00 AM - 10:15 AM	Introduction and Welcome	CULC 144
10:15 AM - 11:00 AM	**Keynote: Ann Pearson** *Do microbial ecosystems have trophic structure?*	CULC 144
11:00 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 - 5:30 PM	Poster Session I	CULC Atrium

Sunday March 29, 2015

Time	Event	Location
8:30 AM -9:00 AM	Breakfast Buffet	CULC Atrium
9:00 AM -11:00 AM	Oral Session III	CULC 144
11:00 AM -12:30 PM	Poster Session II	CULC Atrium
12:30 PM -1:00 PM	Awards Presentation	CULC 144

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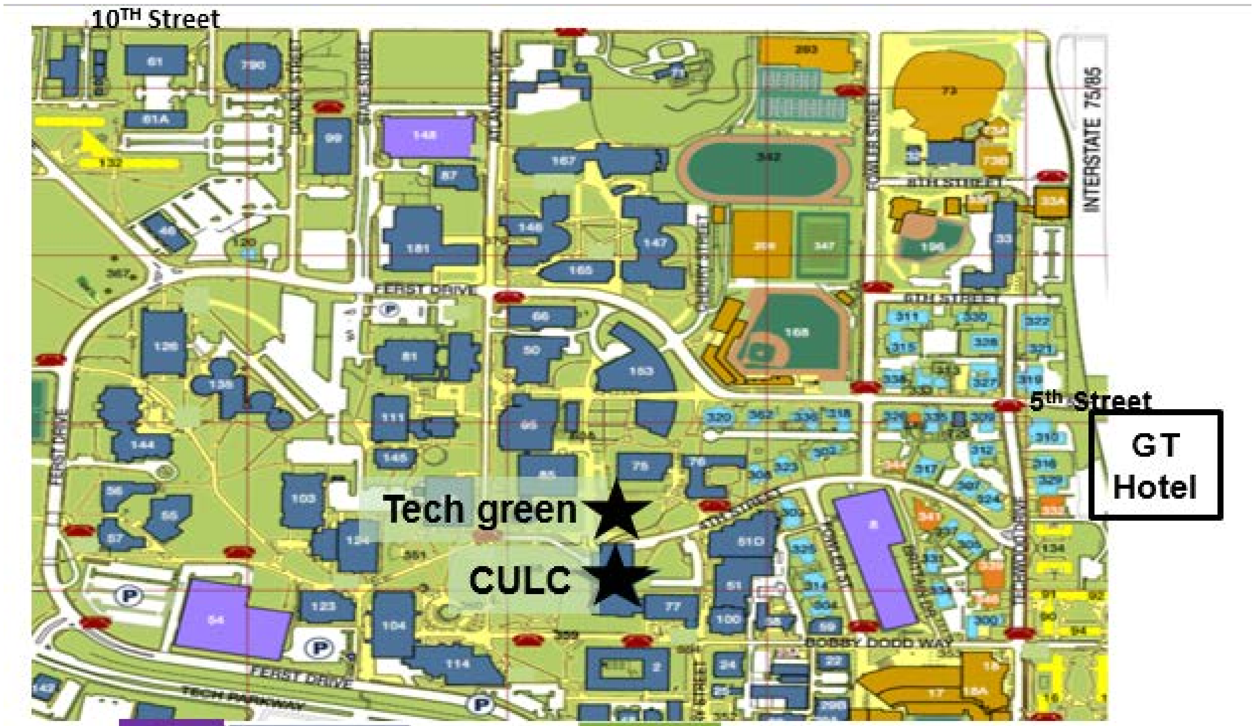
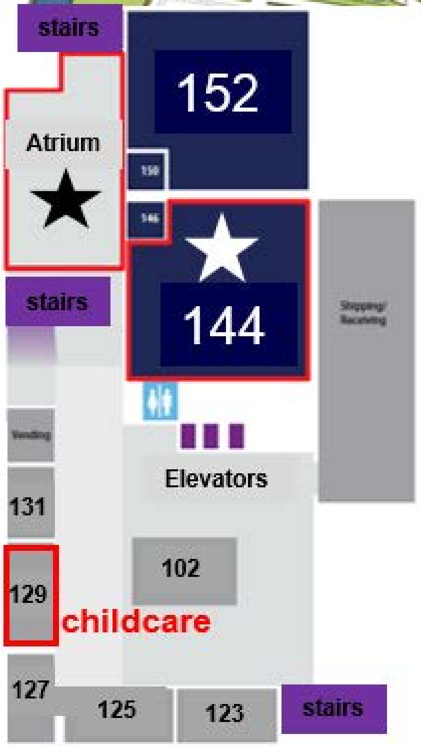
Maps





CULC 1ST floor map

CULC 5th floor map

11:00 AM

1: Microbial Sulfur and Carbon Cycling in Antarctic Sub-ice Environments

Alicia Purcell*, Jill Mikucki, Dhritiman Ghosh, and the WISSARD Science Team

University of Tennessee Knoxville

A dynamic hydrologic system exists beneath Antarctic ice, consisting of subglacial lakes and streams, some of which ultimately drain into the ocean. The Whillans Ice Stream Subglacial Access Research Drilling (WISSARD) project recently sampled two of these sub-ice environments. Subglacial Lake Whillans (SLW) is a subglacial lake 801m beneath the Whillans Ice Stream, West Antarctica. Hydrologic models indicate that SLW drains into the grounding zone, the second target of WISSARD. The grounding zone is the area where the ice stream begins to float on the ocean. Low rates of sulfate reduction and amplification of key genes involved in dissimilatory sulfate reduction and oxidation indicated a sulfur cycling community in SLW surficial sediments dominated by sulfur oxidizers. Sulfur oxidizers would provide chemosynthetic energy to this permanently dark environment. Understanding the uptake and respiration of amino acids in freshwater and marine environments has indicated the dynamic use of amino acids as carbon and nitrogen sources in oligotrophic environments. Incubations with radiolabeled mixed amino acids in SLW and at the grounding zone provided uptake and respiration rates that vary in the water column and surficial sediments. Understanding microbial activity in these sub-ice environments will elucidate the contribution of subglacial outflow to global biogeochemistry.

11:15 AM

2: Observation within Individual Cells of the Calcite-storing Giant Sulfur Bacterium *Achromatium*

Tingting Yang*, Wallace Ambrose, Andreas Teske, Robert Bagnell, Daniel Buckley, and Steve Zinder

University of North Carolina Chapel Hill

Achromatium is a large sulfur-oxidizing bacterium that can oxidize sulfide to elemental sulfur and eventually to sulfate to conserve energy. The most striking features of *Achromatium* are its intracellular granules of calcite for which the formation mechanism and function are largely undecided. *Achromatium* plays a key role in the carbon and sulfur cycles of aquatic sediments in both freshwater and brackish systems but have been poorly described in marine systems. Here, we investigated *Achromatium* cells found in intertidal ponds of the Little Sippewissett Salt Marsh (Falmouth, Massachusetts). Most *Achromatium* cells were found at the sediment surface, which contained oxygen during the day and dissolved sulfides at night. By using scanning electron microscopy (SEM) and scanning electron microscopy-energy-dispersive X-ray spectroscopy (SEM-EDS) which made it possible to map calcite and sulfur intracellularly, the S:Ca ratio was compared between freshly collected *Achromatium* cells and those incubated in oxic sediment. The results indicated the fresh cells contained lower S:Ca value and different morphology than the cells that were incubated. Surprisingly, EDS analysis of numerous small and large granules inside *Achromatium* cells detected calcium but not sulfur in these intracellular granules; sulfur appeared to be distributed through the interstitial spaces between the calcite granules. These results call for an in-depth polyphasic examination of intracellular inclusions found within *Achromatium* cells, and indicate that these large sulfur bacteria can persist under physiological regimes where intracellular sulfur globules are not detectable.

11:30 AM

3: Co-existence of Thiols and Dissolved Iron Species in Coastal Marine Sediments

Eryn Eitel* and Martial Taillefert

Georgia Institute of Technology

Thiols have been proposed to represent efficient electron shuttles in the microbial reduction of Fe(III) oxides as they rapidly reduce Fe(III) oxides abiotically. Indeed, addition of cysteine to pure cultures has resulted in elevated rates and extent of iron reduction suggesting that a microbially-driven thiol cycling may play an important role in the anaerobic respiration of Fe(III) oxides. Interestingly, the prevalence of thiols in the iron reduction zone of natural sediments has not been previously investigated. In this study, salt marsh sediments from Skidaway Island, GA were collected to determine the pore water concentration of thiols and the distribution of the main redox species involved in the transformation of natural organic matter. Four thiols were consistently detected in the pore waters of a variety of sediment across this marsh environment. Three of the thiols reached maximum concentrations in zones of Fe(II) production, while the fourth resulted from sulfidic degradation of plant material. The co-existence of these thiols with Fe(II) as well as soluble organic Fe(III) complexes suggests these electron shuttles are involved in microbial iron reduction, possibly via reduction of organic-Fe(III) complexes produced during the non-reductive dissolution of Fe(III) oxides as proposed for iron-reducing bacteria of the genus *Shewanella*.

11:45 AM

4: Bacterial Community Analysis: Evidence for the Biogenic Origin of the Manganese-Enriched Layer in Lake Superior Sediments

Christine Palermo* and Maria Dittrich

University of Toronto

Lake Superior sediments contain manganese (Mn)- and iron (Fe)-enriched layers that form at specified depths determined by a balance between the downward flux of oxidants and the upward flux of reductants. The roles of bacteria in redox reactions with Mn and Fe are known to be significant, but limited data are available about the indigenous microbial communities in many freshwater environments. This study examined the bacterial communities of Lake Superior sediments in order to evaluate the biogenic origin of Mn-enriched layers. 16S rDNA pyrosequencing revealed that the Mn-enriched layer, compared with the Fe-enriched layer below, exhibited higher bacterial diversity and a higher proportion of classes with known Mn oxidizing members. These classes included Alphaproteobacteria and Betaproteobacteria, containing members of the genera *Pedomicrobium* and *Hyphomicrobium*. The potential for anaerobic Mn oxidation occurring in the Mn-enriched layer was investigated using enrichment cultures, 16S rDNA pyrosequencing, and high resolution electron microscopy and spectroscopic mapping. Electron microscopy revealed bacterial cells encrusted with structures resembling biogenic Mn oxides, suggesting that the accumulation of Mn is linked to bacterial cells. Pyrosequencing of enrichment cultures suggested that these bacteria may be *Bacillus* species, indicating that Bacillus species may be responsible for Mn oxidation under fluctuating redox conditions.

12:00 PM

5: p450nor Amplicon Sequencing Reveals the Spatiotemporal Dynamics of Soil Fungal Denitrifier Communities

Steven Higgins*, Robert Sanford, Joanne Chee-Sanford, Allana Welsh, Luis Orellana, Kostas Konstantinidis, and Frank Löffler

University of Tennessee Knoxville

The nitrogen (N) cycle is Earth's most disrupted biogeochemical cycle. Human technology has altered the N cycle, resulting in increased soil N inputs (e.g., fertilizers) and microbial activity responsible for greenhouse gas release from soils. Denitrification, the formation of gaseous products from nitrate or nitrite, is implicated in increased nitrous oxide (N_2O) release from soils. Although prevailing dogma suggests Bacteria dominate N_2O production, recent evidence implicates Fungi in substantial contributions to soil N_2O emission. Molecular tools to assess fungal denitrification are lacking but needed for elucidating fungal contributions to N_2O formation. Therefore, the diversity of fungal denitrifiers in 62 samples from agricultural soils (Havana and Urbana) in the Midwest cornbelt were examined. The p450nor gene (nitric oxide reductase) was amplified with new primers followed by Illumina MiSeq sequencing. Analyses revealed 78 p450nor OTUs with consistently greater diversity in Urbana soils than Havana soils. Soil moisture and pH were significant drivers of p450nor communities between sites and differences in OTU relative abundances between sites were observed. The p450nor gene-targeted sequencing approach is a novel and useful tool to investigate fungal denitrification in soils, and provides an alternative to shotgun metagenomics, which failed to detect fungal denitrifiers in Havana and Urbana soils.

12:15 PM

6: Mineralogical Constraint of Reverse Weathering Reactions

Emily Saad* and Yuanzhi Tang

Georgia Institute of Technology

Despite the abundance and necessity of Si, aspects of the global Si cycle remain poorly constrained such as the role of coastal regions as a reservoir of reactive Si and the ultimate fate of biogenic silica produced in oceanic surface waters. Consequently, the global biogeochemical Si cycle remains unbalanced. The reverse weathering of biogenic silica to form authigenic clay minerals may act as an unconstrained component of this cycle. The objective of this study is to characterize the biogeochemical reactions involved in the formation of clay minerals during reverse weathering. Initial experiments were performed with varying pH (4.0 and 7.0), Fe(II) concentrations, and combinations of solid phases (amorphous aluminum oxide, ferrihydrite, biogenic silica) under anoxic conditions. Bulk aqueous analysis and solid phase characterization (e.g. electron microscopy) indicate the gradual surface transformation of the silica to Fe(II) rich aluminosilicate phases at pH 7.0 after 3 months of batch reaction. This study provides further constraint of diagenetic processes that occur in typical coastal sediment conditions, which will allow for quantification of reverse weathering in the global Si budget.

12:30 PM

7: The Magnesium Isotopic Composition of Foraminifera: Implications as a Paleoclimate Proxy

Angela Dial*, Sambuddha Misra, Vincent Salters, and William Landing

Florida State University

Accurate records of variations in climate and geochemical processes are limited by proxy robustness. A common and reliable archive used to reconstruct these variations is foraminifera. Over the past 65 Myr (Cenozoic Era), foraminifera have revealed information on global temperature and ice volume ($\delta^{18}O$), ocean pH ($\delta^{11}B$), and chemical weathering of the Himalayan Mountains ($^{87}Sr/^{86}Sr$ and $\delta^{7}Li$). Chemical weathering is of particular interest because the weathering of silicate minerals results in a net removal of atmospheric CO_2, therefore acting as a major control in the global carbon cycle over geological timescales. Since chemical weathering involves primarily carbonate ($CaCO_3$) and silicate (Mg_2SiO_4) minerals, constraining proxies for solely silicate weathering can be difficult. Magnesium is a major cation in silicate minerals and can potentially be a proxy for silicate weathering through time. The present study investigates the Mg isotopic composition in foraminifera to determine whether this isotopic system can be used as a paleoclimate proxy. We analyzed 78 core-top planktonic foraminifera, including 13 species, with an average of $\delta^{26}Mg = -4.63 \pm 0.55‰$ (2σ). Our study demonstrates that there is not species-specific variability. Biomineralization, however, influences the Mg isotopic composition of foraminifera, giving it a distinct value from inorganic calcite ($\delta^{26}Mg = \sim -3‰$).

12:45 PM

8: Why do Dissolved Oxygen Concentrations in Tropical Oceans Increase in a Warming Climate?

Yohei Takano*, Curtis Deutsch, Hartmut Frenzel, and Takamitsu Ito

Georgia Institute of Technology

Global warming and the associated climate change are expected to decrease global mean dissolved oxygen concentrations and the expansion of oxygen minimum zones (OMZs) in tropical oceans. However, the state-of-the-art Earth System Models output shows that dissolved oxygen concentrations in the OMZs of tropical thermoclines are relatively stable or even increase in a warming climate. Changes in dissolved oxygen are determined by the sensitive balance between the lower solubility of dissolved oxygen and reduction in biological consumption. Sensitivity experiments based on an ocean model showed that ocean heating and a decrease in tropical trade winds are the key factors in understanding these counter-intuitive changes in dissolved oxygen in the tropical oceans. Further analysis based on the results from sensitivity experiments revealed the importance of a decrease in water mass age (i.e. ventilation time scale since a water mass leaves the surface) under the warming climate. A decrease in water mass age leads to reduction in cumulative biological loss of dissolved oxygen. On centennial time scales, these dynamics are predicted to lead to a reduction of anoxia in the ocean, even while oxygen is steadily declining globally.

2:00 PM

9: Surface to Depth Transfer Efficiency of the toxic *Pseudo-nitzschia* and Domoic Acid in the Santa Barbara Basin, California

Blaire Umhau*, Claudia Benitez-Nelson, Clarissa Anderson, Robert Thunell, Alexandra Burns, and Christopher Burrell

University of South Carolina

Domoic acid 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 domoic acid have been found at depths up to 540 m in sediment traps in the Santa Barbara Basin, with domoic acid concentrations above the allowable limit in shellfish. From 2009-2011, samples were collected from the upper 150 m of the water column, sediment traps at 150 and 540 m, and from a sediment core collected in 2012. Samples were analyzed for particulate and dissolved domoic acid concentration and *Pseudo-nitzschia* cell abundance. Although only a small percentage of *Pseudo-nitzschia* cells (8-9%) and domoic acid (<1%) from the surface reach the sediment traps, the amount that persists in the environment remains ecologically important. The sediment core shows an increase in domoic acid and *Pseudo-nitzschia* concentrations beginning in the 1990's, consistent with changes in the 540 m sediment trap record and nutrient and production indices that suggest changes in overlying water chemistry have occurred over the past several decades in the Santa Barbara Basin.

2:15 PM

10: Evidence for Shifts in Nutrient Transfer with Range Expansion of Black Mangrove *Avicennia germinans*

Aaron Macy*, Just Cebrian, Ken Heck, Josh Goff, Whitney Scheffel, Shailesh Sharma, Eric Sparks, and Dottie Byron

Dauphin Island Sea Lab

With milder winter temperatures as a result of climate change, the black mangrove *Avicennia germinans* has been extending its range northward in the Gulf of Mexico (GoM) and supplanting *Spartina alterniflora* salt marsh. Both species are ecosystem engineers and often define their habitat. We tracked incipient changes to soil quality, community structure, leaf nutrient composition, herbivory preference, and decomposition rates of marsh and mangrove sites at the most northern documented extent of this mangrove range expansion. We found preliminary evidence to suggest marsh plants encountered little inhibition when trees were small and scarce, but larger trees in greater abundance exclude marsh vegetation. There were similar levels of herbivory for each vegetation species. Decomposition rates were consistently faster in senesced *S. alterniflora* leaf tissue than in senesced *A. germinans* leaf tissue, despite higher nutrient levels in mangrove tissue. Combined, these differences suggest significant changes in energy transfer through our local wetland ecosystems, with implications for carbon storage, erosion, and community structure.

