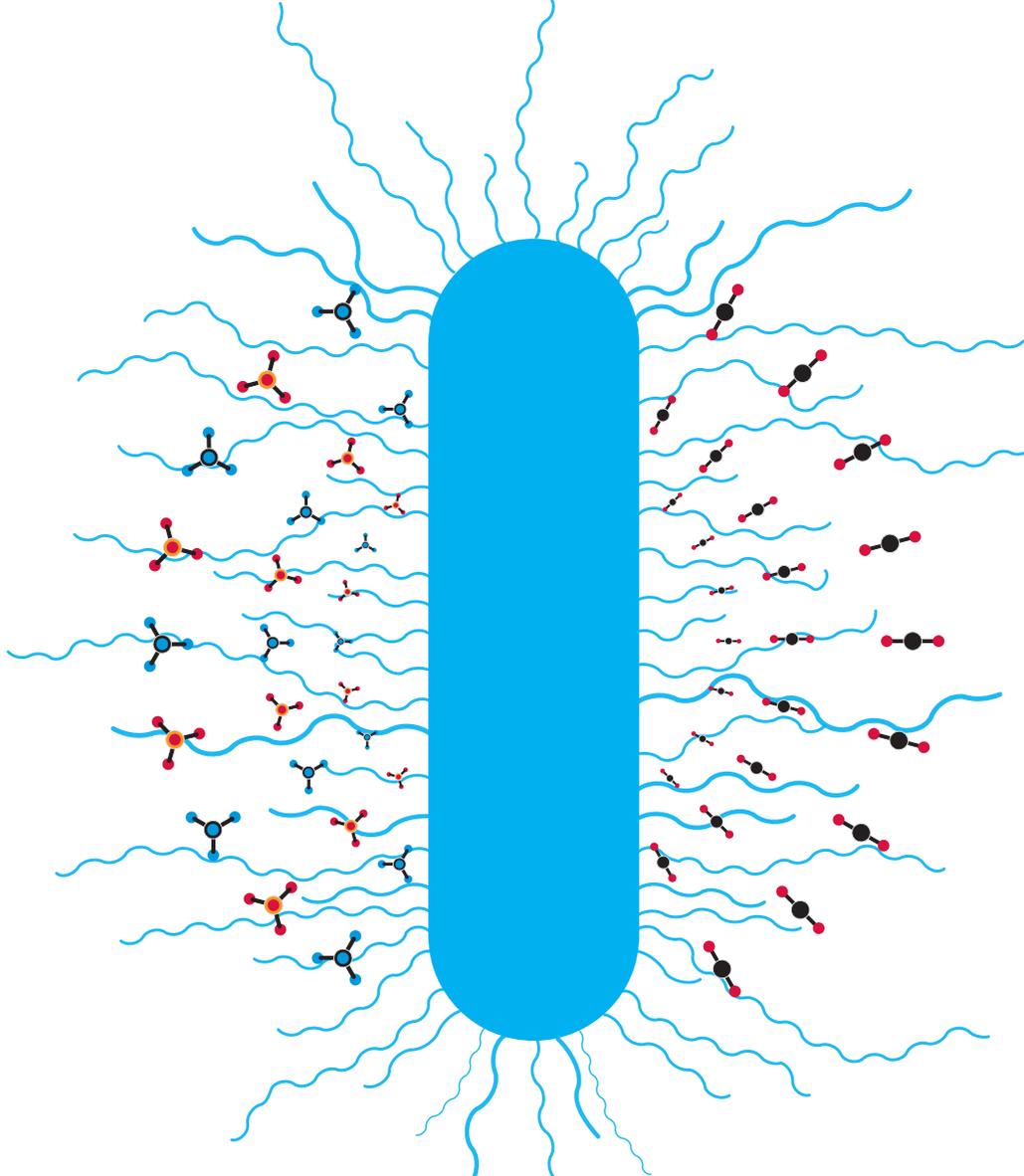


Fourth Annual

SBS



Southeastern Biogeochemistry Symposium

Athens, GA | March 31 - April 2, 2017

Programs and Abstracts

Dr. Jennifer Macalady

2017 SBS Keynote Speaker
The Pennsylvania State
University

Do Microbes Make Caves?

Professor Jennifer (Jenn) Macalady is an Associate Professor and Geomicrobiologist in the Department of Geosciences at the Pennsylvania State University, where she studies microbial life in Precambrian-analog environments. She earned her undergraduate degree in Geology from Carleton College in 1991, and her Ph.D. in Soil Microbiology with Kate Scow at University of California Davis in 2000. She pursued postdoctoral research at the University of California Berkeley under the mentorship of Jillian Banfield, and briefly returned to Carleton College as a Visiting Assistant Professor in 2002.