2:30 PM

11: The Effects of Nitrogen Loading and Low Oxygen Conditions on the Fate of Nitrogen in Coastal Ecosystems

Mary Rogener*, Brian Roberts, Nancy Rabalais, and Samantha Joye

University of Georgia

Excess nitrogen in coastal environments can lead to eutrophication, harmful algal blooms, habitat loss, oxygen depletion and reductions in biodiversity. As such, biological nitrogen (N) removal through the microbially-mediated processes of denitrification are critical ecosystem functions that help mitigate the negative consequences of excess nitrogen loading. Denitrification can release nitrous oxide, a potent greenhouse gas, as a byproduct under some environmental conditions. To understand how excess nitrogen loading impacts denitrification, we measured denitrification in the water column of the Gulf of Mexico "Dead Zone". The Dead Zone is generated by excessive nitrogen loading from the Mississippi River, which leads to a large summer-time hypoxic/anoxic area at the mouth of the river and along the coast of Louisiana. Rates of denitrification ranged from 0.17 to 111 nmol L^{-1} h^{-1}. Maximal rates of denitrification were observed at stations with the lowest oxygen concentrations. Waters exhibiting high rates of nitrate reduction and high methane concentrations also exhibited elevated production of N_2O, a potent greenhouse gas. This suggests coupled nitrate reduction to methane oxidation, releasing N_2O as terminal product, and scrubbing reactive N and methane from the system only to release a more potent, longer lived, and ozone depleting greenhouse gas.

2:45 PM

12: Interactions between Nitrogen Fixation and Methane Cycling in a Boreal Peat Bog

Melissa Warren*, John Christian Gaby, Cecilia Kretz, Xueju Lin, Kait Esson, Peter Morton, Jennifer Pett-Ridge, Stefan Green, Jack Gilbert, Joel Kostka, and Jennifer Glass

Georgia Institute of Technology

Nitrogen fixation supplies significant nitrogen inputs to nutrient-limited peatlands. We coupled major and trace nutrient analyses, rate measurements, gene amplicon and omics sequencing to characterize interactions between nitrogen fixation and methane cycling at the S1 peat bog northern Minnesota. Total dissolved nitrogen, phosphate, and trace metal concentrations in surface peat suggested severe macro- and micro-nutrient limitation. Diazotrophy measured by $^{15}N_2$ incorporation and the acetylene reduction assay was 7-fold higher in anoxic than oxic incubations. Anoxic $^{15}N_2$ incorporation was 3-4x higher in treatments lacking acetylene. Aerobic methanotrophy was completeloraly inhibited by 1% acetylene after a two-day lag phase. The phylogenetic composition of the nitrogenase *nifH* subunit from fresh surface peat revealed notable differences between primer- vs. omics-based sequencing. Metatranscriptomes were dominated by archaeal *nifH* sequences most similar to *Methanosarcina* species, whereas metagenomes were dominated by nitrogenase paralogs. *In silico* analysis of previously used *nifH* primers showed multiple mismatches to methanogenic archaeal *nifH* genes. This study suggests that methanogenic archaea may be important soil diazotrophs that have gone undetected with previous nitrogen fixation methods due to a combination of acetylene inhibition and possible lack of amplification by common *nifH* primers.

3:00 PM

13: Effects of Agricultural Practices on the Quality of Stream Water Dissolved Organic Matter

Peng Shang* and Yuehan Lu

University of Alabama

Agricultural activities influence the quantity and quality of terrestrial dissolved organic matter (DOM) exported into the lotic water, and these influences may have far-reaching impacts on environmental and ecological processes within aquatic environments. To assess the effects of agricultural lands on stream water DOM, we characterized the amount, fluorescence properties, and the quality of DOM from six streams (second to third order) in northern Alabama. These streams drained watersheds along a gradient of percent agricultural lands ranging between 15% and 61%. Samples were collected under base flow conditions monthly since March, 2014. Results show that the concentrations of DOC and the fluorescence intensity of humic-like compounds were positively correlated with the percentage of agricultural lands within watersheds. Relative to DOM from forested streams, agricultural stream DOM comprised higher proportions of humic-like DOM and lower proportions of protein-like DOM, which may be due to that DOM was exported from shallower soil-to-stream flowpaths in agricultural watersheds, whereby lower amounts of humic compounds were removed by soil absorption. This finding contrasts with previous observations showing that anthropogenic disturbance increases the percentages of labile, protein-like compounds. During the 5 d laboratory biodegradation experiments, DOM from agricultural streams showed overall higher % biodegradable DOC, indicating that DOC biodegradability was driven more by elevated concentrations of inorganic nutrients (i.e. nitrite, nitrate, and phosphorus) than by DOM composition.

3:15 PM

14: Biodegradation of Dispersed Oil at Low Seawater Temperature (5°C): A Comparison of Chemistry and Microbiology

Deni Ribicic*, Roman Netzer, Anna Lewin, and Odd Brakstad

University of Tennessee and Norwegian University of Science and Technology

Treatment of oil spills with chemical dispersants may result in small oil droplet dispersions that can enhance biodegradation. The objective of this study was to characterize microbial community associated with the biodegradation of oil compounds in seawater dispersions at cold-environment temperatures. A dispersion of a crude paraffinic oil with defined droplet size was generated in natural seawater from a Norwegian fjord. Samples and sterilized controls with 3 mg/L dispersion were incubated at 5˚C for up to 64 days. Targeted n-alkanes and aromatic hydrocarbons were quantified by GC-FID and GC-MS. Microbial counts were performed by epifluorescence microscopy and by most probable number (MPN) analyses of heterotrophic and oil-degrading prokaryotes. Bacterial community analyses were performed by 16S rRNA gene amplicon sequencing. Total cell counts and MPN results showed increased bacterial activity and growth. Peaked concentrations corresponded to the degradation of n-alkanes and aromatic hydrocarbons which were biotransformed >95% after 31 days. While n-alkane degradation became slower with increased molecular size, aromatics degradation was related both to ring numbers and alkyl-substitution. The most abundant bacterial genera included *Colwellia*, *Oleispira* and *Spongiispira*, related with n-alkanes degradation, followed by later abundances of *Cycloclasticus*, Alteromondaceae and Flavobacteriaceae related strains, associated to degradation of aromatics.

3:30 PM

15: Diazotroph Community Dynamics in Oil-Contaminated Sands of Pensacola Beach, Florida Following the Deepwater Horizon Oil Spill

John Christian Gaby*, William Overholt,
and Joel Kostka

Georgia Institute of Technology

The Deepwater Horizon oil spill contaminated beaches along the northern Gulf of Mexico coastline. Given the high C:N ratio of oil, we hypothesized that diazotrophs would be enriched in oil-contaminated beach sands. Diazotroph abundance, diversity, and community composition were determined in sand cores taken from Pensacola Beach, Florida, where oil from the Deepwater Horizon washed ashore in June of 2010. Oiled sands sampled approximately 2 months after oil came ashore exhibited a 5-fold increase in *nifH* gene abundance (1.82 x105 *nifH* copies/ng extracted DNA) in comparison to clean sands (3.41 x104). Amplicon sequencing revealed that evenness was greatly skewed in the oiled samples by the dominance of a diazotroph whose *nifH* gene was 90% similar to that of *Ideonella dechloratans*. The number of observed diazotroph species at OTU 0.90 was 58 ± 16 in the oiled sands in comparison to 344 ± 59 in clean sands, indicating a nearly 6-fold loss of richness due to oiling. The diazotroph communities in oiled sands showed strong separation from clean sands regardless of the *nifH* primer set employed. To our knowledge, this is the first study to examine diazotroph community dynamics in oil-contaminated beach sands using a cultivation independent approach.

3:45 PM

16: High-Resolution Fluid Advection Rate Estimates from Natural Oil and Bubble Seeps in Deep Ocean Systems: An Examination of Heterogeneity

Leigha Peterson*, Richard Peterson, Samantha Joye,
Christof Meile, Joseph Montoya, and Sarah Weber

Coastal Carolina University

Natural hydrocarbon seeps along the ocean floor supply the overlying water with diffuse carbon and nutrient loads. These deeply-sourced fluid seeps provide critical biogeochemical constituents supporting chemosynthetic communities around the discharge features, yet our understanding of the rate of fluid and material supply relative to the nature of the discharging fluid is limited by our current methods to constrain flux estimates. Remote sensing techniques used to quantify hydrocarbon discharge offer large-scale estimates without characterizing small-scale seepage variability that is important in shaping benthic and pelagic ecosystems. Here, we present a novel method coupling *in situ* pore fluid profile ^{224}Ra observations with laboratory ^{224}Ra ingrowth experiments from several oil and methane rich Gulf of Mexico benthic environments. Using a natural, conservative radiotracer with a 3.6 day half-life, we constrain in-situ production and decay rates of the porewater entrained radium, for each layer in a given profile for use in a 1-dimensional advection-diffusion equation to generate surficial fluid flux estimates to overlying waters. Results indicate advection rates on the order of tens to hundreds of centimeters per day with a high degree of spatial heterogeneity both within sites and among sites (e.g. oil versus methane seeps).

1: Development of a Reverse Flow Injection Analysis Method for the Detection and Quantification of Nanomolar Ammonium in the Oligotrophic Ocean

William Abbott*, Rob Massarini, and Kent Fanning

University of South Florida

Ammonium is the most reduced and bioavailable form of inorganic nitrogen for assimilation by marine microorganisms. Detection and quantification of low levels of ammonium in the surface ocean can enhance the understanding of the marine ecosystem and the greater impacts of primary production on the environment such as carbon sequestration. Current methods for open ocean measurements of ammonium on a nanomolar scale are not capable of long term deployments or do not adequately correct for background interference in the signal. Reverse flow injection analysis is capable of removing background fluorescence from each seawater sample and allows for a detection limit of approximately 6 nM (calculated as 3 times the standard deviation of replicate blanks). On a reconfigured high sensitivity nitrogen analyzer developed in house, a sulfite-formaldehyde reagent is mixed with a sample stream and then injected with an o-phthaldialdehyde (OPA) reagent before being heated. Fluorescence of the sample stream is measured before and at the peak of the OPA injection, differentiating the background fluorescence from the analyte signal. Experiments to optimize the instrument configuration were conducted: parameter selection, linearity across dynamic range, salinity effects and interference species. The developed method offers robust advantages to achieve long-term deployments for high resolution analysis of low nutrient seawater.

2: Insights into the Adsorption of Arsenates on γ-AlOOH: A Flow-Adsorption Microcalorimetry Study

Nicholas Allen*, Christopher Tran, Adrian Gale, and Nadine Kabengi

Georgia State University

Arsenate poisoning is a serious problem in soil regions with naturally high arsenic concentration. The arsenates from natural sources leach into groundwater, causing cases of arsenic poisoning worldwide. This study focuses on investigating the binding interactions between various arsenate ions and a commonly occurring aluminum oxyhydroxide, boehmite (γ-AlOOH)). In addition to inorganic arsenates at different protonation states, experiments will also employ two of the most prevalent methylated arsenate species: monomethylated arsenate (MMA) and dimethylated arsenate (DMA). Analysis will be carried out using flow adsorption microcalorimetry (FAMC). By observing trends in the molar heats of adsorption in repeated adsorption and desorption cycles, experimental data will be used to discern aspects of both inner- and outer-sphere reactions, as well as the ratio of monodentate versus bidentate complexation of arsenate to boehmite. The enthalpy data from FAMC will be used to elucidate transition states and reaction kinetics. The combined data and calculations can then be used to improve computer modeling and understanding of ionic interactions with aluminum oxyhydroxide crystal structures, as well as verify current geochemical models and theories.

3: Oil Distribution and Transformation in the Gulf Sediments after the 2010 Macondo Blowout: A Multi-Tracer Approach

Lydia Babcock-Adams*, Jeffrey Chanton, Samantha Joye, and Patricia Medeiros

University of Georgia

In the spring of 2010, ~700 million liters of oil were released into the Gulf of Mexico waters following the Macondo wellhead blowout. Surface and subsurface sediment samples collected in May, September, and December of 2010, as well as in July of 2011, 2012, and 2013 have been analyzed for biomarker and isotope compositions. Molecular biomarkers were used to calculate specific ratios in order to track chemical transformations of oil-derived compounds. Degradation ratios indicate a preferential degradation of low molecular weight n-alkanes in September 2010, followed by significant degradation of isoprenoids by December 2010. Source parameter ratios (18α-22,29,30-trisnorneohopane/17α-22,29,30-trisnorhopane, C24 tricyclic terpane/C23 tricyclic terpane, 17α,21β(H)-30-norhopane/17α,21β(H)-hopane) calculated for September and December match well to those observed for the BP crude oil, especially near the wellhead, which is consistent with the idea that part of the oil released was deposited on the seafloor. $\delta^{13}C$ and $\Delta^{14}C$ values further support the hypothesis of oil deposition onto the seafloor peaking in late fall 2010. Interpretation of results is complicated by inputs of oil from natural seeps, use of dispersants in the early stages of the spill, and transport of sediments via bottom currents.

4: Biogeography of Microbial Organic Matter Breakdown in the Central Arctic Ocean

John Paul Balmonte* and Carol Arnosti

University of North Carolina Chapel Hill

The shrinking 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 geographically, with depth and with sea-ice, we compared the enzymatic capabilities of natural microbial communities from high Arctic regions subjected to different sea-ice regimes, from open water to fully ice-covered. We used a suite of peptide and polysaccharide substrates—which represent natural compounds found in marine dissolved organic matter pools—to investigate substrate utilization patterns of Arctic microbial communities. We find that total hydrolysis rates of peptide substrates are higher in open water and partially-ice covered regions, and lower in the fully ice-covered stations. In addition, the spectrum of hydrolyzed polysaccharide substrates are more similar in geographically-near regions. These measurements of microbial heterotrophic activity are among the first in the Central Arctic and point to a biogeography in the capabilities of Arctic microbial communities to access different pools of marine dissolved organic matter.

5: Iron Reduction Rate Increases during Shorter Redox Fluctuations in Slurries of Luquillo CZO Soils

Diego Barcellos*, Jared Wilmoth,
and Aaron Thompson

University of Georgia

Interactions between soil organic carbon and soil iron phases can influence how much carbon is mineralized stabilized in soils. A key influence on Fe-C interactions is shifts in O_2 concentration in soils, which can alternate oxidation and reduction of soil Fe. Our overall research question is how fluctuations in soil redox influence the nature of Fe-C interactions and the stabilization or destabilization of carbon? In this work we examined how the frequently redox fluctuations influence Fe reduction rates by subjecting soils from the upper 10 cm of the Bisley Watershed, Luquillo CZO, Puerto Rico, to different redox fluctuation frequencies over a 40-day experiment, fixing the time each treatment was exposed to anoxic vs. oxic conditions at 6:1. By measuring 0.5 M HCl-extractable Fe(II) every 12 h to 4 days we found Fe(II) concentrations increased during each anoxic cycle and decreased during each oxic cycle, as expected. However, when we changed the frequency of the redox cycles from 280 h to 70 h, the rate of Fe(II) production increased remarkably (from 0.3 to 1.0 mmol kg^{-1} h^{-1}), suggesting shorting frequencies lead to faster Fe reduction rates. Our next experiment will examine how redox fluctuations influence carbon stability by monitoring CO_2 production.

6: Bacterial-Viral Interactions and Marine Biogeochemistry

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Viruses are abundant in the marine environment, where they actively infect marine bacteria and contribute to biogeochemical cycles. Temperate bacterial viruses (phage) display two distinct lifestyles: they can either immediately lyse their hosts or they can integrate into the host genome and lie dormant until environmental conditions trigger their induction to a lytic cycle. In a limited number of well-studied phage-host systems, genome-integrated phage (prophage) have been able to provide their hosts immunity against infection by other phage. The extent to which this immunity is prevalent in marine bacteria and influences the occurrence of lytic events has not been well studied. We have isolated a marine bacterium, *Sulfitobacter* sp. CB2047, and its temperate-infecting phage (ϕCB2047-A). The bacterium contains a prophage with high sequence similarity (79% identity) to ϕCB2047-A. Interestingly, infection of *Sulfitobacter CB2047* with ϕCB2047-A results in a lytic infection, indicating the prophage does not provide immunity. In contrast, infection of a related strain of *Sulfitobacter* strain that lacks a prophage results in lysogeny. These data increase our understanding of the biotic factors that stimulate prophage induction and provide an ecologically relevant mechanism by which genetic information is transferred in the marine environment.

7: Linkages between Particulate and Dissolved Organic Phosphorus Composition across Tidal and Seasonal Time-Scales

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and Kelly McCabe

University of South Carolina

There are few investigations that specifically focus on the linkages between the compositions of particulate and dissolved organic phosphorus (POP, DOP) and the availability of P across multiple time-scales, particularly in coastal ecosystems. In this study, molecular characterizations of marine POP and DOP were conducted over both a tidal and seasonal cycle in North Inlet, SC (a part of the National Estuarine Research Reserve System). Organic P composition was determined using a combination of analytical techniques: Solid and liquid-state ^{31}P nuclear magnetic resonance (NMR), fluorometric determination of polyphosphate (polyP), and chemical extractions for lipid-P quantification. Notably, DOP isolation was accomplished using electrodialysis and reverse osmosis. Preliminary results from this work will be presented with differences in P speciation from winter to spring and over a range of salinities associated with a tidal cycle presented.

8: Toward Understanding the Functional Role of Deeply-Branching Microbial Communities in Marine Sediments from IODP Leg 347: Baltic Sea Paleoenvironment

Jordan Bird*, Joy Buongiorno, Hector Castro, Eric Tague, Expedition 347 Scientists, Brandi Reese, and Karen Lloyd

University of Tennessee

Microbial communities in the marine sediment subsurface are dominated by “deeply-branching” bacteria and archaea whose metabolisms remain unknown. Utilizing single-cell genomics, 16S tag libraries, and metametabolomics we characterized the deeply-branching microbial communities at IODP Exp 347 sites near Anholt Island and Lille Belt in the Baltic Sea. In addition, we present non-reactive tracer and 16S tag library data that provides the first evidence of acquisition of native single-cell genomes from low-contamination drilled marine sediments. Thirteen such single cell amplified genomes from 5 bacterial and 1 archaeal lineages were sequenced. The lineages include: *Desulfobacterium* sp., Chloroflexi, OPB41, Aminecenantes, Aerophobetes, and Marine Group II archaea. OPB41 draft genomes represent the first ever genomic sampling of this lineage, and all bacterial lineages are frequently associated with marine sediment in sequence databases. Metametabolomes provide a chemical inventory to assess the validity of proposed metabolic strategies as well as a means to further characterize sediment horizons at these sites. Presented here is evidence for putative metabolic strategies, including sulfate reduction, phenolic compound degradation, and sugar degradation pathways. Combining culture-independent techniques has allowed us to leverage multiple lines of evidence when characterizing deeply-branching communities in marine sediment.

9: Anaerobic Oxidation of Methane Coupled to Metal Reduction in Tropical Lake Sediments

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Georgia Institute of Technology

Microbial anaerobic oxidation of methane (AOM) is the dominant methane sink in anoxic ecosystems and can be coupled to sulfate, nitrate or nitrite reduction. However, many tropical methane-rich wetland environments contain very low levels of these electron acceptors. Recent geochemical evidence suggests that AOM coupled to Fe(III) reduction (Fe-AOM) occurs in marine and freshwater sediments although the microorganisms mediating Fe-AOM remain enigmatic. In this study, we enriched for Fe-AOM mediating microorganisms in sediments from Lake Matano, Indonesia, a stratified tropical lake with anoxic methane-rich deep waters. Lake Matano sediments contain abundant Fe(III) due to erosion of lateritic soils and scarce (<100 nM) nitrate and sulfate, forming ideal conditions for enrichment of microbes mediating Fe-AOM. We incubated Fe(III)-amended Lake Matano sediments from 0-5, 5-10 and 10-15 cm below the sediment-water interface in the presence and absence of methane. Methane stimulated Fe(III) reduction in initial incubations by 8-fold over nitrogen headspace controls. The dominant 16s rRNA gene sequences in methane-amended enrichments (79, 40 and 27% in 0-5, 5-10 and 10-15 cm) were Betaproteobacteria in the Rhodocyclaceae family. The enrichment with highest AOM activity (measured by ^{13}C-methane incorporation into DIC) was dominated by 16s rRNA gene sequences with highest similarity to the perchlorate-reducing bacterium *Azospira suillum* strain PS. Ongoing work is focused on culture isolation and characterization with omics and microscopy.

10: Expression of Orange Guaymas *Beggiatoa* spp. Proteins in *E. Coli* to Elucidate Nitrogen Metabolic Pathways

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Species of the family Beggiatoaceae are characterized as large, filamentous, sulfide-oxidizing bacteria growing in freshwater or marine environments. Representative members contain a large central vacuole that accumulates nitrate that could be used in sulfide oxidation. The Guaymas Basin in the Gulf of California has numerous sulfide-rich seeps and hydrothermal vents; colonies of *Beggiatoa* spp. are readily identified in these areas as mats up to several

meters in diameter. The Orange Guaymas *Beggiatoa* spp. (BOGUAY) is uncultivable, and not unique in that respect among the marine Beggiatoaceae. Physiologic experiments result in the destruction of sample material, which can only be collected from the benthic environment. To reduce the amount of initial sample material used, and maximize protein available for enzymatic assays, amplified BOGUAY gDNA was used to create recombinant-proteins in E. coli for use in cell-free enzymatic studies. Two genes currently targeted are BOGUAY_2967 and BOGUAY_2386, which putatively code for nitrite reductase and octaheme nitrite reductase respectively, and may be involved in the metabolism of stored vacuolar nitrate. The genes represent parts of a proposed nitrate reduction pathway in BOGUAY. The goal of the project is to introduce a novel approach for cell-free physiologic characterization of *Beggiatoa* metabolic pathways.

11: Coexpression of Benzylsuccinate and M-Hydroxybenzylsuccinyl-CoA Synthases in Anaerobic Aromatic Hydrocarbon Oxidation by *Geobacter daltonii* Strain FRC-32

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Fe(III)-reducing bacterium *Geobacter daltonii* is capable of oxidizing aromatic hydrocarbons anaerobically via the radical forming enzyme benzylsuccinate synthase (Bss). Annotation of the *G. daltonii* genome revealed the presence of a homologue to Bss with 76% identity named m-hydroxybenzylsuccinyl-CoA synthase (Mbs). The highly significant up-regulation of these genes in *G. daltonii* cultures grown on benzene as the sole carbon source suggested that Mbs is utilized during benzene degradation. Using site directed mutagenesis and cloning techniques, Bss and Mbs, along with their activating subunits, will be isolated and purified. The main aim of this study is to compare the catalytic activity of Bss and Mbs and to elucidate the mechanism involved in anaerobic oxidation of benzene by *G. daltonii*. We hypothesize that Mbs is used to induce the first step of benzene degradation in *G. daltonii*, methylating it to toluene using a radical s-adenosyl methionine site on its activating subunit.

12: Quantification of Archaea and Bacteria in Deeply Buried Marine Sediments from IODP Leg 347: Baltic Sea Paleoenvironment

Joy Buongiorno*, Alexander Shumaker, IODP Leg
347 Shipboard Scientists, and Karen Lloyd

University of Tennessee Knoxville

Recent work on uncultured microbes, often called microbial dark matter, in buried sediments suggests that these organisms actively participate in global biogeochemical processes. This highlights the importance of enhancing our knowledge of sub-seafloor communities. Here, we present quantitative PCR (qPCR) data on sediment samples from IODP Expedition 347 sites Landsort Deep, Little Belt, and Anholt Basin within the Baltic Sea. Primers targeting total bacteria and archaea were used to show that bacteria outnumber archaea at each site, although total microbial abundance decreases with depth. Total organic carbon (TOC) profiles suggest that organic matter loading to these sedimentary basins may play a role in microbial abundance, though the reason for bacterial dominance is not yet clear. In addition, the new phylum Bathyarchaeota (formerly Miscellaneous Crenarchaeota Group) and methanogen-like archaea (ANME) within the archaea were also targeted for qPCR. Across all sites, Bathyarchaeota are a minor component of total archaeal biomass, and decrease in abundance with depth. Finally, depth profiles of ANMEs covary with methane concentrations, suggesting that they either produce or oxidize methane. Coupling qPCR biomass quantifications with geochemistry shows promise in aiding the ongoing characterization of the Baltic subsurface biosphere.

13: Dimethylsufoniopropionate (DMSP), Osmolytes, and Oxidative Stress in *Ruegeria pomeroyi* DSS-3

Andrew Burns* and Mary Ann Moran

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Dimethylsulfoniopropionate (DMSP) is an abundant biogenic molecule in the marine environment that contributes heavily to the global sulfur cycle. Some heterotrophic bacteria—such as the Roseobacter *Ruegeria pomeroyi*—take up DMSP and metabolize it via two distinct pathways. Both pathways provide carbon and energy to the bacterium but only one pathway, demethylation, retains the sulfur group within the organism. Cleavage of DMSP produces the volatile gas dimethylsulfide (DMS), which is potentially lost from the environment and represents ~50% of global biogenic sulfur released to the atmosphere. The complete role of DMSP within the *R. pomeroyi* cell is not fully understood but it is thought to act as an osmolyte, a sulfur and carbon source, and have a role in oxidative stress.

Using *R. pomeroyi* as a model organism, we looked at how the addition of other potential osmolytes/antioxidants affected the generation of both end products of DMSP metabolism. Additionally, a cell viability assay was used to determine cell survival during oxidative stress supplemented with DMSP and alternative osmolytes. Both approaches detail how physiological conditions of the bacterium affect metabolism of DMSP and ultimately the fate of the sulfur group in the ocean.

14: Impact of Exogenous Nutrients on Biotic Mn(II) Oxidation and Biogeochemical Cycling Among Caves of the Southern Appalachian Mountains

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Manganese-oxidizing microbes are common in a variety of environments, including cave and karst systems, and can act as indicators of water quality and/or bioremediators within their natural environments. The microbial ecology of Mn oxide deposits is not well understood and even less is known about the factors that stimulate Mn-oxidizing microbes *in situ*. Preliminary results from this study suggest that bacterial Mn oxidation can be stimulated with the addition of organic acids (i.e. arabinose, succinic acid, and casamino acids), while fungal Mn oxidation can be stimulated with the addition of simple sugars (i.e. glucose and malt extract), as well as complex carbohydrates (i.e. wood, cotton and cellulose). Results also indicated that fungal growth without biotic Mn oxidation can be stimulated with the addition of carbon. This lack of simple correlation between Mn oxidation and additional exogenous carbon suggests that other environmental factors need to be considered in order to fully define the triggers of biotic Mn oxidation within cave systems. The aim of this study is to further constrain the factors that stimulate biotic Mn-oxidizing activity in situ and to determine how anthropogenic impacts can alter biogeochemical cycling within cave ecosystems.

15: Kinetics of Abiotic N_2O Production via Nitrification Intermediates and Redox-Active Metals in Seawater

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and Jennifer Glass

Georgia Institute of Technology

Nitrous oxide (N_2O) is a potent greenhouse gas that has nearly 300 times the global warming potential of CO_2. Anthropogenic activities have caused eutrophication of coastal waters that promotes N_2O production from microbial nitrification and denitrification. Abiotic reactions can also produce N_2O from intermediates in these biological processes, but the mechanism remains unclear. One such reaction is the oxidation of the nitrification intermediate hydroxylamine (NH_2OH) by Mn(IV) or Fe(III), which is thermodynamically favorable in seawater at circa neutral pH. River runoff may supply ammonia for nitrification and particulate metals; this reaction may contribute to N_2O production in coastal environments. In this study, the kinetics of NH_2OH oxidation in seawater at circumneutral pH was investigated from real time data recorded by N_2O microelectrodes. Our initial findings suggest that N_2O production is a second order reaction with respect to NH_2OH for both Fe(III) and Mn(IV) reduction. We are now in the process of calculating the rate constants from this data set. These rate constants may contribute to future models of aquatic N_2O production and can be used to determine the mechanisms of this reaction.

16: Maximizing the Recovery of Dissolved Organic Matter from Saltwater Samples with Coupled ED and PPL Resin

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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 (ED) system was constructed and coupled with a PPL resin extraction method to concentrate DOM from small volume (2 to 10 L) samples by removing dissolved salts. Seawater samples were processed by preforming a PPL extraction and saving the waste to run on the ED system. DOM recoveries are up to 82% when processing the samples with PPL then ED and 76% when processing with ED followed by PPL. The recoveries with this coupled process generally increased the recovery of DOM by approximately 8% when compared to only processing on the ED and 12% when compared to only PPL. ED and PPL were chosen to be coupled since they preferentially extract complementary subsets of compounds. ED has an affinity for larger uncharged particles while PPL better extracts the smaller charged particles. This means processing a sample using PPL then ED will maximize the recovery over the entire spectrum of compounds.

17: Impact of Clay Flocculation of Algal Blooms on Pond Microbial Community

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One of the major environmental concerns of clay flocculation in harmful algal blooms control is the ecological impact of the clay and modified clay. Here we investigated the impact of the clay flocculation technique on the microbial composition in water samples collected in June 2014 at eutrophic ponds in Datong, China. Successional changes in the microbial community structure due to the clay flocculation for algal cells removal were determined by deep sequencing of 16S rRNA genes. Quantitative PCR was used to quantify the biomass in water samples. In addition, total phosphate, soluble reactive phosphate, total nitrate, NH_4-N, and NO_3-N were measured. The 16S data revealed that microbial community structure significantly changed after clay flocculation in pond water. Water samples were dominated by Actinobacteria, Spartobacteria, Betaproteobacteria, Acidimicrobiia, and Synechococcophycideae before clay flocculation, whereas Actinobacteria, Sphingobacteriia and Betaproteobacteria were dominant during the first 10 days after flocculation, and Actinobacteria decreased dramatically in the following 5 days. Deltaproteobacteria as well as Gammaproteobacteria and Bacilli were dominant in water samples on the 11th day and 15th day. In addition, the total coliform test results indicated a decrease of indicator bacteria after clay flocculation. This study provides an ecological impact assessment of clay flocculation for harmful algae blooms in pond water.

18: The Genome Sequence of a Psychrophilic *Marinobacter* Strain Reveals Insights for Adaptation to Blood Falls, a Cold, Hypersaline, Antarctic Subglacial Ecosystem

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and Jill Mikucki

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Psychrophiles are organisms with an optimal growth temperature at or below ~15°C. These slow growing, cold-loving organisms are underrepresented in culture collections, with relatively few samples from Antarctic subglacial environments. This is due to difficulty in accessing subglacial materials below thick ice covers. Here we present a physiological and genome characterization from *Marinobacter* sp. strain BF05_4, the first Antarctic subglacial isolate genome to be sequenced. BF05_4 was isolated from Blood Falls, a cold, saline, iron-rich subglacial outflow of the Taylor Glacier in the McMurdo Dry Valleys, Antarctica. BF05_4 is a psychrophile and moderate halophile containing genes encoding potential low temperature adaptations, including translation and protein folding efficiency. Genes encoding proteins for compatible solute biosynthesis and transport are important for saline environments and were found in BF05_4. BF05_4 produces increased concentrations of membrane unsaturated fatty acids for maintaining cell membrane fluidity. *Marinobacter* species have been isolated from other cold and saline environments in the McMurdo Dry Valleys and permanently cold environments globally. The genetic mobile elements in BF05_4 could provide it with adaptations to various environments through gene disruption and rearrangement. Descriptions of isolates, such as BF05_4, from subglacial environments are important in understanding how ecosystems can survive below glaciers.

19: Contribution of Diazotroph Nitrogen to Particulate Organic Matter and Mesozooplankton Related to Diazotroph Diversity in the Southwest Pacific

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The Southwest Pacific Ocean is characterized by its high oligotrophy and nitrogen (N) limitation. Even though a variety of diazotrophs, including *Trichodesmium* spp., unicellular cyanobacteria and gammaproteobacteria, have been reported to occur in this region, studies on diazotrophs in these waters are still scarce and none have evaluated the actual contribution or efficiency of diazotrophic nitrogen (ND) transfer through planktonic food webs for this region. In this study, we use the natural abundance of ^{15}N to estimate the contribution of ND to suspended particles (PN) and mesozooplankton in the context of diazotroph diversity along a track extending from the Australian East Coast to a point in between Fiji and the Vanuatu islands. We found that biological N_2 fixation is a major source of nitrogen, supporting both primary and secondary production in the South West Pacific with ND contributions reaching up to 100% in PN and up to 54% in zooplankton. Strong spatial variations were observed and suggest that nitrogen derived from *Trichodesmium* spp. and picoplanktonic-UCYN are more efficiently transferred to the ecosystem than ND coming from nanoplanktonic-UCYN. ND transfer efficiency also varied between mesozooplankton size fractions, and larger mesozooplankton (1000-4000 µm) incorporated more ND than smaller mesozooplankton.

20: Phytolith Content Variability for Short-Form *Spartina alterniflora* in the Northern Gulf of Mexico

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Salt marshes provide a variety of ecologically important services and are regions where carbon, nitrogen, phosphorus and sulfur undergo complex biogeochemical transformations. While less studied, in the last decade there has been an increased understanding about how these regions alter silicon during travel from its continental origin to the ocean, and silicon cycling in these regions has been shown to be highly dynamic. Silicon can be stored in plants as phytoliths. Determination of phytolith content in the grass *Spartina alterniflora* has been made in the northeastern United States marshes but few data are available from Gulf of Mexico, despite nearly half of the salt marshes in the United States occur in this region. Here we discuss changes in the phytolith content of short-form *Spartina alterniflora* during a growing season (May through September) at multiple sites on Horn Island, Mississippi—a long and thin barrier island that is part of the Gulf Islands National Seashore. During this period, temperatures increased to >30°C and salinity was dynamic. Our aim is to determine whether phytolith silica is variable among the sites (<0.5 km spatial scales) and over monthly time scales in response to the strong changes in environmental forcing.

21: Quantifying Nutrient Fluxes in Relation to Water Budgets for Two Stormwater Detention Ponds in Coastal South Carolina

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Due to their ability to retain pollutants and minimize nutrient impact on surrounding water bodies, stormwater detention ponds are commonly used stormwater management practices. Stormwater engineers construct ponds to moderate peak flow intensities and to allow residence time of the water within the pond to enhance nutrient removal prior to discharging into surrounding rivers. This study aims to compare hydraulic effectiveness of two stormwater detention ponds located in coastal South Carolina to theoretical design plans. A high resolution water budget is necessary to effectively quantify nutrient variability associated with seasonal rainfall events. Inflow components of the water budget include surface inflow (sheetflow runoff and engineered drainage networks), groundwater inflow, and precipitation. Outflow components include evaporation and surface outflow. Preliminary results indicate during rain events, sheet flow is the dominant contributor of nutrient inputs, with piped inflow contributing a less significant, but substantial nutrient flux. Groundwater supports a lower fraction of nutrient inflow following a rain event, but for a longer duration of time. This research aims to provide an estimate of performance expectancies in residential stormwater detention ponds as structural best management practices along coastal South Carolina.

22: The Fate and Transport of Terrestrial Organic Carbon in New Zealand Fjord Sediments: A Multiple Biomarker Approach with Global Implications

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Active margin systems have been proposed as sites of enhanced terrestrial organic carbon (OC) burial because of the shorter residence time of watershed soils and mass-wasting events that enhance carbon transport to coastal waters. In this study, we present sediment and terrestrial end-member biomarker data from three fjords in Fiordland, New Zealand. We provide comprehensive comparisons of lignin-derived phenols, fatty acids (FA), and other organic proxies for tracing the sources of organic carbon in fjords to highlight the efficiency of terrestrial OC burial, both in this system and fjords globally. A combined lignin-phenols and FA approach allowed for quantitative separation of soil versus vascular plant inputs. End-member models indicate that 31%, 35%, and 34% of OC in Fiordland sediments were contributed by marine algae, soil, and fresh vascular plants, respectively. The OC in fjord sediments was found to be less degraded compared to other coastal systems. We estimate that ~22% and ~7% of the terrestrial and marine OC buried in marine sediments occurs within fjord systems. Our results suggest that the watershed soil residence times, fjord water depth, and dissolved oxygen levels were the main factors controlling OC burial in fjord systems.

23: A Coupled Spatially Explicit Modelling Approach to Assess the Influence of Soil Erosion and Deposition on the Redistribution of Soil Organic Carbon at the Watershed Scale

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Whether soil erosion is a net source or a sink of soil organic carbon (C) is not well understood but is significant to the regional and global C cycle. Coupled spatially-explicit modelling may help quantify C fluxes and reduce uncertainty. To simulate the effects of erosion on the C cycle we developed a distributed model of soil organic C (SOC) dynamics, tRIBS-ECO (Triangulated Irregular Network-based Real-time Integrated Basin Simulator - Erosion and Carbon Oxidation), within an existing physically-based hydro-geomorphic model. tRIBS-ECO includes feedbacks among complex processes, and systematically accounts for the fate of eroded SOC across the landscape. We applied tRIBS-ECO to the Calhoun Experimental Forest, which is recovering from severe land degradation prior to the mid-20th century. A point comparison against the model SOrCERO (Soil Organic Carbon, Erosion, Replacement, and Oxidation) showed that the dynamic representation of soil erosion and management practices in tRIBS-ECO is important to SOC redistribution. Watershed-integrated soil-atmosphere C fluxes ranged from a source of 14.5 g m^{-2} yr^{-1}, to a sink of 18.2 g m^{-2} yr^{-1}. We estimated that 34% of eroded C has been replaced by C sequestration. tRIBS-ECO captures the significant influence of topography and management on the soil's capacity to serve as a CO_2 source or a sink.

24: Microbial Diversity Fluctuations within Mangrove-Associated Sediments that Harbor the Lucinid Bivalve, *Phacoides pectinatus*, and their Free-Living Bacterial Endosymbionts

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Microbial taxonomic and functional diversity responsible for sulfur, nitrogen, and carbon cycling in shallow marine sediments associated with seagrass and mangroves is poorly understood. Some microbes colonizing these sediments are free-living cells that can also live in chemosymbiotic associations with lucinid bivalves. Lucinids, the most taxonomically diverse chemosymbiotic bivalves, acquire endosymbionts throughout their lifetime from the environment. Endosymbiont metagenomes from *Phacoides pectinatus* near Ft. Pierce, Florida, suggest taxonomically diverse gammaproteobacterial groups capable of sulfur oxidation, methane oxidation, and nitrate reduction. Because of the range in bacterial metabolic capabilities, and because lucinids acquire symbionts from the environment, lucinid-endosymbiont associations may be affected by changes in habitat sediment microbial communities. This study's goal was to define geochemical controls on microbial communities within sediments associated with *P. pectinatus*, and to evaluate the potential free-living symbiont reservoir. Highest *P. pectinatus* abundances occurred within the top 30 cm of sediment parallel to the mangrove coastline. Geochemical gradients differed tidally and where there was vegetation. Proteobacteria dominated the sediment microbial diversity, and gammaproteobacterial abundances differed with depth. The abundance of Gammaproteobacteria from porewaters varied, whereas sediment taxonomic changes were consistent. Free-living cells may be more prevalent in porewater, which could affect lucinid distribution and endosymbionts.