She accepted a permanent position at Penn State in 2004, where she serves as Director of the Center for Environmental Geochemistry and Genomics, Faculty-in-charge of the Graduate Program in Biogeochemistry, and Member of the Penn State Astrobiology Research Center.

Her research is focused on the microbial ecology of sulfur-rich, oxygen-poor ecosystems. She can often be found underground in the deep and sulfidic Frasassi cave system, Italy, or with cave divers exploring inland blue holes and stratified aquifers in the Caribbean. Her group aims to discover ecological rules and genomic constraints governing how microbial populations distribute themselves into environmental niches, with an eye toward how geochemistry influences biosignatures preserved in Earth's geologic record and potentially on other planets.



<http://www3.geosc.psu.edu/~jlm80/>

2017 SBS UGA Graduate Student Steering Committee

Hilde Oliver
Maite Gahzaleh
Mary Katherine Rogener
Frank Xavier Ferrer-Gonzalez
Jason Westrich
Andy Montgomery
Ryan Sibert

2017 SBS Faculty Steering Committee

Samantha Joye (University of Georgia), Chair
Julia Diaz (Skidaway, University of Georgia)
Patricia Medeiros (University of Georgia)
Christof Meile (University of Georgia)
Erin Lipp (University of Georgia)
Catherine Pringle (University of Georgia)
Amy Rosemond (University of Georgia)

Participating Universities

Coastal Carolina University, Dauphin Island Sea Lab, East Carolina University, Florida State University, Georgia Institute of Technology, Georgia State University, Iqra National University, Oak Ridge National Laboratory, Shanxi Agriculture University, Skidaway Institute of Oceanography, The Pennsylvania State University, University of Georgia, University of Florida, University of North Carolina Chapel Hill, University of North Carolina Charlotte, University of South Alabama, University of South Carolina, University of Tennessee Knoxville, Virginia Tech

Sponsors

Agouron Institute
University of Georgia (UGA) Department of Marine Science
Joye Research Group
UGA Graduate School
UGA OVRP
UGA Franklin College of Arts and Sciences
UGA Department of Microbiology
UGA Odum School of Ecology
ECOGIG
Georgia Sea Grant



Locations

1. Courtyard-Marriott

166 North Finley St, Athens, GA 30601

2. Holiday Inn

197 East Broad St, Athens, GA 30601
706-549-4433

3. Transmetropolitan

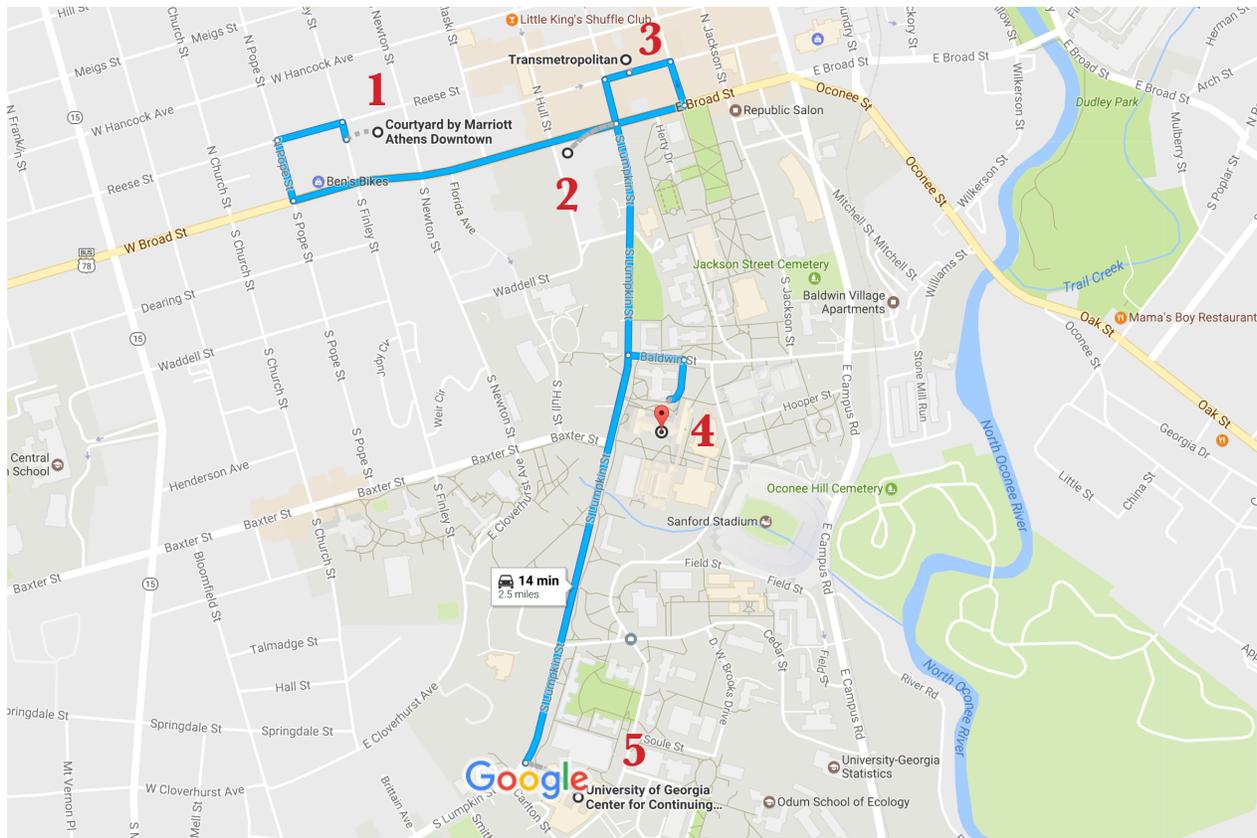
145 E Clayton St, Athens, GA 30601
<http://www.transmetathens.com/menu/>
706-613-8773