25: Particle Export and Scavenging in the Chukchi Sea Derived from ^{234}Th

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The polar waters of the Chukchi Sea are becoming increasingly exposed to sunlight, leading to alterations in the timing, magnitude, and composition of the biological food web. These ecosystem modifications will likely alter the overall nutrient load available to the Arctic Ocean, further influencing food web community structure and the exchange of organic carbon between the sediment and water column. To determine spatial and annual shifts of nutrient flux, the short lived radionuclide, thorium-234, and the disequilibrium from its parent element uranium-238, were compared to abundances of carbon, nitrogen and phosphorus, as well as total suspended particulate matter during two summer cruises as part of the ICESCAPE (Impact of Climate Change on the Ecosystem and Chemistry of the Arctic Pacific Environment) Program. The initial cruise took place during 2010 between June and July, collecting 150 thorium samples from 24 stations (4 ice cores and 22 water column). The second cruise occurred roughly one year later during the same time period, collecting 152 samples from 29 stations (3 ice cores and 26 water column). Here we will present the initial findings.

26: Alum and Rainfall Effects on Ionophores in Runoff from Surface-applied Broiler Litter

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Polyether ionophores (IPAs) are antiparasitic drugs used in broiler production and may be present in broiler litter (BL) (bird excreta plus bedding material). Long-term BL application to pastures may lead to IPA contamination of surface waters. We quantified IPA loss to runoff in response to (a) addition of aluminum sulfate (alum) to BL and (b) length of time between litter application and the first simulated rainfall event. The factorial experiment consisted of unamended (~pH 9) vs. alum-amended BL (~pH 6), each combined with simulated rainfall at 0, 2, or 4 weeks after BL application. Runoff from alum-amended BL had 33% lower monensin and 48% lower salinomycin concentrations compared to runoff from unamended BL when averaged across all events of rainfall. Delaying rainfall for 2 or 4 weeks after litter application lowered ionophore concentrations, loads and fractions lost to runoff relative to applying rainfall immediately after litter application. Our data suggest that ionophore losses in surface runoff can be reduced by adding alum to BL, or by applying BL when 2 or more weeks of subsequent dry weather are expected before rainfall.

27: The Missing Link: Characterizing Trace Elements within the Atmosphere, Sea Surface Microlayer, and Underlying Water Column

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Natural and anthropogenic aerosols are a significant source of trace elements to oligotrophic ocean surface waters, where they provide episodic pulses of limiting micronutrients for the microbial community. Opportunistic bacteria have been shown to experience rapid growth during deposition events and may influence trace element limitation for other microorganisms. However, little is known about the fate of trace elements at the air-sea interface, i.e. the sea surface microlayer. In this study, aerosols, sea surface microlayer, and underlying water column samples were collected in the FL Keys in July 2014 and analyzed for a suite of dissolved and particulate trace elements. Sea surface microlayer samples (~ 50 μm) were collected using a cylinder of ultra-pure SiO_2 (quartz glass); a novel adaptation of the glass plate technique. Total concentrations as well as fractional solubilties for the aerosols and particulate samples from the microlayer and water column were measured. Characterizing the trace metal distributions within these three regimes is an important step towards our overall goal of understanding the specific effects of aeolian dust deposition on heterotrophic microbes in the upper ocean.

28: Did the Deepwater Horizon Petrocarbon enter the Planktonic Food Web in the Gulf of Mexico?

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An unprecedented amount of ^{13}C-depleted oil and gas ($\delta^{13}C$ = –27‰ and –57‰, respectively) was released to intermediate waters of the Gulf of Mexico during the Deepwater Horizon (DWH) accident in 2010. This carbon affected a broad range of the water column, as oil/gas moved in surface slicks as well as deep plumes that spread laterally at 1000-1200m depth. In a series of cruises beginning in Autumn 2010, we measured the $\delta^{13}C$ of particles and zooplankton to assess the potential movement of petrocarbon into the planktonic food web. In 2010, methane-C had a greater impact at the depth of the plumes than oil-C did at the surface ($\delta^{13}C$ of suspended particles < –25‰), accounting for up to 25% of particulate carbon standing stock at depth. Low $\delta^{13}C$ values in small size-fraction zooplankton documented the movement of petrocarbon into the mixed layer food web, with a variable contribution of 5-15% of zooplankton biomass. In 2011, the low $\delta^{13}C$ (< –25‰) of petrocarbon appeared in particles distributed throughout the water column. Interestingly, the ^{13}C of all zooplankton size fractions decreased by roughly 1‰ between 2010 and 2011, reflecting the penetration of petrocarbon into the planktonic food web during the first year after the accident.

29: Transformation of Lignin by Coastal Marine Bacteria

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Lignin is the most abundant aromatic polymer in nature. Due to the impressive amount of carbon in this material, it offers incredible potential as a source of valuable hydrocarbon products; however, lignin's structural complexity renders it resistant to both abiotic and biotic deconstruction. While it is generally understood that lignin is predominantly degraded by fungi, we have demonstrated that bacteria of the marine *Roseobacter* lineage can utilize a pretreated lignin as a sole carbon and energy source, issuing large structural changes to the lignin biomass. In a pilot study assessing the relative ability of different roseobacters to transform lignin, we identified 4 strains that were capable of robust growth on a pretreated (Organosolv) lignin. 2D NMR analysis of the lignin before and after incubation with roseobacters suggests that these organisms modify specific features in the lignin including beta-O4 linkages, ferulate esters, as well was phenylcoumaran and pinoresinol units. Here we present data from an expanded lignin mesocosm study whose results corroborate those of the pilot study and offer additional insight into the progression of roseobacter-mediated lignin conversions over time. These findings provide an enhanced understanding of bacterial lignin degradation and offer potential to unveil novel enzymes involved in lignin deconstruction.

30: Standard Filtration Practices Significantly Distort Planktonic Microbial Diversity Estimates

Sangita Ganesh*, Cory Padilla, Shelby Gantt, Alex Huhman, D. Joshua Parris, Neha Sarode,
and Frank Stewart

Georgia Institute of Technology

Filtration is the standard method for isolating planktonic microbial biomass for analysis. It is unclear how the taxonomic composition of biomass on a filter changes as a function of filtered water volume, potentially due to filter clogging. Using seawater from a marine oxygen minimum zone, we conducted experiments to quantify the 16S rRNA gene composition of biomass on a prefilter (GF/A, 1.6 um pore size) and a downstream collection filter (Sterivex, 0.2 um) over a range of typical collection volumes, from 50 to 5000 mL. Significant community shifts occurred in both filter fractions, and were most dramatic in the prefilter community. Sequences affiliated with Vibrionales decreased from ~40-60% of the prefilter datasets at low volumes (50-500 ml) to less than 5% at higher volumes, while groups such as the Chromatiales and Thiohalorhabdales followed opposite trends, increasing from minor representation to become the dominant taxa at higher volumes. Taxa shown previously to be associated with marine particles, including diverse members of the Deltaproteobacteria, Planctomycetes and Bacteroidetes, were among those showing the greatest increase with filter volume (4 to 27-fold). Metrics of taxon richness also varied significantly with volume, and in opposing directions depending on filter fraction, highlighting potential biases in community complexity estimates. These data raise serious concerns for studies using filter fractionation to separate biomass for quantitative comparisons of aquatic microbial diversity, for example between free-living and particle-associated communities.

31: Archaeal Enrichment in the Shelfwide Hypoxic Zone in the Northern Gulf of Mexico

Lauren Gillies*, J. Cameron Thrash, Sergio deRada, Nancy Rabalais, and Olivia Mason

Florida State University

Areas of low oxygen have spread exponentially over the past 40 years, and are cited as a key stressor on coastal ecosystems. The world's second largest coastal hypoxic (≤ 2 mg of O_2 L^{-1}) zone occurs annually in the northern Gulf of Mexico (nGOM). The net effect of hypoxia is the diversion of energy flow away from higher trophic levels to microorganisms. This energy shunt is consequential to the overall productivity of hypoxic water masses and the ecosystem as a whole. In this study, water column samples were collected at 39 sites in the nGOM during the July 2013 hypoxia event, 21 of these samples were hypoxic. We characterized the microbial community along a hypoxic to oxic dissolved oxygen gradient using "iTag" sequencing and quantitative polymerase chain reaction (Q-PCR) of 16S rRNA genes and Q-PCR of archaeal ammonia-oxidizing genes (amoA). These analyses revealed that the relative abundances (iTag) of a Thaumarchaeota species 16S rRNA genes, the absolute abundance (Q-PCR) of Thaumarchaeota 16S rRNA genes and archaeal amoA gene copy number (Q-PCR) were significantly higher in hypoxic samples. The relative abundance of the Thaumarchaeota species was >40% of the microbial community in some hypoxic samples. The relative abundance of a MGII Euryarchaeota species was also significantly higher in hypoxic samples. Spatial interpolation of both the microbial and chemical data revealed a continuous, shelf wide band of low dissolved oxygen waters that were dominated by Thaumarchaeota, amoA genes and high concentrations of phosphate in the nGOM, thus implicating physicochemical forcing on microbial abundance.

32: Impacts of Cold Seeps on Nutrient Distributions in the Northern Gulf of Mexico

Kristen Goehring*, Sarah Weber,
and Joseph Montoya

Georgia Institute of Technology

The Gulf of Mexico is home to many natural hydrocarbon seeps. Our group carried out two cruises to the Gulf of Mexico in 2013 and 2014 in which we visited several of these seep sites as part of the ECOGIG (Ecosystem Impacts of Oil and Gas in the Gulf) Consortium. On these cruises, we sampled at GC600, one of the largest known seeps, as well as three other seep sites. We used CTD rosette systems and flow injection nutrient analysis to sample and measure phosphate, silicate, nitrate, and nitrite concentrations around cold seeps in the Northern Gulf. At these sites, we see

nutrient profiles that vary highly both spatially and temporally. Nutrient availability plays a central role in regulating biological productivity in marine ecosystems, and this contrast in nutrient concentrations between a major cold-seep and its environs represents a fundamental change in the biogeochemical environment. High phosphate availability will favor nitrogen fixation as a pathway for nitrogen acquisition, promoting fundamentally different nutrient dynamics in areas affected by seepage. Cold seeps may play a central role in structuring nutrient and production dynamics in offshore ecosystems of the Northern Gulf of Mexico.

33: Direct Measurement of Intracellular Carotenoids in Macroalgae and Phytoplankton

Taylor Goodie*, Robert Barletta, Jeffrey Krause, and Hijrah Sabe

University of South Alabama

Carotenoid pigments are ubiquitous in nature. In marine primary producers, they serve an important function as UV-protectants and expand the spectrum of light available for photosynthesis. From a taxonomic standpoint, carotenoid distributions can be used as marker pigments, changing from species to species. In photosynthetic organisms, carotenoids are typically measured both qualitatively and quantitatively on bulk samples relative to chlorophyll concentrations, using pigment extraction followed by HPLC analysis. While sensitive and selective, this approach is destructive and requires a large amount of biomass. Further, it provides no information on variance within a given population. This limitation precludes a systematic study of environmental factors as well as the impact of species-specific parameters on pigment production. To remedy this deficiency in characterization technology, we have investigated the use of high spatial resolution, non-destructive techniques such as Raman spectroscopy for qualitative and quantitative analysis of cell pigments. Using both cultured and wild species, intracellular fucoxanthin and β-carotene have been directly quantified using resonance Raman microscopy. In *P. antarctica,* for example, the dominance of fucoxanthin pigments within this clone was confirmed and a variation of mean fucoxanthin concentration with UV and PAR intensity of >40x was found.

34: Distribution and Fluxes of Dry Season Dissolved Organic Carbon (DOC) in Two Urbanized Versus Two Non-Urbanized Small Sub-Tropical Rivers, Tampa Bay, Florida

David Gordon*, Ryan Moyer, and Amanda Chappel

Mote Marine Laboratory

Small tropical and sub-tropical rivers deliver significant amounts of carbon, to coastal estuaries and the adjacent ocean and estuaries can serve as sites of intense biogeochemical processing. Coastal development and urbanization, however, have dramatically altered the watersheds of many rivers and estuaries. Tampa Bay receives inputs from four rivers, each representing a continuum of urbanization. In this study, the dry season distribution and fluxes of dissolved organic carbon (DOC) were measured in riverine, estuarine, and coastal waters along the four major rivers draining into Tampa Bay. DOC concentrations ranged from 91–1670 μmol L^{-1} across all rivers, and no significant difference was observed between riverine end-member concentration in the two urbanized rivers (Hillsborough and Manatee R.) versus the least urbanized river (Little Manatee R.). Riverine end-member DOC was significantly higher in the Alafia River, which has undergone little urbanization, but drains a catchment with extensive phosphate mining. The Alafia R. also had the highest total flux of DOC, with no significant difference between fluxes in the Hillsborough and Little Manatee Rivers. The non-urbanized Little Manatee was the only river to exhibit an estuarine source of DOC, while both the Hillsborough and Alafia Rivers served as sinks of DOC.

35: Quantifying Extracellular Enzyme Activity in Deep-Sea Sediment from the Mediterranean Sea through the use of Fluorometric Assays

Shane Hagen*, Nagissa Mahmoudi, Andrew Steen, and Terry Hazen

University of Tennessee Knoxville

The Mediterranean Sea is home to a diverse community of heterotrophic microbes responsible for cycling much of the organic carbon that enters its waters. The subset of those organisms that utilize macromolecules produce extracellular enzymes as a means of carbon degradation. However, this hydrolytic community is poorly characterized at water column depths greater than a few hundred meters where physical properties, such as pressure and temperature, create a unique environment for influencing enzyme behavior. Here we describe enzyme activities of a suite of hydrolases in surface sediment collected at four sampling stations in the Mediterranean Sea at water depths ranging from 800-2200m. In total, nine enzymes were studied- three peptidases, one esterase, and five glycosidases. Fluorometric assays revealed alkaline phosphatase and aminopeptidase to be active on the magnitude of 100x the other enzymes studied here. Furthermore, assays revealed a significant correlation between activity and depth for a majority of the studied community, indicating adaptation to environmental conditions. A qualitative assessment of the data also showed difference in the activity of enzymes from cores taken from the same site, suggesting variability in hydrolytic potential over a short (approximately 1 m) spatial scale.

36: Microbial Diversity Analysis of Pineola Bog, North Carolina

Austin Harbison* and Suzanna Bräuer

Appalachian State University

Peat-forming wetlands are one of the largest natural sources of atmospheric methane and important contributors to global climate change. Little is known about the novel microbes in these anaerobic environments, which slowly decompose plant material and produce H2, CO2, acetate and other methane precursors. In this study, peat was collected from Pineola Bog, a relatively acidic Sphagnum-dominated bog located in Pineola, North Carolina. DNA was extracted, and analyses of microbial diversity were conducted via TA cloning and Sanger sequencing. A total of 95 sequences (~291 bp) were analyzed with 81.1% corresponding to the domain Bacteria, 15.8% corresponding to the domain Archaea and 3.2% reported as unclassified, according to the Ribosomal Database Project Classifier. Within the bacterial and archaeal domains 44.2% and 66.7% (respectively) represented unclassified species below the phylum level (80% confidence), highlighting the diversity of novel organisms at this site. Alphaproteobacteria represented approximately 12% of the retrieved Bacteria sequences, of which the clones shared low identity to a novel anaerobe in the family Hyphomicrobiacea, *Candidatus* Microrhizomicrobium pineolum strain CS4, recently isolated from Pineola Bog. Illumina sequencing is currently underway to capture a greater depth of sequencing.

37: Point of Zero Net Charge on Titanium Dioxide

Tyler Hawkins* and Nadine Kabengi

Georgia State University

This study uses Flow Adsorption Microcalorimetry (FAMC) to investigate surface charge of two common components of Titanium dioxide (TiO_2), rutile and anatase. TiO_2 is extensively used in nanotechnology for pigment and photocatalytic applications, yet little is known about how these materials behave in the soil environment. Recent studies suggest TiO_2 may act as a temporary sink for toxic metals, making these materials a pathway for contamination. The point of zero net charge (PZNC) is the point at which the anion exchange and cation exchange are equal. Determining the PZNC enables an accurate prediction of how the surface will behave under various environmental conditions. FAMC allows direct quantitative measurement of the heat of a surface reaction; these heats are directly proportional to surface charge. The pH at which the heats of cation exchange (CE) and anion exchange (AE) are equal indicates the PZNC. The heat of CE and AE were measured at pH 3.25, 5.8, and 10.0. Heats of AE were measured using 50 mM NaCl and $NaNO_3$; heats of CE were measured using 50 mM NaCl and KCl. To determine the PZNC, heat (mJ/mg sample) was plotted against pH.

38: Multi-biomarker Characterization of Particulate and Sedimentary Organic Carbon Influenced by the Amazon River Plume

Ding He*, William Berelson, and Patricia Medeiros

University of Georgia

Particulate and sedimentary organic carbon were collected along the Amazon River plume in May 2010 during high flow discharge. Sources and levels of particulate organic carbon (POC) from surface samples and from sediment traps (placed at ~150 m deep), as well as from underlying top sediments (~ 4000 m) were assessed using a biomarker approach. Major contributions to surface POC included low molecular fatty acids (saturated and unsaturated) and mono- and disaccharides, i.e., short-lived compounds and indicators of fresh inputs. These compounds are presumably derived from algal blooms (primarily diatoms) observed along the core of the plume. Solvent-extractable terrestrial biomarkers were minor in surface samples and generally restricted to stations closest to the Amazon River mouth. Interestingly, terrestrial biomarker inputs, including plant wax homologous series, di- and triterpenoids became relatively more important in the sediment traps and, especially, in the underlying top sediment samples, which better preserved the terrestrial signature of the Amazon River.

39: Surveying the Northern Gulf of Mexico Microbial Community with a Combination of Cultivation-Dependent and -Independent Techniques

Michael Henson*, David Pitre, Jessica Weckhorst, and J. Cameron Thrash

Louisiana State University

The purpose of this study is to combine cultivation and cultivation-independent techniques with biogeochemical data to survey the microbial community in the coastal Louisiana environments of the northern Gulf of Mexico (nGOM). Reported here are the preliminary findings from the first eight months of a three-year project, including the first four cultivation experiments from Barataria Bay (BT), Calcasieu Jetties (CJ), Atchafalaya River Delta (ARD), and Mississippi Birdfoot (JLB). Marine chemistry (DO, SiO_4, NH_4, NO_3, NO_2, pH) distinguished the sites indicating that each has different influences. High throughput culturing experiments resulted in 17, 15, 1, and 61 positive wells (2.3, 2.5%, 0.1%, 6.8 culturability) for BT, CJ, AD, and JLB, respectively. From this initial set, 36 of 94 cultures were capable of being repeatedly transferred. Of the cultures that have been identified via 16S rRNA gene Sanger sequencing, twelve isolates were identified as pure cultures of OM182, OM252, OM60, *Pseudoalteromonas* sp., and Glacieacola sp. from Gammaproteobacteria, *Roseobacter* sp. and Altererythrobacter sp. from Alphaproteobacteria, and Micrococus sp. from the Actinobacteria. These results will help evaluate the efficacy of the cultivation efforts, quantify seasonality of microbial communities at each site, and to assess there are unique biogeographic distributions of taxa across the nGOM.

40: Mapping the Potential for Soil Iron Reduction using Electromagnetic Induction

Caitlin Hodges* and Aaron Thompson

University of Georgia

Iron minerals play important roles in governing soil nutrient availability and carbon dynamics. Periods of intermittent anoxia (low-oxygen) in upland soils can drive microbial reduction and dissolution of iron minerals. However, quantifying ecosystem-scale iron reduction in upland soils is challenging. We hypothesized that regions of the landscape with higher conduction of electromagnetic current will exhibit a higher capacity for iron reduction. To test this, we conducted monthly surveys of three watersheds at the Calhoun Forest in South Carolina using electromagnetic induction (EMI). EMI intensity is typically correlated with soil moisture, but it is unknown if this method can predict regions of potential iron reduction. From the EMI maps we have pinpointed locations of probable anoxia and have outlined a plan for testing the iron reduction capacity of these sites using a passive iron rod sampling method. EMI holds promise as a low-effort method for better understanding the dynamics of nutrients significant to ecosystem function on a watershed scale.

41: Sediment Oxygen Demand and Benthic Nutrient Flux: Comparison of Techniques and Prediction from Sediment Constituents

Alexandria Hounshell, Camia Charniga*, Philip Murphy, and L. Kellie Dixon

Mote Marine Lab

Water quality models are often used to predict changes due to natural and anthropogenic phenomena and pollutants. The influence of sediments on the overlying water column requires the parameterization of both sediment oxygen demand (SOD) and sediment nutrient flux (NUTX). Previous determinations of demands and flux have depended on day-long incubations of in situ benthic chambers, limited to a single site per sampling day. This project compared the results of SOD and NUTX from both field incubations and laboratory-incubated cores collected from Old Tampa Bay, Florida. Bulk sediment parameters (organics, grain size, aluminum, iron, manganese, ammonium, nitrate-nitrite, total Kjeldahl nitrogen, and total phosphorus) were investigated for potential prediction of SOD and NUTX. The project demonstrated generally comparable SOD and NUTX rates from both field and laboratory incubations at most stations. SOD rates ranged by a factor of 3 or more depending on the time period selected for quantification. There was no bias between field and laboratory techniques for phosphorus fluxes. Patterns of fluxes of nitrogen and oxygen implied that observed differences may be due to heterogeneous distribution of biological influences. Significant regression models of SOD included ammonium and some measure of sediment porosity (% organics, % sand, or aluminum).

42: Biochar Stability Evaluation: Application of Thermal Analysis and Solid State NMR

Rixiang Huang*, Justin Von Bargen, William C. Hockaday, and Evan Kane

Georgia Institute of Technology

Quantitative evaluation and prediction of the stability of biochar from anthropological and natural sources are of great relevance to carbon sequestration and carbon cycle modeling. In this study, we used thermogravimetric analysis (TGA) and differential scanning calorimetry (DSC), with the help from ^{13}C solid-state nuclear magnetic resonance

*indicates presenting author

spectroscopy (NMR) to evaluate the stability of biochars from diverse sources. By correlating the thermal patterns with NMR spectra, we found that the labile and stable fractions quantified by thermal analysis were equivalent to sp3-hybridized and sp2-hybridized carbon fraction measured by NMR, respectively. Thermal stability indices calculated for the respective two fractions behaved differently. The results suggest that parameters characterizing the whole sample may not accurately reflect the stability of biochar, due to the presence of at least 2 pools of differing thermal stability and heterogeneous composition of biochar. In accordance with findings from the environmental stability of biochars, in which there is a concurrence of initial fast decomposition and long term stability, the labile fraction is likely to be responsible for the initial fast decomposition while the stable fraction contributes to the long term stability of biochar. Ancient forest fire charcoals were also tested to understand the relevance of thermal stability evaluation to environmental stability.

43: Impacts of Artificial Pulse Flooding on the Age, Composition, and Flux of Carbon in the Colorado River

Rory Kates*, Thomas Bianchi, Peter Raymond, David Butman, Karl Flessa, and Hector Zamora

University of Florida

River ecosystems receive, process, and transport organic carbon from terrestrial systems. Flooding events deliver carbon stored within soils and plant litter into rivers and streams. The influence of flood duration and intervening dry periods between flooding events on regional carbon budgets is poorly understood. A new treaty agreement between the United States and Mexico (Minute 319), signed in late 2012 to allow for greater sharing of water from the Colorado River, resulted in a planned flooding event, from March 2014 to May 2014, to release water into the dry Colorado River channel in Mexico. Here we examine carbon cycling dynamics during an artificial pulse flood within the dry lower reaches of the Colorado River, providing a unique opportunity to investigate how carbon stored within dry, arid soils becomes mobilized and reactivated with flooding and how the age and composition of stored carbon pools changes with flood progression. Bulk parameters such as the concentration and stable/radio-isotopic composition of dissolved organic carbon (DOC), and particulate organic carbon (POC) were measured along with chemical biomarkers such as lignin phenols and amino acids. The concentration of DOC and POC ranged from 3.4-6.8mg/L and 0.18-0.62mg/L, with the highest concentrations occurring during peak river discharge. Likewise, lignin phenol concentrations (Λ_8) ranged from of 0.09-1.32. Interestingly, the ratio of dissolved lignin to DOC decreased with enhanced runoff. An increased frequency of flooding events is one potential impact of global climate change, allowing greater exchange between terrestrial and aquatic carbon pools. Thus, it is critical that we improve our understanding of the influence of flooding events on carbon cycling dynamics.

44: Marine Sediment Incubations Provide Evidence for Redox Coupling of Iron and Nitrogen

Nicole Kiriazis* and Martial Taillefert

Georgia Institute of Technology

Fixed nitrogen is essential for organisms, yet scarce on Earth. In marine sediments, ammonium is produced from the decomposition of organic matter then oxidized aerobically to nitrate and nitrite (NO_x^-), which are then reduced anaerobically to N_2 by denitrification, anammox, or dissimilatory nitrate reduction to ammonium (DNRA). As NO_x^- is rapidly produced and consumed, it does not typically build up in marine sediments. In this study, incubations were conducted using sediment from the Congo deep-sea fan, 800 km from the mouth of the Congo River in western Africa, where a significant peak in NO_x^-concentration was observed almost one centimeter below the depth of oxygenation penetration in several sediment cores. The sediments were amended with ammonium to stimulate ammonium oxidation coupled to iron reduction. Over a period of 90 days, an increase in nitrate was observed in correlation with iron reduction, supporting the hypothesis that the two processes are coupled in the absence of dissolved oxygen. If confirmed, the iron-dependent anaerobic nitrification process may play an important role in the nitrogen cycle, as it could generate significant concentrations of NO_x^- to fuel denitrification either via heterotrophic denitrification or anammox in non-sulfidic environments.

45: Taxonomic and Functional Shifts in Peatland Microbial Communities Coupled to Methane Dynamics and Peat Decomposition

Max Kolton*, Xueji Lin, and Joel Kostka

Georgia Institute of Technology

Peatlands store about one-third of total terrestrial carbon. Nevertheless, the role of the microbial communities in the carbon cycle of these ecosystems remains poorly understood. Microbial communities from representative peatland sites in northern Minnesota were integratively characterized through determination of greenhouse gases emissions rates, characterization of microbial community compositions, in silico prediction of microbial functional content, and quantification of functional gene expression (*pmoA*, *mcrA*, *nifH*). The peatland microbial communities shared similar stratification with peat depth in taxonomic and functional gene diversity, pointing to 3 depth zones (acrotelm, mesotelm, catotelm). Vertical stratification in microbial communities paralleled changes in methane production rates and organic carbon composition to indicate peat decomposition. Depth zones characterized by shifting microbial community from Alpha/Gammaproteobacteria domination at the surface to a Deltaproteobacteria domination at depth, decreasing microbial diversity, and by an increase in archaeal methanogen abundance with a depth. Moreover, potential rates of methane production, methane consumption, and nitrogen fixation were positively correlated with the expression of *mcrA*, *pmoA* and *nifH* genes that codes for essential enzymes in the corresponding pathways. The similarity in microbial community structure and function among representative peatland sites probably will simplify the prediction of this ecosystem response to climatic change.

46: Microbial Diversity and Distribution in Deep Subsurface Methane Hydrate Bearing Sediments

Cecilia Kretz*, Brandi Reese, Neha Sarode, Peter Girguis, Despina Tsementzi, Kostas Konstantinidis, Frank Stewart, and Jennifer Glass

Georgia Institute of Technology

Methane is a critical chemical component of the deep subsurface. However, relatively little is known about microbial metabolisms in deep sediments containing methane hydrates. In this study, we coupled geochemical data with microbial community composition and functional gene diversity using 16S rRNA sequences and metagenomes from ODP Leg 204 Site 1244 drilled below Hydrate Ridge, offshore Oregon. We targeted four geochemically distinct depths: near surface (2 mbsf), sulfate-methane transition zone (4 and 8 mbsf), iron and manganese reduction zone (18 and 20 mbsf) and deep subsurface (35 and 68 mbsf). 16S rRNA taxonomic analysis revealed large depth-specific differences in community composition. Near-surface samples were dominated by Archaea (57% total sequences), while deeper sediments were dominated by Bacteria (51-90% total sequences). In the near-surface, archaeal sequences were dominated by Marine Benthic Group B (MBGB; 22-29%) and Miscellaneous Crenarchaeotal Group (MCG or “Bathyarchaeota”; 20%). In contrast, sequences from the deeper zones were dominated by the OP9 candidate phylum JS1 “Atribacteria” (60-87%). In the iron-manganese reduction zone, the microbial community was significantly different from bordering zones, with resurgence of uncultivated archaeal groups (10% SAGMEG, 16% MBGB). Ongoing metagenomic analysis will investigate functional gene diversity within geochemical zones of interest in deep subsurface sediments.

47: Soil Microbial Respiration and Community Structure in Response to Severe Drought and Precipitation Events

Charles Paradis*, Nagissa Mahmoudi, Damani Driver, Kaela O’Dell, Julian Fortney, Sindhu Jagadamma, Sean Schaeffer, and Terry Hazen

University of Tennessee Knoxville

There is strong evidence of an increasing trend of severe drought and precipitation events in the Unites States (US) due to greenhouse gas emissions. However, there is a considerable knowledge gap between these severe weather events and soil microbial respiration. The objective of this study was to quantify soil microbial respiration and assess microbial community structure under ambient and heavy weekly precipitation drying/wetting cycles and continuous drought conditions. Laboratory microcosms were constructed using soil native to the southeastern US. Soil moisture and CO2 were measured periodically during the 6-week experiment. Soil microbial DNA (16S rRNA) was extracted and analyzed before and after incubation. The rate of CO_2 production in the drought treatment was substantially less compared the ambient and heavy moisture treatments after 2 weeks. The cumulative CO_2 production in the ambient and heavy moisture treatments were similar. The rate of CO_2 production was substantially higher immediately after wetting of the drying soil (wetting effect) in the ambient treatment compared to the heavy moisture treatment. The microbial community taxa was similar among the treatments before and after incubation. These results suggested that extended drought may result in decreased respiration and the wetting effect becomes negligible during frequent heavy precipitation. Further, our study suggested that severe drought or precipitation events may simply decrease or increase respiration, respectively, of taxa already present rather than select for specific microbial communities.

48: Phenotypic and Genomic Heterogeneity among *Colwellia psychrerythraea* Strains from Distant Deep-Sea Basins

Stephen Techtmann*, Savannah Stelling, Dominique Joyner, Sagar Uttukar, Austin Harris, Noor Alshibli, Steven Brown, and Terry Hazen

University of Tennessee Knoxville

16S rRNA sequencing is routinely used to investigate the diversity of prokaryotes in environmental settings. Evidence suggests that microbes with nearly identical 16S rRNA genes can have genotypic heterogeneity. To better understand the diversity within a single microbial species, we characterized the phenotypic and genomic heterogeneity of three strains of *Colwellia psychrerythraea*. *Colwellia* are psychrophilic heterotrophic marine bacteria ubiquitous in cold ecosystems. We have recently isolated two *Colwellia* strains: ND2E from the Eastern Mediterranean and GAB14E from the Great Australian Bight. The 16S rRNA of these two strains are greater than 98.2% identical to the type strain *C. psychrerythraea* 34H, which was isolated from Arctic sediments. Carbon source utilization profiles for these strains were determined using the Biolog phenotype microarrays. The carbon source utilization profiles were distinct with less than half of the carbon sources being shared between all three strains. Whole genome sequencing revealed that the genomes of these three strains were quite diverse with some genomes having up to 1600 unique genes. These findings suggest that a single microbial species can exhibit substantial phenotypic and genomic heterogeneity. This diversity must be taken into account when trying to interpret 16S rRNA sequencing data from complex environmental microbial communities.

9:00 AM

17: ^{57}Fe Isotope Labelling of Reactive Fe Solid Phases during Redox Transitions in a Tropical Forest Soil using Variable Temperature Mossbauer Spectroscopy

Jared Wilmoth* and Aaron Thompson

University of Georgia

Reactive Fe solid phases collectively form a biogeochemical hub in redox transitioning environments, coupling microbial metabolism, carbon transformations and nutrient cycling. We labeled a soil from the Bisley Watershed, Luquillo Critical Zone Observatory, PR with ^{57}Fe in laboratory suspensions over a 7 d anoxic: 1 d oxic: 7 d anoxic cycle to study physical changes in the natural Fe solid phases. The Fe(II) solution generated during native microbial Fe(III) reduction was separated after the first anoxic 7 d by centrifugation and replaced by a similar aqueous solution enriched in ^{57}Fe(II). The labeled suspension was oxidized under atm air for 24 hrs and complete incorporation of the isotope into the soil was confirmed by mass spectroscopy. Mössbauer spectroscopy at 4.5 K shows added ^{57}Fe partitioned proportionately among nano-αFeOOH and paramagnetic Fe(III) detected during solid phase incorporation. Samples analyzed at 4.5 K from the end of the final 7 d anoxic period show that ^{57}Fe (III) label from each of the detected Fe(III) phases was utilized as a terminal electron acceptor during microbial Fe(III) reduction to generate Fe(II). A portion of this Fe(II) displays weak magnetic ordering and quadrupole splitting at low temperature consistent with Fe(II) on the surface and/or internal structure of short-range-order Fe(III) (oxyhydr)oxides.

9:15 AM

18: Influence of the Amazon River on Nitrogen Fixation and Export Production in the Western Tropical North Atlantic

Sarah Weber*, Edward Carpenter, Victoria Coles, Patricia Yager, Joaquim Goes, and Joseph Montoya

Georgia Institute of Technology

The Amazon River forms an extensive surface plume that extends well into the Western Tropical North Atlantic, delivering nutrients and promoting N_2-fixation and carbon sequestration far offshore. During research cruises to the Amazon Plume as part of the ANACONDAS program, we used shipboard underway seawater systems to characterize the diverse biogeochemistry and phytoplankton communities associated with surface waters. Building on previous work, we found that the aging plume supports high abundances of diatom-diazotroph assemblages (DDAs) through the delivery of phosphate and silicate to the nutrient-limited oceanic waters. Within the outer reaches of the plume, we measured significant biological consumption of Si and low δ^{15}N values in particulate organic matter, reflecting the incorporation of DDA-derived N into the food web. We additionally saw evidence for enhanced carbon export in regions with these DDA blooms.

9:30 AM

19: Expansion of the Denitrification Regime in the Eastern Tropical North Pacific from 1972 - 2012

Rachel Horak*, Bess Ward, and Allan Devol

American Society for Microbiology

The Eastern Tropical North Pacific (ETNP) is a large region of anoxic water that hosts widespread water column N loss (denitrification). There is some disagreement about the long-term trends of anoxia and denitrification in oxygen deficient regions such as the ETNP, and long-term studies of water column denitrification within the anoxic zone are lacking. In this study, we compared hydrographic measurements, water column O_2, and dissolved inorganic nitrogen (DIN) data from the ETNP in 2012 to data from the same transect in 1972, 1994, and 2007. We show that geochemical markers for cumulative N loss indicate denitrification was highest in 2012. Low oxygen conditions have expanded into shallower isopycnals from 1972 to 2012. Oxygen and N loss changes in the world's largest ODZ for 2012 could not fully be explained by the Pacific Decadal Oscillation. Finally, any increase in N loss due to vertical expansion of anoxia should be muted by a negative feedback on productivity.

9:45 AM

20: What Happens to Lignin in the Ocean? Evidence of Bacterial Lignin Degradation in Marine Microcosms

Hannah Woo*, Kaela O'Dell, Stephen Techtmann, and Terry Hazen

University of Tennessee Knoxville

The microbial transformation of allochthonous terrestrial organic matter, particularly recalcitrant aromatic lignin, is a significant but poorly understood phenomenon in the marine ecosystem. We aim to elucidate the diversity and metabolic potential of a marine bacterial community subsisting on lignin. Seawater from the oxic and ultra-oligotrophic Mediterranean Sea, near the Egyptian Nile Delta, was amended with lignin and incubated for 2 weeks. Microbial activity was assessed by CO_2 respirometry and enzyme assays. Community structure and metabolic potential of the microcosms were assessed using 16S rRNA gene amplicon sequencing, and metagenomic sequencing. Lignin amendment caused higher respiration rates and oxidative enzyme activity in comparison to the control. *Halomonas*, *Idiomarina*, *Thalassospira* spp. were several of the dominant OTUs in the microbiome. The metagenome of the lignin-amended microcosm had higher abundance of genes encoding information storage and processing, and aromatic catabolism. Conversely, the unamended control metagenome had signs of starvation conditions, such as higher abundance of genes encoding desiccation stress, spore protection, and plasmid function that were not found in the lignin-amended metagenome. We believe the positive effect of lignin on microbial activity and abundance of aromatic catabolism genes supports the notion of lignin degradation by marine microbes

10:00 AM

21: NC10 Bacteria in a Marine Oxygen Minimum Zone

Cory Padilla*, Laura Bristow, Neha Sarode, Catherine Benson, Annie Bourbonnais, Emilio Garcia-Robledo, Mark Altabet, Peter Girguis, Bo Thamdrup, and Frank Stewart

Georgia Institute of Technology

Bacteria of the NC10 phylum perform anaerobic oxidation of methane (AOM) coupled to denitrification. Nitrite, typically at nanomolar levels in oxic ocean waters, may accumulate under oxygen depletion, notably in oxygen minimum zones (OMZs) where anaerobic microbial metabolisms contribute to oceanic nitrogen loss. We test the hypothesis that denitrification-dependent AOM (D-AOM) bacteria are present and active in the world's largest OMZ, the Eastern Tropical North Pacific. 16S rRNA genes matching NC10 bacteria were detected with highest abundances between the nitrite and methane maxima. Particulate methane monooxygenase genes clustered phylogenetically with NC10 isolates, being most closely related to sequences from South China Sea sediments, suggesting a marine-specific NC10 clade. Community RNA sequencing confirmed the expression of genes with top matches to the NC10 bacterium '*Candidatus* Methylomirabilis oxyfera'. 'M. oxyfera'-like transcripts increased in relative abundance with depth into the OMZ and included genes of aerobic methanotrophy and denitrification, with high expression of nitric oxide reductase, hypothesized to play a role in an O_2-yielding dismutation reaction. These findings expand the known range of D-AOM bacteria to include the pelagic ocean, identify an unrecognized linkage between OMZ methane cycling and nitrogen loss, and suggest the potential for oxygen production in an anoxic water column.