4. Zell B. Miller Learning Center (MLC)

48 Baxter St, Athens, GA 30602
706-542-7000

5. Georgia Center

1197 S Lumpkin St, Athens, GA 30602
706-542-3537



Schedule

Friday March 31, 2017

Time	Event	Location
6:00 PM - 9:00 PM	Welcome Reception	Transmetropolitan

Saturday April 1, 2017

Time	Event	Location
8:30 AM - 9:30 AM	Registration/Breakfast	MLC; 4th Floor Rotunda
9:30 AM - 9:45 AM	Introduction/Welcome	MLC; Room 101
9:45 AM - 10:00 AM	Keynote Speaker	MLC; Room 101
10:00 AM - 10:15 AM	Coffee Break	MLC; 4th Floor Rotunda
10:15 AM - 11:45 AM	Oral Session I	MLC; Room 101
11:45 AM - 12:45 PM	Lunch	MLC; 4th Floor Rotunda
12:45 PM - 2:15 PM	Oral Session II	MLC; Room 101
2:15 PM - 2:30 PM	Coffee Break	MLC; 4th Floor Rotunda
2:30 PM - 4:00 PM	Oral Session III	MLC; Room 101
4:00 PM - 5:30 PM	Poster Session I	MLC; 4th Floor Rotunda
5:45 PM - 6:30 PM	Dinner	MLC; 4th Floor Rotunda

Sunday April 2, 2017

Time	Event	Location
8:30 AM - 9:00 AM	Breakfast	MLC; 4th Floor Rotunda
9:00 AM - 10:30 AM	Oral Session IV	MLC; Room 101
10:30 AM - 12:00 PM	Poster Session II	MLC; 4th Floor Rotunda
12:00 PM - 12:15 PM	Coffee Break	MLC; 4th Floor Rotunda
12:15 PM - 12:45 PM	Awards	MLC; Room 101

Oral Session I
10:15 – 11:45 AM
Saturday April 1, 2017
Miller Learning Center

10:00 AM
Coffee Break

10:15 AM
**1. Succession of Microbial Populations
Linked to Surface Residual Ball Degradation
in Pensacola Beach Sands Impacted by the
Deepwater Horizon Oil Spill**

Boryoung Shin*, Markus Huettel, Joel Kostka

Georgia Institute of Technology

The Deepwater Horizon oil spill contaminated large areas of coastline from Louisiana to Florida and oil was buried as deep as 55 cm in sandy beaches. Buried oil is protected from photodegradation and mechanical erosion and thus microbial decomposition may play a key role in its degradation. Although our group and others have examined biodegradation in oiled sands and surface residual balls (SRB), the rates and mechanisms of biodegradation of buried SRBs is less clear. Thus, the main objectives of this study are (i) to determine rate of SRB degradation in situ in dry beach sand, (ii) to investigate the succession of microbial communities in simulated SRBs, and (iii) to elucidate the linkage between nitrogen fixation and hydrocarbon degradation. Replicate standardized SRBs were buried from 5 to 55 cm depth in Pensacola Beach sand and sampled from October 2010 to December 2013. Microbial communities were characterized using next generation sequencing of 16S rRNA gene amplicons from SRBs sampled with time series. Results indicate pronounced change in microbial composition with time but little change with depth. All SRB samples were predominated by members of Alphaproteobacteria and Gammaproteobacteria. At least a five-fold increase of relative abundance of Rhizobiales was detected, which implicates an enrichment of nitrogen fixing taxa. *Alcanivorax*, *Hyphomonas*, *Phenylobacterium*, and *Mycoplana* were enriched after 2 months of burial and decreased in their abundance. *Pseudomonas* was enriched after 6 months of burial and *Parvibaculum* was enriched after a year of burial. Quantitative PCR of *nifH* gene implicates increased nitrogen fixing potential. Results thus support field data, which point to a succession

from early responding taxa, mainly members of the Gammaproteobacteria capable of alkane degradation, to other groups capable of degradation of more recalcitrant compounds such as PAHs. Overall results will help better understand persistence and impact of buried oil in Gulf Coast beaches and point to methods that could improve bioremediation.

10:30 AM
**2. No Laughing Matter: Nitrous Oxide
Production by Chemodenitrification in the
Ferruginous Proterozoic Ocean**

Chloe Stanton*, Chris T. Reinhard, James F. Kasting,
Tim W. Lyons, Jennifer B. Glass

Georgia Institute of Technology

Dimmer solar luminosity required an enhanced greenhouse effect to sustain liquid water on Earth's surface prior to ~2 Ga, but evidence for liquid water throughout Earth's history is incontrovertible. Solutions to this "Faint Young Sun Problem" are often attributed to CO₂ and CH₄ because the more potent N₂O molecule would have photodissociated in the anoxic Archean atmosphere. However, an N₂O greenhouse may have existed after the Great Oxidation Event at ~2.4 Ga when atmospheric O₂ levels rose to 0.001 - 0.1 PAL, though the deep ocean remained anoxic and Fe²⁺-rich (~3 mM). Chemodenitrification, the abiotic reduction of dissolved oxidized nitrogen to gaseous forms, could have been an important source of Proterozoic N₂O. To achieve N₂O concentrations allowing above-freezing temperatures with modern CO₂ and CH₄ at 0.001-0.1 PAL O₂, 10-500x modern fluxes are needed. We measured N₂O production rates in anoxic seawater with Fe²⁺, NO₂⁻, NO₃⁻, or NO. Minimal N₂O was produced with single substrates, less than 0.01% of NO₂⁻ was converted to N₂O with Fe²⁺, and greater than 25% of NO was converted with Fe²⁺. Increasing NO from 13 to 44 μM led to 2.9x higher N₂O yield. Increasing Fe²⁺ from 10 to 500 μM led to 4.5x higher N₂O yield, yielding rate orders of 0.7 and 0.3 with respect to NO and Fe²⁺, respectively, and a rate constant of 3.6x10⁻⁷ sec⁻¹. We hypothesize that chemodenitrification could have helped to solve the

* Indicates Presenting Author

“Faint Young Sun Problem” in the Proterozoic.

10:45 AM

3. Formation of The Subsurface Iron Maximum by the Simultaneous Release of Iron and Ligands from Organic Particles

Anh Le-Duy Pham*, Takamitsu Ito

Georgia Institute of Technology

The micronutrient iron (Fe) can limit biological productivity in about half of the world's oceans. However, processes that drive the ocean Fe cycling are not yet fully understood and accurately represented in ocean biogeochemistry models (OBMs), which leads to the limited ability of these models in reproducing recent Fe observations from GEOTRACES transects. In this study, we perform a suite of computational simulations in an OBM with an improved scheme for the ocean Fe cycling to better understand the mechanisms behind the observed Fe distribution. Specifically, we parameterize organic ligands, which protect dissolved Fe (dFe) from being removed in the seawater, as functions of dissolved organic matter and remineralization as opposed to a spatially homogeneous ligand assumed in previous studies. Model-data comparison shows that our model starts reproducing some important observed Fe features such as the subsurface maximum of dFe in the tropical Atlantic, which is not captured by many state-of-the-art Fe models. Sensitivity experiments show that this subsurface maximum is formed in our model by the simultaneous remineralization of Fe and ligands from organic particles. This remineralization source of Fe and ligands also sustains the long-range transport of dFe to Fe-limited biomes with implications for the ocean productivity and carbon uptake.