10:15 AM

22: Environmental and Physiological Controls of DMSP Metabolism in *Ruegeria pomeroyi*

Qiuyuan Huang* and William Whitman

University of Georgia

Dimethylsulfoniopropionate (DMSP) is a compatible solute and potential osmolyte, an abundance source of reduced carbon and sulfur, and a precursor for the climatically active gas dimethylsulfide (DMS) for marine phytoplankton and bacteria. Based on previous studies of DMSP assimilation and degradation by natural populations of marine bacteria, we expected that the bacterial response to DMSP will depend first on its availability. By controlling the concentrations of DMSP, the salinity and carbon source of medium, and another potential osmolyte glycine betaine, the regulation of DMSP metabolism was investigated in *Ruegeria pomeroyi*, a cultured representative of the roseobacters with the ability to carry out both demethylation and cleavage pathways of DMSP degradation. Our results suggested that at low DMSP levels (μM range), DMSP could act as a precursor for both methanethiol and DMS. Despite the fact that DMSP could protect the cells from osmotic stress, it is not a preferred function when the DMSP concentration was low. Overall, DMSP metabolism in *Ruegeria pomeroyi* is closely related to the environmental conditions, such as DMSP availability, salinity, and carbon source.

10:30 AM

23: Metatranscriptomic Analysis of Bacterial Arsenic and Sulfur Cycling Along a Redox Gradient in Alkaline, Hypersaline Mono Lake

Christian Edwardson* and James Hollibaugh

University of Georgia

We analyzed metatranscriptomes in samples taken along a redox gradient (10-31 m, oxycline at 12-15m) in alkaline (pH 9.8), hypersaline (~90 g L-1), Mono Lake, CA, to examine changes in the composition of microbial communities and their potential contribution to biogeochemical cycles in the lake – specifically arsenic and sulfur cycles. The average taxonomic distribution of hits to protein coding sequences in the samples was 68% bacterial, 30% eukaryotic, 1% archaeal, and 1% viral. Bacterial reads were dominated by Proteobacteria (43-61%) at all depths. Bacteroidetes (14%), Actinobacteria (13%) and Verrucomicrobia (10%) were abundant at 10 m, whereas Firmicutes (18-32%) were the second most abundant at all other depths. Bacteria involved in sulfur cycling were abundant at all depths below 15m. Transcripts from two chemolithotrophic sulfur-oxidizing Gammaproteobacteria (*Thioalkalimicrobium* sp. and *Thioalkalivibrio* sp.) previously isolated from Mono Lake were the most abundant transcripts in samples from 15 to 31 m (18-27% of transcripts). Analysis of molybdopterin oxidoreductase transcripts revealed that anaerobic arsenite oxidation was dominant at 15 m compared to arsenate reduction which was more prevalent at 18 and 25 m.

10:45 AM

24: Geochemical Control of Methanogenesis in Cape Lookout Bight, North Carolina

Richard Kevorkian*, Jordan Bird, and Karen Lloyd

University of Tennessee Knoxville

We endeavored to identify the organisms that are responsible for the methane produced in marine sediments, and to determine 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, North Carolina, 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 was methane produced. Quantitative PCR data suggest that ANME-2, other Methanosarcinales, and Methanomicrobiales increase when sulfate is depleted. 16s rDNA analysis supports the increase of ANMEs and other methanogens relative to other organisms after sulfate concentrations have declined while sulfate reducing bacteria maintain similar population levels throughout the duration of the experiment. Total cell counts demonstrate a decline in cells with the decrease of sulfate until a recovery corresponding with production of methane. Our results suggest that hydrogen concentrations influence what metabolic processes can occur in marine sediments, and ANME can grow without first being given access to methane.

1: Characterization of Iron-Binding Organic Ligands in Marine Sediment Pore Waters

Jordon Beckler*, Eryn Eitel, David Bostwick,
and Martial Taillefert

Mote Marine Laboratory

Although organic-Fe(III) complexes that can provide a significant flux of Fe to the overlying waters appear to be pervasive in marine sediments, the origin of these complexes and their mechanism of formation remains unknown. In this work, a novel extraction scheme was developed to extract Fe-specific binding ligands from the bulk of pore water natural organic matter (NOM). The overall objective of this study was to attempt to identify the composition of the Fe-binding ligands to determine the source of these complexes. Fe-reactive ligands from the pore waters of a variety of sites across a coastal marsh in southern Georgia, US, were fractionated by an immobilized-metal affinity chromatography (IMAC) procedure that first eluted pore waters through Fe(III)-coated Chelex® resins to accumulate the ligands, then collected the ligands by rinsing the column with EDTA. The non-polar and moderately polar ligands were subsequently concentrated through hydrophilic-lipophilic balanced solid-phase extraction cartridges (HLB-SPE) and eluted with methanol/H_2O. Finally, liquid chromatography / electrospray ionization mass spectrometry (LC/ESI-MS) was used to characterize the fractionated molecules. Results revealed that pore waters contained a few low-molecular weight ligands (< 200 Da) that were unique to sediments undergoing microbial Fe(III)-reduction. On the other hand, natural organic matter standards (SRHA) did not generate any significant individual peaks on the LC/ESI-MS chromatograms. These results suggest that organic ligands produced during the overall microbial Fe(III)-reduction processes may ultimately be responsible for maintaining Fe(III) in a soluble form, which may ultimately flux from sediments and provide a source of a limiting nutrient to the oceans.

2: Water Swap

Ann-Marie Harik*, Stephen Techtmann, Julian
Fortney and Terry Hazen

University of Tennessee Knoxville

To determine change in microbial community structure and hydrocarbon degradation rates when placed in foreign waters, as compared to ambient waters. Microbial directed biodegradation has a large impact on hydrocarbon degradation; from naturally occurring oil seeps and from spills. The microbial communities from two separate Angola ocean waters, one surface and one deep water, were removed via 0.22 µm filter then either placed back in their original water source or placed into the other depth's water by flipping the filter and filtering the water back through it. 16S rRNA sequencing and GC analysis are being performed, we expect there to be differences in microbial community structure and hydrocarbon degradation rates of the communities in their ambient waters versus their swapped waters. If it is found that microbial community structure plays a much larger role than nutrients on biodegradation than oil drilling locations whose microbial communities are not capable of high rates of oil biodegradation will need to have a more extensive spill response than those locations whose microbial communities are well equipped. However, if nutrients are found to be the major factor then spill response procedures can include supplementing the waters with necessary nutrients.

3: Hydraulic Fracturing Flowback Water: A Look into the Subsurface Microbial Community and Intrinsic Bioremediation

Maria Fernanda Campa*, Stephen Techtmann,
Sheridan Brewer, Amanda Garcia de Matos Amaral,
Justin Wright, Nikea Ulrich, Regina Lamandella,
and Terry Hazen

University of Tennessee Knoxville

Treatment and reuse of hydraulic fracturing flowback water is the best alternative to handle the enormous volume of wastewater produced. Intrinsic bioremediation and bioaugmentation are efficient ways to treat the high salinity and chemical content of this water. The microbial community in flowback water can provide an insight into what facilitates bioremediation. Thus, raw and treated flowback waters from the Marcellus Shale were collected. The microbial community from the flowback water, and how it changes at different stages of the treatment process was determined by sequencing of 16S rRNA amplicons. Furthermore, aerobic and anaerobic bacteria with physiologies of interest were isolated. Samples were plated on marine broth and ORN7a supplemented with oil. High growth of halophilic bacteria as well as the presence of sulfate reducing bacteria was observed. The isolates will be sequenced (16S rRNA amplicon) and compared to the microbial community structure data. The isolates that are most representative of the community will be selected for high-throughput phenotypic microarray analysis. The study is currently in progress. Characterizing the microbial community structure of the flowback water and understanding its function will help develop and optimize a bioremediation strategy so that flowback water can be inexpensively treated and reused.

4: Deepwater Horizon Impacts on the Pelagic Food Web: Stable Isotope Constraints on Zooplankton Carbon and Nitrogen Sources

Drake Lee-Patterson*, Sarah Weber, Ana Fernandez, and Joseph Montoya

Georgia Institute of Technology

The offshore ecosystem of the Northern Gulf of Mexico is affected by inputs of oil and gas from natural seeps as well as accidental releases, such as the Deepwater Horizon (DWH) incident in 2010, which discharged an unprecedented volume of oil and gas into pelagic waters. We collected zooplankton from the Northern Gulf one month after the DWH wellhead was sealed and have resampled the system annually. We use stable isotope measurements to quantify the incorporation of low δ13C petrocarbon and low δ^{15}N material from nitrogen fixation into the marine food web. Immediately after the spill, we found low δ^{13}C values, particularly in the small size fraction of animals collected during the day in the mixed layer, and a shift to higher δ13C values at night. These diel changes reflect the integration of petrocarbon and recently fixed nitrogen fixation into the pelagic food web, and imply that incorporation of both petrocarbon and recently fixed nitrogen occurred primarily in the mixed layer. Zooplankton collected in subsequent years do not show consistent diel shifts in δ13C, though surface δ15N values were generally lower during the day than at night. Our data imply that the DWH spill made a measurable contribution to zooplankton production, and that this direct impact was relatively short-lived.

5: Alaskan Arctic Soils: Relationship between Microbes and Soil Composition

Hongyu Li* and Lori Ziolkowski

University of South Carolina

Carbon stored in Arctic permafrost carbon is sensitivity to climate change. Microbes are known to degrade Arctic soil organic carbon (OC) and potentially release vast quantitates of CO_2 and methane. We studied the microbial community and soil OC composition along a latitudinal transect that varied in vegetation, temperature and moisture on the North Slope of Alaska. Isotopic (^{13}C,^{15}N) and elemental analysis of bulk soil OC, the total phospholipid fatty acids (PLFA) composition were used at five sites to a depth range of 0-32cm. Surface soil (0-4cm) is generally organic rich and contains predominantly straight-chain PLFA compounds. As the soils get deeper, the relative proportion of OC decreases dramatically and decreases in bulk C/N ratios, while the proportion of branched and unsaturated PLFA compounds increase. These results indicate that the vegetative inputs to surface soils are degraded in deeper soils where microbial signals dominate. Microbial community changes as a function of location will also be discussed in this presentation. Future work includes using radiocarbon of both bulk OC and the microbial community to study the microbial incorporation of soil OC to assess microbial carbon sources as a function of composition and bioavailability of the surrounding soil OC changes.

6: Crude Oil Biodegradation and Microbial Community Changes in Deep Oceans

Jiang Liu*, Julian Fortney, Stephen Techtmann, Dominique Joyner, and Terry Hazen

University of Tennessee, Knoxville

Crude oil contamination in the ocean from oil spills becomes a huge concern to the public and governments. Very limited information is available on the oil degradation potential and microbial community response to crude oil contamination in deep oceans. In this study, we investigated the response of microbial communities to crude oil in various deep-sea basins from around the world where oil exploration is anticipated (Eastern Mediterranean Sea, Central Mediterranean Sea and Great Australian Bight). Microcosms were set up aerobically in three different conditions: seawater, seawater + oil and seawater + oil + oil dispersant (Corexit). CO_2 evolution followed a similar pattern in all of the basins sampled. The treatment of seawater + oil + Corexit had the highest CO_2 production. In addition, there was a clear succession of microbial communities during degradation of oil. The microbial diversity decreased in all of the microcosms over time. The relative abundance of Proteobacteria increased drastically while the population of archaea decreased. In particular, the percentage of Betaproteobacteria increased in samples from the Central Mediterranean Sea. However, Gammaproteobacteria increased in abundance in the microcosms from the Eastern Mediterranean Sea and Great Australian Bight, which was very similar to GOM.

7: Key Factors Controlling the Solubility of Iron in Saharan Dust

Amelia Longo*, Yan Feng, Barry Lai, William Landing, Athanasios Nenes, Nikos Mihalopoulos, Kaliopi Violaki, and Ellery Ingall

Georgia Institute of Technology

Biological productivity in many oligotrophic ocean regions is limited or co-limited by the availability of nutrient iron; in these regions, atmospheric deposition can play a key role in supplying iron. Understanding iron composition in aerosols is critical for determining the factors controlling iron solubility and ultimately its potential bioavailability to marine organisms. The Sahara Desert is a major source of iron containing dust, with traces found across the Atlantic

Ocean and Mediterranean Sea. Aerosol composition and oxidation state were investigated using iron X-ray Absorption Near Edge Structure (XANES) spectroscopy, X-ray fluorescence mapping, and measurements of total and soluble iron collected in samples from the Atlantic Ocean, Bermuda, and Crete. Bulk composition was largely iron(III) oxides, with fractions of iron phosphates, silicates, and sulfates increasing with atmospheric transport. Iron(II) is generally considered to be the more soluble than iron(III), and iron became more reduced as with increasing distance from the Sahara Desert. However, in these samples, higher iron(II) levels did not correlate with increased iron solubility. This suggest that atmospheric processes, rather than composition or oxidation state, plays a key role in the solubility of aerosol iron in Saharan dust.

8: Reconstructing Depositional Environments of the Devonian Chattanooga Shale in Northeastern Alabama Using Sedimentological and Geochemical Analyses

Man Lu*, Yuehan Lu, Takehito Ikejiri, and Ibrahim Cemen

University of Alabama

The depositional environments of the Chattanooga Shale remain controversial. In the present study, two Chattanooga Shale outcrops near Fort Payne and Collinsville in northeastern Alabama were investigated to reconstruct the depositional environments, combining sedimentological and geochemical data. The two outcrops share similar sedimentological, that is, thinly laminated fissile grayish shale strata in lower part and nearly homogeneous black blocky shale in upper part. The two outcrops also exhibit similar trends in geochemical proxies. The predominance of short-chain n-alkanes (nC15-19) over long-chain n-alkanes (nC27-31) and low terrigenous to aquatic ratio indicate that the organic matter was dominated by algal materials. Low values of ratios of pristane to phytane (1.1±0.6) with frequent fluctuations indicate that the shales were deposited in anoxic environments with episodic oxygenation. The concentrations of monomethyl alkanes (nC12-20) relative to total normal alkanes, an indicator of inputs of cyanobacteria, suggest that the inputs increased from the lower to the upper parts. Relative to the lower part, the upper part show elevated long-chain n-alkane concentrations, higher ratios of quartz to clay mineral, lower values of Pr/Ph and lower δ^{13}Corg and TOC values. These data suggest a depositional environmental shift from deeper water conditions to shallower, more nutrient-rich and anoxic conditions during the deposition of the Chattanooga.

9: Investigating the Determinants of Soil Bacterial Community Structure in a Mongolian Climate and Land-Use Change Experiment

Aurora MacRae-Crerar*, Eric Johnston, Pierre Liancourt, Laura Spence, Bazartseren Boldgiv, Daniel Song, Jack Gilbert, Sarah Owens, Jarrad Hampton-Marcell, Brenda Casper, and Peter Petraitis

University of Pennsylvania

Soils contain some of the most diverse bacterial communities and much remains to be explored about how these communities are structured. We investigated how these communities vary within a landscape between years and with warming and grazing. We undertook a multi-year experiment to test these effects on soil bacterial communities in northern Mongolia, a region where air temperatures have increased by 1.6°C since 1960 and traditional grazing patterns are shifting. We used open-top chambers and fencing to manipulate warming and grazing regimes, respectively and subsequently sequenced soil bacterial DNA from these experimental plots using the Illumina platform. We used constrained analysis of proximities to test the effects of year (2010 and 2011), slope location (lower and upper), warming and grazing on bacterial community composition, which was measured using Bray-Curtis dissimilarities. Community composition varied with year and slope, but not warming or grazing. Three environmental gradients were significant: total available nitrogen, soil temperature and moisture. These gradients could be correlated with significant phylum abundance gradients for Verrucomicrobia, Planctomycetes, and Firmicutes. Such results give us hints as to the ecological attributes of these phyla. Future analysis of 2012 data is forthcoming and, interestingly, preliminary results show a significant effect of warming.

10: Further Examination of Biogeochemical Consequences of Mesoscale Eddies in the Sargasso Sea

Israel Marquez*, Jeffrey Krause, and Michael Lomas

Dauphin Island Sea Lab

The Bermuda Atlantic Time Series (BATS) is an ongoing 25-year biogeochemical record in the North Atlantic subtropical gyre. Contemporaneous data on the particulate phases of four major bioreactive elements: C, N, P, Si only exist during two years and also for a companion project (Trophic BATS, i.e. TBATS). Diatoms, the only 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 synchronal measurements of four elements has left a knowledge gap regarding the coupling of the Si cycle with that of C, N, P. Data from BATS and TBATS provide an opportunity to improve our understanding about the coupling of C, N, P, and Si in the water column and exported material. Preliminary results suggest that the eddies positively and negatively affect water column inventories of dissolved and particulate element phases, elemental ratios of exported material, and particle residence times outside of typical seasonal observations at the BATS site since 2000. Trends were not conserved among elements, within eddy type, or among seasons; suggesting eddies can induce strong shifts in how elements are cycled in this region.

11: Characterization and Quantification of Dissolved Organic Phosphorus in Aquatic Systems

Kelly McCabe*, Doug Bell,
and Claudia Benitez-Nelson

University of South Carolina

The dissolved organic phosphorus (DOP) fraction of the marine phosphorus pool has been recognized as a significant, biologically available source of P for phytoplankton. Yet our lack of understanding regarding DOP composition and cycling has hindered efforts to understand nutrient limitation and its subsequent impacts on the marine food web. In order to constrain the composition of marine DOP, a bench-top electrodialysis (ED) reverse osmosis (RO) instrument was constructed to isolate material for chemical characterization. Recent work suggests an ED/RO instrument is highly effective for characterizing dissolved organic matter (DOM), but has not been specifically tested for DOP composition. To determine the instrument's ability to isolate various DOP compounds, artificial seawater was spiked with eight known DOP compounds (triplicate measurements of two phosphodiesters, short and long chain polyphosphate, phosphonate, and complex phospholipids) and processed using ED/RO. High-resolution time-series measurements of total dissolved and soluble reactive phosphorus (TDP, SRP, respectively) were taken to determine DOP recovery over the course of desalting, concentrating, extracting, and cleaning stages. Nuclear magnetic resonance spectroscopy (^{31}P NMR) was used to determine compound integrity following isolation. Preliminary data shows variable, but consistently high specific-compound DOP recovery (66-81%) with little to no alteration of sample integrity.