11:00 AM

4. Methanogenesis Marker Protein 10 Methylates Arginine at the Active Site Region of Methyl-Coenzyme M Reductase

Zhe Lyu*, Chau-wen Chou, Hao Shi, Ricky Patel, Evert C. Duin, and William B. Whitman

University of Georgia

Catalyzing the key step for anaerobic methane production and oxidation, methyl-coenzyme M reductase or MCR arguably controls global methane cycling and holds great promise for conversion of methane into high density liquid fuel. The MCR

possesses up to five modified amino acids at its active site, but neither the enzymes catalyzing those modifications nor their effects on enzyme activity or structure are known. Bioinformatic analyses had previously suggested that methanogenesis marker protein 10 (Mmp10) played an important role in methanogenesis. To examine its role, MMP1554, the gene encoding Mmp10 in *Methanococcus maripaludis*, was deleted, resulting in the specific loss of the 5-(S)-methylarginine modification of residue 275 in the α subunit of MCR. The methylation was restored when the gene was complemented by the wild-type gene in a methanococcal expression plasmid. The rates of methane formation in whole cells were reduced by 40% in the deletion mutant compared to the wild-type and complemented strains. This study presents the first evidence for a functional role of the posttranslational modifications on the activity of MCR. Lastly, a bioinformatic survey in the public genome database showed that Mmp10 homologs were present in most but not all methanogen lineages, indicating that the diversity of MCR posttranslational modifications may be larger than previously anticipated.

11:15 AM

5. Bacterial Transcriptional Response to Sequential Co-Culture with a Marine Dinoflagellate and Diatom

Marine Landa-Bezweirchy*, A.S. Burns, S.J. Roth, M.A. Moran

University of Georgia

A large fraction of the fluxes of major elements in the ocean results from heterotrophic bacterial activity. Because phytoplankton are intimately linked to bacteria in their role as primary producers, the taxonomic, functional and physiological diversity of phytoplankton is expected to modulate marine bacterial metabolism. This study investigates the transcriptional response of bacteria to a change in the taxonomy of phytoplankton and the organic compounds they release. The model marine bacterium *Ruegeria pomeroyi* was grown in microcosms first with the dinoflagellate *Alexandrium tamarense*, then with the diatom *Thalassiosira pseudonana* as it gradually outcompeted the dinoflagellate. Samples were taken throughout the 30-day co-cultures to track shifts in bacterial gene expression. Our data indicate that during growth with the dinoflagellate, sulfur-containing compounds such as DMSP and taurine, as well as methylated amines and polyamines, served as the main sources of carbon and energy. During growth with the diatom, dihydroxypropane sulfonate, glycolate, xylose and ectoine were the important

* Indicates Presenting Author

compounds fueling bacterial metabolism. Expression patterns of genes for quorum sensing, gene transfer agent and motility suggest that processes related to cell communication and signaling were important during growth with the dinoflagellate. Our results indicate that *R. pomeroyi* differentially regulates the expression of its genome during a shift in phytoplankton regime, with implications for biogeochemical cycling of sulfur and carbon in the surface ocean.

11:30 AM

6. Divergent Gene Expression Among Phytoplankton Taxa in Response to Upwelling

Robert H. Lampe*, Natalie R. Cohen, Kelsey A. Ellis, Kenneth W. Bruland, Maria T. Maldonado, Tawnya D. Peterson, Claire P. Till, Mark A. Brzezinski, Sibel Bargu, Kimberlee Thamatrakoln, Fedor I Kuzminov, Benjamin S. Twining, Adrian Marchetti

University of North Carolina, Chapel Hill

Frequent blooms of phytoplankton occur in coastal upwelling zones creating hotspots of biological productivity in the ocean. As cold, nutrient-rich water is brought up to sunlit layers from depth, phytoplankton are also transported upwards to seed surface blooms that are often dominated by diatoms. The physiological response of phytoplankton to this process, termed shift-up, is characterized by rapid growth rates and increases in nitrate uptake. To examine the molecular underpinnings behind the shift-up phenomenon, metatranscriptomic analysis was applied to a simulated upwelling experiment using natural phytoplankton communities from the California Upwelling Zone. An increase in diatom growth following five days of incubation was attributed to the genera *Chaetoceros* and *Pseudo-nitzschia*. Here we show that certain bloom-forming diatoms exhibit a distinct transcriptional response that coordinates shift-up during upwelling. Diatoms exhibited greater transcript reallocation following upwelling; however, comparison of co-expressed genes exposed overrepresentation of distinct sets within each group. The analysis revealed that diatoms frontload genes involved in nitrogen assimilation likely in order to outcompete other groups for available nitrogen during upwelling events. We speculate that the evolutionary success of diatoms may be due, in part, to this proactive response to frequently encountered changes in their environment.