11: Extracellular Peptidase Activities in Subsurface Sediments of White Oak River, North Carolina

Katherine Mulligan*, Shane Hagen, Shannon Ryan,
and Andrew Steen

University of Tennessee Knoxville

Heterotrophic microorganisms have been observed in subsurface sediments in which the only organic matter available for metabolism is chronologically old and extensively degraded. Microorganisms produce extracellular enzymes (EEs), which break down polymeric organic matter, contributing to nutrient cycling. Extracellular enzyme activity (EEA) has previously been measured for a small number of peptidase substrates (specifically leucine-AMC) and rarely in sediment greater than 10 cm deep. This study measures EEAs for a broader range of peptidase substrates using marine sediment from the White Oak River Estuary in North Carolina from up to 82.5 cm below the sediment-water interface. The activity of ten different peptidase substrates was measured using high-throughput fluorescent measurements at various depths to determine how EEAs for various peptidases change as a function of depth. Peptidase activity was observed at all depths, and a general decrease in enzyme V_{max}, roughly proportional to cell abundance, was observed as sediment depth increased. This phenomenon possibly reflects lower microbial activity at deeper depths due to the parallel decrease in quality of organic matter as depth increases. In addition, all peptidase substrates were not hydrolyzed with equal V_{max} values, suggesting that subsurface heterotrophic microorganisms have specificities for different substrates.

12: Investigating the Effects of Shifting Phytoplankton Composition and Bacterial Organic Sulfur Sources on Dimethylsulfoniopropionate Fate in the Ocean

Brent Nowinski*, Jessie Motard-Côté, Christina Preston, Roman Marin III, Andrew Burns, Marine Landa, Ronald Kiene, and Mary Ann Moran

University of Georgia

Marine bacteria play a major role in the determining the fate of dimethylsulfoniopropionate (DMSP), a reduced sulfur and carbon osmolyte produced by phytoplankton. Upon uptake, bacteria process DMSP through either the demethylation pathway, where DMSP breakdown products remain in the marine food web, or through the cleavage pathway, in which the volatile gas DMS is produced and oxidized to sulfates that act as cloud condensation nuclei and impact global climate. The prominent hypothesis to explain which pathway is favored poses that demethylation is favored when DMSP is the dominant sulfur source present, but when other sulfur compounds are more abundant, DMSP will be cleaved. Phytoplankton vary in the types and abundances of sulfur compounds they produce, so shifts in phytoplankton community composition will alter sulfur source availability and may impact bacterial DMSP metabolism. To test this hypothesis in the field, we are studying gene expression and biochemical properties of marine phytoplankton and bacteria over a 31-day field deployment during a fall phytoplankton bloom period in Monterey Bay.

13: Recovery of Denitrification Rates in Restored North Carolina Oyster Reefs and Salt Marshes

Kathleen Onorevole*, Suzanne Thompson,
and Michael Piehler

University of North Carolina Chapel Hill

Coastal restoration can bolster important ecosystem services, such as nutrient cycling and wave attenuation. As restored systems age, it may be useful for managers to anticipate ways in which corresponding ecosystems services will change over time. Salt marshes and intertidal oyster reefs are often restored together, and previous research has indicated that both habitats can enhance denitrification, the process by which nitrate is converted to non-bioavailable dinitrogen gas. This study used a space-for-time chronosequence to assess denitrification rates in Southern Outer Banks salt marshes and oyster reefs that were restored 0-20 years ago. In summer 2014, sediment cores were collected from multiple elevations in each habitat and incubated in a continuous flow-through system. Water samples from each core were analyzed for N_2 gas flux, indicative of denitrification, using a Membrane Inlet Mass Spectrometer (MIMS). Results suggest that denitrification rates peak approximately 6 years after restoration, and that lower elevations support higher denitrification rates in both habitats. These results may inform restoration planning in areas where N cycling is a particular concern.

14: Seasonal and Spatial Changes in Nitrogen Cycle Potential in Midwestern Agricultural Soils as Revealed by Metagenomics

Luis Orellana*, Joanne Chee-Sanford, Robert Sanford, Frank Löffler, and Konstantinos Konstantinidis

Georgia Institute of Technology

Assessing the impact of fertilizer overuse on the activities of soil microbial communities is important for better a understanding of the cycling of key nutrients like nitrogen and the effects on climate change. We analyzed short-read metagenomes obtained from two agricultural sites with contrasting soil textures (sandy versus silty-loam) during four seasons in 2012 at two depths. The predicted protein-coding sequences revealed a clear separation between surface and deep samples. For instance, genes related to light-dependent stress, DNA repair and nutrient uptake were more abundant (> 2-fold) in the surface samples in both soils (p-adjusted < 0.05). Different archaeal populations and nitrogen metabolism genes were characteristic of the deep samples. For example, three predicted AmoA proteins, each encoded by a distinct archaeal population, became abundant in the deep sandy samples when seasonal nitrogen fertilization was applied. By binning contigs, the draft genome of the most abundant population (comprising 0.36% of the metagenomic sequences or 35X coverage) related to the Thaumarchaeota phylum was obtained. All together, our study identified key microbial populations and genes responding to seasonal and human-induced perturbations (e.g., fertilization practices) and controlling the fate of nitrogen in agricultural soils.

15: Distribution of Deep Sea Sedimentary Microbial Populations in the Northern Gulf of Mexico

Will Overholt*, David Hollander, and Joel Kostka

Georgia Institute of Technology

Deep sea benthic microbial communities are vastly understudied in comparison to their planktonic counterparts in marine ecosystems. In order to understand the response of sedimentary microbes to oil disturbance at the seafloor, the natural structure of deep sea microbial communities needs to be understood. The objective of this research is to interrogate the distribution, community composition, and diversity of sedimentary microorganisms in the northern Gulf of Mexico (nGoM). Microbial communities were elucidated through the generation of 80 million Illumina MiSeq SSU rRNA amplicon sequences from 700 samples representing 23 sites. Results indicate large variations in microbial communities on small spatial scales that increase with sediment depth. Surficial sediment microbial communities are structurally similar across the nGoM, and communities diverge with increasing sediment depth. The statistical power of this dataset has enabled a generalized, depth stratified microbial community structure to be constructed for deep ocean sediments across the nGoM. Microbial community structure is linked to oxygen penetration depth and sediment geochemical regime, which are likely controlled by carbon delivery. The distributions of key microbial populations can be calculated and we foresee these distributions being incorporated into predictive ecosystem models that assess large scale disturbances, such as the Deepwater Horizon oil discharge.

16: Cryopreservation of Model Organisms: A Great Tool for Biogeochemistry Research

Estefania Paredes* and Peter Mazur

University of Tennessee Knoxville

Cryopreservation can be very powerful biotechnological tool in the lab, allowing the preservation of cells or organisms at your disposal for future experiments, to preserve special genomes, provide out of season stock of organisms that can allow you to work all year round with your desired test specie. No matter if it is among the classical animal models, NHI recommended models or emerging model organisms, cryopreservation can be very useful. Vitrification is achieved by rapidly cooling a liquid through the glass transition. In our lab we have demonstrated that one of the key issues of survival is not only the high cooling rate but for the high warming rate needed to prevent the recrystallization during warming. In order to achieve warming rates fast enough we are using an IR laser pulse. We have taken part in developing cryopreservation protocols for several model or test organisms (marine microalgae, freshwater microalgae, fungus, marine invertebrates and mice) and now we will be revisiting several of those cryopreservation protocols using vitrification with IR laser warming to try to increase survivals and we are working on sensitive cell types. We will go over the protocols for some test species interesting in biogeochemistry research.

17: H_2O_2 Photoproduction in Marine Waters: A Simple Proxy for Estimating Direct CO_2 Photochemical Fluxes from Riverine Impacted to Oligotrophic Waters

Leanne Powers* and William Miller

Skidaway Institute of Oceanography

CO_2 is the largest identified product of dissolved organic matter (DOM) photochemistry in natural waters, but its analysis in seawater is hampered due to high background DIC concentrations and the lack of sensitive detection methods. Hence, a quantitative description of its photochemical efficiency remains poorly constrained, especially for the open ocean. However, the photoproduction of H_2O_2 (sub-nanomolar detection limits) appears to be a simple proxy for CO_2 photoproduction with an average CO_2:H_2O_2 molar ratio of 6.89 ± 1.64 determined in a variety of marine waters ranging from a tidal creek to offshore stations near the Gulf Stream. Even when corrected for photobleaching, accumulation of both H2O2 and CO_2 was not linear beyond 12 hours of constant irradiation, with interval rates indicating that production efficiency for both products decreased with prolonged exposure. Direct measurements of O_2^- photoproduction, together with its dark thermal decay to H_2O_2, indicate that O_2^- may be the best proxy for photochemical DOM oxidation to CO_2. Given the short irradiation times needed to determine O_2^- production rates (~5 minutes), determination of O_2^- photoproduction rates may provide robust estimates for initial CO_2 photoproduction rates even in blue water, allowing greatly improved estimates for the global significance of DOM photooxidation.

18: Impact of Environmental Gradients of Nonconsumptive Effects (NCEs)

Jessica Pruett* and Marc Weissburg

Georgia Institute of Technology

Predators not only exert influence on prey through direct consumption but also their presence causes plastic responses in prey that can cascade down to lower trophic levels and have strong impacts on community structure. The importance of these nonconsumptive effects (NCEs) depends on the area around the predator in which prey respond, known as the predator active space. Chemically-mediated cues are known to be important in many NCEs, but there are few estimates of active space and chemical cues can be altered by surrounding environmental conditions which may result in differences in antipredator responses across flow environments. This study aims to determine the predator active space of blue crabs on mud crabs and cascading NCEs on oysters at different flow sites and tidal types. In field caging experiments, preliminary results suggest that predator active space decreases with increasing mean flow velocity, but oyster foraging suppression and mud crab refuge use increase. Yet, in higher flow velocities and turbulence intensity, mud crab foraging appears to be limited by physical constraints imposed by flow and NCEs have little impact. Thus, hydrodynamics may modulate where and when NCEs are important in a nonlinear fashion and understanding the perceptual effects of environmental forces can provide a framework to examine NCEs in both aquatic and terrestrial chemical systems, as well as those where prey use different sensory modes.

19: Enrichment and Characterization Of Petroleum Hydrocarbon-Oxidizing, Fe(III)- and Sulfate Reducing Prokaryotes from Salt Marsh Sediments Impacted by the Deepwater Horizon Oil Spill

Michael Sanderson*, Rebecca Rossetti, William Furin, and Kuk-Jeong Chin

Georgia State University

Fe(III)-reducing (FeRP) and sulfate-reducing prokaryotes (SRP) play an essential role in the remediation of crude oil in anoxic environments by coupling oxidation of petroleum hydrocarbons (PHC) with reduction of Fe(III) and sulfate. In this study, FeRP and SRP were enriched from oil-contaminated Louisiana salt marsh sediments with crude oil as the sole carbon and electron source. The molecular proxies, alkylsuccinate synthase (*assA*), benzyl succinate synthase (*bssA*), naphthylmethylsuccinate synthase (*nmsA*), 2-naphthoyl-CoA reductase (*ncr*) and dissimilatory (bi)sulfite reductase (*dsrAB*) genes were surveyed for metabolically-active PHC-oxidizing FeRP and SRP. Phylogenetic analyses by pyrosequencing of 16S rRNA cDNA demonstrated that Fe(III)-reducing enrichments are dominated by unclassified Deltaproteobacteria. Isolation of two novel anaerobic PHC-oxidizing prokaryotes from Fe(III)- and sulfate-reducing enrichments was performed using agar shake dilutions. Ongoing PCR analysis and microscopy of isolated colonies suggested 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.

20: Activities and Lifetimes of Extracellular Peptidases in River Sediments

Jenna Schmidt*, Austen Webber, Richard Kevorkian, and Andrew Steen

University of Tennessee Knoxville

Heterotrophic microbes produce extracellular enzymes in order to hydrolyze organic macromolecules so that they can be brought into the cell and used for energy. Doubling times of cells in subsurface sediments have been estimated on the order of thousands of years, implying a need for similarly long-lived enzymes. Measuring the activity of these enzymes in sediments provides insight into their role in organic carbon metabolism in subsurface sediments. A fluorogenic substrate-based enzyme assay was performed using L-Phe-AMC, D-Phe-AMC, and Orn-AMC substrates on the full length of a 63 cm sediment core sampled from the White Oak River in North Carolina. Autoclaved samples retained residual enzyme activity, however, implying the presence of highly stabilized enzymes. In order to determine activation energy for enzyme degradation, a heating experiment was performed using Tennessee River sediment. The sediment samples were heated for various amounts of time at temperatures between 70 and 100°C, allowing estimation of in situ rates of enzyme decay. An accurate estimate of extracellular enzyme lifecycle length is crucial to our understanding of subsurface microbial life because long living, robust microbes would likely not exist without long-living extracellular enzymes.

21: Competitive Degradation of Co-Contaminants 1,4-Dioxane, Tetrachloroethylene (PCE), and Trichloroethylene (TCE) by a Microbial Driven Fenton Reaction

Ramanan Sekar* and Thomas DiChristina

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Hazardous contaminants of heightened concern include the chlorinated solvents tetrachloroethene (PCE) and trichloroethene (TCE) and the solvent stabilizer 1,4-dioxane. Recent concern over these contaminants in contaminated waters and sediments is driven by several factors, including widespread use and improper disposal practices by industry, high miscibility in water, recalcitrance to conventional degradation processes, and classification as probable human carcinogens. Current remediation technologies entail carbon absorption, distillation, UV based advanced oxidation processes and ex situ pump-and- treat procedures that are neither cost effective nor able to effectively remove co-contaminants such as 1,4-dioxane, PCE, and TCE. The objective of this study was to evaluate the ability of a microbially driven Fenton reaction to competitively degrade1,4-dioxane, TCE, and PCE singly and in double and triple combinations as co-contaminants. The microbially driven Fenton reaction operates at circumneutral pH and does not require continual addition of the Fenton reagents Fe(II) and peroxide. *Shewanella oneidensis*, an Fe(III)-respiring facultative anaerobe was used as a biocatalyst to generate hydroxyl radicals via the Fenton reaction. Hydroxyl radicals were produced by providing *S. oneidensis* batch cultures with Fe(III) and alternating between aerobic/anaerobic conditions with lactate as electron donor. Previous batch reactor studies demonstrated that rates of hydroxyl radical production and 1,4-dioxane degradation were optimal with aerobic/anaerobic cycling frequencies of 3 h.In the present study, 1,4-dioxane degradation was carried out in the presence of the co-contaminants TCE and PCE. The high volatility of PCE and TCE necessitated the development of fed-batch reactor configurations to generate hydroxyl radicals without loss of TCE and PCE during the hydroxyl radical-producing aerobic/anaerobic cycling periods. The fed-batch reactor system degraded 1,4-dioxane, TCE, and PCE singly and in double and triple combinations as co-contaminants, while the contaminants were not degraded in control experiments carried out with bacterial cells (abiotic control) or Fe(III) omitted. The newly designed degradation fed batch reactor system is currently being optimized to improve rates of co-contaminant degradation by examining effects of varying bacterial cell density and the concentrations of Fe(III), oxygen, and the three co-contaminants.

22: The Role of Reactive Iron Phases in Stabilizing Organic Matter along a Deltaic Soil Chronosequence

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Reactive iron phases are reported to be significant factors in controlling carbon burial in both marine and lacustrine sediments. Here, we examine the role of this constituent in preserving organic carbon in deltaic soils and sediments. The Wax Lake Delta, Louisiana, has become a model for deltas in an active progradational stage. These systems are unique in that they receive organic carbon via fluvial sedimentation and a coincident pulse during soil formation once the delta becomes subaerial. We report the proportion, δ^{13}C, lignin phenol content, and fatty acid content of organic carbon associated to iron along a chronosequence of soil development in the delta topset. We found that over 20 % of the organic carbon in the top 0.5 meters of the delta topset was associated to reactive iron phases and was terrestrial in origin. Moreover, the type of binding shifts from 1:1 sorption in the sediment dominated region to chelation/co-precipitation in the soil dominated region. These results add to our knowledge of the carbon burial processes in young deltas, and provide insight into an added benefit of restoring the Mississippi River Delta.

23: Anaerobic Hydrocarbon Degradation under Iron- and Sulfate-reducing Conditions by Sedimentary Microorganisms

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This study investigates the rates and the microbial communities that catalyze anaerobic hydrocarbon degradation in areas of the Gulf of Mexico seafloor that were impacted by the Deepwater Horizon blowout. Sediment samples were collected on research cruises from 2012 to 2014. Enrichment cultures were initiated under iron- or sulfate-reducing conditions with Macondo oil, hexadecane, or phenanthrene as the sole carbon source. Microbial activity was confirmed by quantification of electron acceptor utilization and microbial communities were characterized using Illumina sequencing of SSU rRNA gene amplicons. Enrichments grown on hexadecane showed the fastest hydrocarbon mineralization, followed by phenanthrene and crude oil under iron- or sulfate-reducing conditions. Phylogenetic analysis of SSU rRNA sequences indicated that the members of the Deltaproteobacteria consist 12-46% of the total community in all enrichments studied. Bacterial groups belonging to the families Anaerolineae and Desulfobacteraceae were highly enriched under sulfate-reducing conditions. Enrichment of known hydrocarbon fermenters and secondary scavengers suggests the potential for syntrophic hydrocarbon degradation under sulfate-reducing conditions. Surprisingly, known sulfate-reducing bacterial groups such as the families Thermodesulfovibrionaceae and Desulfobulbaceae were highly enriched under iron-reducing conditions. All isolates obtained from enrichment cultures grown on phenanthrene under sulfate-reducing conditions were phylogenetically clustered within the Desulfovibrionaceae and Pelobacteraceae.

24: Faster Nitrate Uptake and Chlorophyll Turning Over under Elevated Atmospheric CO_2

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The concentration of CO_2 in the atmosphere is expected to double by the end of this century. This will profoundly change the carbonate chemistry in aquatic ecosystems and is likely to have an impact of aquatic primary producers. In this study, we grew a single species phytoplankton culture with different starting nitrate concentration under 380 ppm and 700 ppm CO_2 and monitor the trajectory of chlorophyll and nitrate changes. We fit a dynamic model to the experimental data to investigate how elevated atmospheric CO_2 influences phytoplankton growth and nutrient uptake. We found that high nitrate concentrations results in fast chlorophyll production. High CO_2 leads to faster nitrate uptake and chlorophyll turning over. But chlorophyll standing stock was not significantly changed. Together with previous studies, this study suggests that the influence of high CO_2 is not reflected as accumulation of primary producers, but an accelerated cycle of carbon and nutrients.

25: Methanotroph Identification from Hudson Canyon Gas Seeps

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The emission of methane from continental shelf gas seeps has the potential to release this greenhouse gas into the atmosphere. However, the methane emitted from these seeps can be oxidized by aerobic microbes in the surrounding water column, reducing or eliminating flux to the atmosphere. The recent discovery of at least 50 gas seeps along the tectonically inactive US Atlantic Margin prompted an investigation into the fate of this methane and the microbes that may consume it. Water samples were collected from methane seeps ranging from 450 meters below sea level (mbsl) to 682 mbsl, in the Hudson Canyon (offshore NY) in July of 2014. Methane concentrations reached 100 nM or more in the water column. Methane oxidation rates were measured using a ^{13}C tracer technique, suggesting that methane-oxidizing bacteria were active in water samples. 16S rRNA gene sequencing and additional isotope labeling experiments will be conducted to identify these bacteria.

26: Metagenomic Analysis of the Microbial Communities in a Cassava Flour Processing Plant

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Human-mediated ecosystems represent an interesting niche to study microbial diversity and a potential source of novel enzymatic functions and molecules. Cassava fermentation tanks contain cyanogenic glycosides, starch, free monosaccharides and cellulose. We characterized the composition of microbial community present in a cassava mill using a shotgun metagenomic approach. DNA was extracted from a cassava tank at three different points during a 30 day-fermentation. 16S rRNA-encoding reads was used for taxonomic characterization. Functional annotation of protein-coding sequences was performed using MetaGeneMark (gene prediction), SwissProt database (functional annotation) and Gene Ontology (functional categories). Approximately 70% of the community was dominated by members of *Lactobacillus* (28%), *Acetobacter* (27%) and *Prevotella* (15%) genera. Most proteins were associated with protein degradation, carbohydrate metabolism and lactate fermentation, suggesting that organic acid production and fermentation are active mechanisms in the community. Hydrolase-encoding genes, peptidases, and transcarbamylases were identified in sequences affiliated to *Lactobacillus*. Proteins participating in oxidation of alcohol and sugars, belonging to the *Acetobacter* genus, were also present. Our functional analysis contributes to understanding the functional interplay of active populations involved in the cassava fermentation process and confirms the genetic diversity that can thrive in such environments.

27: Total and Soluble Trace Element Concentrations of Aerosol Dust in the Indian Ocean

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To estimate the atmospheric deposition of trace elements to the Indian Ocean, aerosol dust samples were collected during three CLIVAR/CO_2 Repeat Hydrography Indian Ocean transects (I5, I8S/I9N, and I6S). Bulk aerosols were collected on polycarbonate track etched filters (PCTE), while samples for solubility and size-fractionated studies were concurrently collected using mixed cellulose ester (GN6) filters. Soluble trace metal concentrations in aerosols were determined by subjecting two subsets of GN6 filters to instantaneous leaches of either ultrahigh purity (UHP) water (pH 5.6) or 0.2 µm filtered seawater at natural pH. Bulk concentrations were measured by Energy Dispersive X-Ray Fluorescence (ED-XRF) at the NOAA/PMEL laboratory, and UHP water soluble concentrations were measured by ICP-MS at FSU/NHMFL. Atmospheric fluxes of lithogenic elements were highest within the Bay of Bengal and near Australia (e.g., 5-10 µmol Al m^{-2} d^{-1} and 2-4 µmol Fe m^{-2} d^{-1}, but frequently fell below ED-XRF detection limits in samples from the central Indian Ocean and Southern Ocean. Aerosol lead concentrations were highest in the Bay of Bengal as well, suggesting a significant industrial component of aerosol dust. Ultimately, these aerosol concentrations will be compared with concurrent studies of marine suspended particulate matter and modeled dust inputs based on surface dissolved Al concentrations.

28: Oceanographic Parameters Affect Biodegradation Potential in the Northeastern Gulf of Mexico

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Contrasting conclusions have been reported in previous studies regarding nutrient limitation of hydrocarbon biodegradation in the Gulf of Mexico, and rate measurements are needed to support oil plume modeling. Thus, this study focuses on the rates and controls of biodegradation in seawater and sediments, largely in the deep sea. Sediment and seawater samples were collected on research cruises in the northern Gulf from 2012 to 2014, where the seafloor was impacted by the Deepwater Horizon (DWH) oil spill. Biodegradation was clearly limited by both nitrogen and phosphorus availability in surface waters with significant rates of CO_2 production only observed in nutrient amended treatments. In bottom waters, degradation was observed in both unamended and nutrient–amendment treatments. Further analysis of degradation process on individual hydrocarbon compounds has been conducted to better understand the persistence of specific compounds in the environment. Effects of temperature on shaping microbial communities were also investigated. Enrichment cultures under room temperature and in situ temperature showed very distinct community compositions, both with the capability of hydrocarbon degradation. This suggest that functional redundancy exists in the deep sea sediment.

29: Reconciling Diatom Productivity and Iron Flux in the Southern Ocean

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Iron plays an important role in the regulation of biological productivity and the carbon cycle of the Southern Ocean. Recently, synchrotron X-ray spectromicroscopy was used to quantify a significantly higher molar Fe:Si ratio in diatom samples from the Antarctic region relative to the ratio found in Circumpolar Deep Water. Thus diatom production preferentially depletes iron relative to silica in the Antarctic. Combining dissolved iron and silicic acid datasets with an inverse box model we estimate the regional coupled iron and silica budget. The upwelling of subsurface waters cannot supply enough iron to balance losses due to diatom production, indicating that the closed budget requires additional sources of iron. To evaluate the impacts of high Fe:Si ratios, a three-dimensional ocean biogeochemistry and ecosystem model is used to simulate the sensitivity of ocean productivity and nutrient cycling to a range of Fe:Si ratios in diatoms. We find that higher Fe:Si ratios strongly decrease subpolar productivity with moderate increases in subtropical productivity. Surface iron decreases globally while macro-nutrient concentrations increase in the subtropics, suggesting that productivity responds to reorganization of nutrient cycling. Our results indicate that the iron has global impacts through the distribution of micro- and macro-nutrients.

30: Diel and Seasonal pCO_2 Variability in the New River Estuary, North Carolina

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High rates of organic matter delivery generally cause estuaries to be sites of intense carbon remineralization. Previous studies have shown well-mixed, high latitude estuaries to be strong CO_2 sources to the atmosphere, roughly in balance with the continental shelf sink. However, human and natural nutrient loading (and other factors) may cause autochthonous C fixation (photosynthesis, nitrification) to exceed respiration within temperate, microtidal systems like the New River Estuary (NRE), NC, causing them to become autotrophic over daily or seasonal time scales. In an effort to better constrain the magnitude of air-sea CO_2 exchange, bi-monthly surveys were conducted in the NRE between July 2013 and the present. The use of consecutive dawn-dusk-dawn sampling periods enabled diel pCO_2 variability to be investigated, a critically important factor in shallow estuaries like the NRE where trophic change is the norm, not the exception. Initial results indicate that the competing factors of respiration and production can cause large pCO_2 excursions of over 1,000 uatm between dusk and dawn. Environmental and climatic factors such as temperature, vertical stratification, and freshwater flushing time appear to play important roles in modulating both rates of biological activity as well as the physical factors responsible for air-sea gas exchange.

31: Sapelo Island Microbial Carbon Observatory (SIMCO)

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Bacterioplankton control the flux of dissolved organic carbon (DOC) into the coastal microbial food web and influence the release of inorganic carbon to atmospheric reservoirs. Yet the nature of the carbon decomposition through the coastal continuum is still a matter of considerable controversy. Thousands of compounds make up the DOC pool, each with different biological turnover rates. This complex DOC pool is processed by a community of heterotrophic bacteria composed of hundreds of taxa with varying ecological strategies for the uptake and metabolism of carbon using largely uncharacterized biochemical pathways. The goal of this project is to characterize the functional network for bacterioplankton communities processing marine DOC: the bioreactive components, the metabolic pathways used to transform them, and the partitioning of ecological niches. The explicit goals are to identify: What are some of the major bioreactive compounds of DOC? Which microbial taxa are most active in transforming DOC? How do these linkages change seasonally? Biological complexity of carbon turnover was analyzed through a study of bacterioplankton messenger RNAs via metatranscriptomics focused on transcripts representing bacterial transporters. As a result key components of the biologically labile DOC pool and major bacterial taxa responsible for transformation of these components were determined.

32: Sediment Denitrification Overcomes Sulfides Inhibition Under Low Salinity Environment

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Previous studies carried out in the northern Gulf of Mexico detected low rates of nitrification, denitrification and, hence, low N removal. The inhibitory effects of porewater sulfide on these processes may limit rates in this region. To test this hypothesis, mud flat sediments were collected seasonally from locations with differing salinities. We predicted that in lower salinity habitats, the inhibition of HS$^-$ would be limited and nitrification and denitrification would be higher than in the high salinity habitats. Potential nitrification rates were low (0.06-0.25 nmol N g^{-1} h^{-1}) at both sites. Although 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} compared to the high salinity site). *nrfA* gene, a proxy for dissimilatory nitrate reduction to ammonium (DNRA), was abundant and positively correlated with the genes associated with sulfate reduction, *dsrB* (Spearman's Rho=0.64, p=0.0008). Contrary to our hypothesis, nitrification remained low in both high and low salinity environments, but potential denitrification was higher under lower salinity, indicating that salinity is not the only factor influencing these processes. Additionally, other N pathways, such as DNRA, may also play an important role regulating N removal in Mobile Bay, AL.

33: Gene Expression of *hao* Affects the Molecular Basis of Nitrogen Transformations in *Methylococcus capsulatus* Bath, a Nitrifying Methanotroph

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Methylococcus capsulatus strain Bath ("*MCB*") is an aerobic methane-oxidizing bacterium that can oxidize ammonia to nitrite via the intermediate hydroxylamine. *MCB* can assimilate (by ADH or GS-GOGAT) ammonium obtained directly from the environment or produced by reduction of N$_2$ (*nif*) or nitrate (*nasA* & *nirB*). *MCB* was thought for decades to oxidize hydroxylamine with cytochrome P460 (*cytL*), until the discovery of a functional hydroxylamine dehydrogenase gene (*haoA*, HAO). By using qPCR analyses of cDNA from *MCB* incubated +/- 5 mM ammonium, we have shown earlier that *haoA* steady-state mRNA levels increased >15-fold in response to ammonium while mRNA levels for *cytL* were not affected by ammonium. We also reported that a conserved open reading frame located 3' of *haoA* in *MCB* and in in all known AOB genomes, *haoB* (formerly *orf2*) was co-transcribed with *haoA* at increased mRNA levels in the presence of ammonia; however, no function of the *haoB* gene has been identified. We also determined mRNA levels for additional genes that encode proteins involved in N-oxide detoxification: cytochrome *c*´-beta (CytS) and nitric oxide reductase (NorCB), both implicated in NO reduction. Whereas *cytS* mRNA levels increased ~ 30-fold in response to ammonium, the co-transcribed *norCB* mRNA did not; the opposite is observed under N-oxide stress. By extending this work with the goal to discover a function for the putative HaoB protein, we succeeded in generating a *haoAB* knock-out mutant as well as a mutant that lacks the stemloop in the 5' end in the *haoB* gene. The latter is implicated in differential transcription of the *haoAB* gene cluster. Determined steady-state mRNA levels of above listed N-transformation inventory in *MCB* WT and isogenic mutants under ammonium stress implicate the *haoB* gene product in the modulation of nitrite levels by a yet unknown mechanism, which is subject to ongoing investigation.

34: Quantifying the Importance of the Rare Biosphere in Adaptation of Freshwater, Planktonic Microbial Communities to Perturbation by Organic Pollutants

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Freshwater communities found in Lake Lanier can include thousands of low abundance, 'rare' organisms. It is hypothesized that rare species play a major role in environmental adaptation. We tested the hypothesis by setting up mesocosms with lake water and perturbing them with 2,4-dichlorophenoxyacetic acid (2,4-D), 4-nitrophenol (4-NP) or caffeine. 2,4-D was removed in 10 days and multiple additions of the same substrate led to faster degradation rates. 16S rDNA analysis and genome sequencing assigned the isolated 2,4-D degrader to the genus *Burkholderia*, and revealed the presence of the *tfdABCDEF* operon. Comparison of metagenomic reads revealed that *Burkholderia* was present at a very low abundance originally, and increased by at least four orders of magnitude (~0.82% of total) due to perturbation. Close examination of the *Burkholderia* sp. draft genome sequence revealed the presence of three *tfd* gene clusters on a circular plasmid (~600 kb), which appeared to be a recombination product of two 2,4-D degradation plasmids, pM7012 and pJp4. Collectively, our results revealed that rare microorganisms in Lake Lanier are capable of utilizing various chemicals as sole carbon and energy source for growth, and play an important role in community adaptation to perturbation.

35: The Generation of DOC and POC by Viral Infection of Marine Bacteria

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Oceanic microbial communities are important in the transformation and recycling of dissolved organic matter (DOM). With 50% of primary production occurring in marine systems, it is important to understand how viruses shape the portioning of organic carbon into a wide range of size fractions. Bacterial cell disruption due to viral lysis releases potentially labile compounds into the dissolved phase, which may serve as a significant carbon source for other organisms. Some of this biomass, along with other remnants of lysed cells, may aggregate into the particulate phase, which can potentially be transferred to higher trophic levels or sink out of the euphotic zone. This “viral shunt” was simulated using a model marine gammaproteobacterium (*Vibrio alginolyticus*) and a phage specific to this bacterium. Here we report the effects of viral lysis on this system and the size fractions of organic carbon generated. To gain a better understanding of how viruses affect this process we used varying multiplicities of infection (MOIs). By changing the percentage of infected cells, we hope to understand how the organic carbon released during viral lysis of bacterial cells partitions between dissolved and particulate phases. In addition to tracking the fate of microbial biomass, we used immunological staining techniques and microscopy to characterize and distinguish cells with double-stranded DNA, cell-like structures without double-stranded DNA, and amorphous polysaccharide-rich structures. The results are presented in an effort to demonstrate how viral activity contributes to a continuum of size classes of organic carbon and further our understanding of how viruses shape the marine carbon cycle.

36: Particulate Trace Metal Cycling at Station ALOHA

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Phytoplankton in oligotrophic marine deserts depend on remote sources to supply trace nutrients. In the low nutrient low chlorophyll regions of the central North Pacific Ocean, episodic inputs of bioactive trace elements (e.g., Fe, Zn, Co, Cd, and Cu) could alleviate nutrient limitation and stimulate phytoplankton blooms. However, the events that stimulate these blooms can be just as scarce and sporadic as the blooms themselves. To better observe and understand the sources and cycling of trace elements in this region, suspended particulate matter (SPM) samples were collected during a near-continuous occupation of Station ALOHA (July-August 2012) and analyzed for a suite of major and trace elements. The results from daily surface and four vertical profile samples were used to estimate residence times, temporal variability, and contributions from aerosol, sedimentary, and biological influences. In the absence of atmospheric inputs, biological cycling dominated particulate trace metal distributions. Elemental ratios in SPM were comparable to literature values from both field and laboratory cultures. Ongoing research includes the comparison of dissolved and particulate trace metal concentrations and the resolution of discrepancies between source and removal fluxes.

37: Integrated Metagenomic and Metatranscriptomic Analyses of Microbial Communities in the Meso- and Bathypelagic Realm of the North Pacific Ocean

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Although emerging evidence indicates that deep-sea water contains an untapped reservoir of high metabolic and genetic diversity, this realm has not been studied well compared with surface seawater. The study provided the first integrated meta-genomic and -transcriptomic analysis of the microbial communities in deep-sea water of North Pacific Ocean. DNA/RNA amplifications and simultaneous metagenomic and metatranscriptomic analyses were employed to discover information concerning deep-sea microbial communities from four different deep-sea sites ranging from the mesopelagic to pelagic ocean. Within the prokaryotic community, bacteria is absolutely dominant (~90%) over archaea in both metagenomic and metatranscriptomic data pools. The emergence of archaeal phyla Crenarchaeota, Euryarchaeota, Thaumarchaeota, bacterial phyla Actinobacteria, Firmicutes, sub-phyla Betaproteobacteria, Deltaproteobacteria, and Gammaproteobacteria, and the decrease of bacterial phyla Bacteroidetes and Alphaproteobacteria are the main composition changes of prokaryotic communities in the deep-sea water, when compared with the reference Global Ocean Sampling Expedition (GOS) surface water. Photosynthetic Cyanobacteria exist in all four metagenomic libraries and two metatranscriptomic libraries. In Eukaryota community, decreased abundance of fungi and algae in deep sea was observed. RNA/DNA ratio was employed as an index to show metabolic activity strength of microbes in deep sea. Functional analysis indicated that deep-sea microbes are leading a defensive lifestyle.

38: The Distribution of Dissolved Zinc in the South Atlantic as Part of the UK GEOTRACES Programme

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We present the first comprehensive dataset of dissolved zinc along the South Atlantic 40°S latitudinal line as part of the UK GEOTRACES programme. Previously, there was little understanding of the supply of zinc, an essential requirement for phytoplankton, to this productive region of the Atlantic. To address this issue we utilized a modified Flow Injection Analysis method, with a detection limit of 14 pM. Along the 40°S parallel, the vertical and horizontal distributions of zinc showed distinct gradients associated with the water masses present. Concentrations ranged from 15 pM in open ocean surface waters to 8 nM in Antarctic Bottom Waters. Growth limiting mixed layer zinc concentrations resulted from the lack of a direct return path for zinc to the South Atlantic pycnocline with Sub-Antarctic Mode Water. Low zinc in this return path was identified by a linear correlation between zinc and soluble reactive phosphorus that showed a kink at ~500 m, much deeper than that observed in other oceanographic regimes. This research has led to the development of a new tracer (Zn*) that can map the low dissolved zinc concentrations delivered to pycnocline waters of the Southern Hemisphere by the upper branches of Meridional Overturning Circulation.

39: Sources of Organic Matter in Sediments of the Colville River Delta, Alaska: A Glimpse of River Impact and Coastal Dynamics

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Arctic permafrost represents about half of the total belowground global carbon pool, and thus the fate of this pool, as it thaws in the wake of global warming, warrants close attention. The Colville River is the largest North American Arctic River with a continuous permafrost watershed. Sediments from last ~50 years were collected from Colville River delta and the adjacent lagoon and analyzed for bulk organic carbon proxies, biomarkers (including lignin phenols and sterols), and compound-specific ^{13}C isotope analysis (CSIA) of fatty acids. Based on lignin and sterol results, there are distinct spatial patterns in the distribution of soil and peat inputs to the delta and the lagoon. Stations close to the river mouth show greater inputs of soil and litter derived terrestrial material, in addition to more pulsing events, than stations in the lagoon. The distal eastern region of the lagoon has greater inputs of peat from coastal erosion. β-sitosterol may prove to be another biomarker for peat inputs in the Arctic. CSIA of fatty acids shows decadal shifts in algal and terrestrial inputs, due to changes in river inputs and variability of phytoplankton abundance.