* Indicates Presenting Author

Oral Session II
12:45 – 2:15 PM
Saturday April 1, 2017
Miller Learning Center

12:45 AM

**7. The Biogeochemistry of Trace Elements
in the Sea Surface Microlayer: Response to
Atmospheric Deposition**

Alina Ebling*, Jason Westrich, Erin Lipp, Kristen
Buck, Rachel Shelley, Angela Knapp, Thomas Kelly,
William Landing

Florida State University

The aeolian transport of aerosols is an important process for introducing trace elements (TEs) which impact marine primary production to the surface ocean. All material that enters the ocean from the atmosphere must pass through the sea surface microlayer (SML) at the air-sea interface. The SML is the physical link between the sea surface and lower atmosphere and processes that occur in this layer are a key component of the global biogeochemical cycling of TEs. A novel technique, a hollow cylinder of pure silica glass, was developed to collect the SML for the determination of dissolved and particulate Al, Mn, Fe, Co, Cu, Zn, Cd, and Pb. Aerosol and seawater samples were collected simultaneously in the Florida Keys over a one-month period. Concentrations of TEs increased by factors of 2-5 in the SML during significant Saharan dust events. Residence times (RT) of dissolved TEs in the SML ranged from 9.3 min for Mn to 94 min for Pb. RTs of particulate TEs ranged from 0.7 min for Co to 3.4 min for Pb. While the relatively short particulate RTs suggest rapid settling of particles out of the SML, the longer dissolved RTs could be due to the solubilization of TEs in the microlayer immediately being complexed by organic ligands. Heterotrophic bacteria (*Vibrio* spp.) as well as dissolved organic nitrogen (DON) in the SML increased by factors of 2-4 after the passage of a Saharan dust event, which suggests that there was an initial pulse of bioavailable TEs and other nutrients to the SML.

1:00 PM

**8. Direct Metabolic Evidence for Adaptations
to Deep Subsurface Life**

Jordan T. Bird*, Eric Tague, Laura Zinke, Brandi
Reese, Ian Marshall, Gordon Webster, Andrew
Weightman, Hector Castro, Shawn Campagna, Karen
G. Lloyd

University of Tennessee

Despite extreme energy-limitation, microbes in deep marine sediment communities appear to be active, persisting in a maintenance state with negligible growth for >100,000 years. Little is known about the specific mechanisms used to overcome energy stress within marine sediment microbial communities. The effect of energy limitation on concentrations of a wide array of small biomolecules has been studied extensively in model organisms, but never before in the deep marine sediment biosphere. We were able to link small organic molecules that denote specific adaptations to extreme energy limitation with the microbial clades that interact with them, by combining single cell genomics with metagenomics, metatranscriptomics, and untargeted small organic molecules identification. We found that some strategies for long term energy limitation such as the accumulation of protective trehalose and maintenance of NAD⁺ pools are shared across phyla. Other mechanisms such as the degradation of allantoin seems to be specific to Atribacteria. Additionally, toxin-antitoxin systems are common and expressed in these communities and may play key roles in attenuating growth and promoting gene acquisition in these slow growing populations. Here we provide the first direct evidence that deeply buried microbial communities utilize the available small organic molecule pools and toxin-antitoxin systems to overcome the stresses of extreme energy limitations.

* Indicates Presenting Author

1:15 PM

9. Bacterial Fe(III) Reduction Via a Cryptic Sulfur Cycle

Andrew Burns*

Georgia Institute of Technology

Microbial Fe(III) respiration is an ancient metabolism that is key to the global carbon and iron cycles. Yet, the diversity and function of microbial species capable of this metabolism are poorly understood. Geochemical profiling of saltmarsh sediments in coastal Georgia indicated overlapping high concentrations of Fe(II) and thiol species. Thiol species can abiotically reduce Fe(III) oxides to Fe(II), becoming oxidized to disulfide species as a result. As these disulfides can act as terminal electron acceptors for anaerobic respiration producing two thiol equivalents, these overlapping signals of thiols/Fe(II) may represent a cryptic sulfur cycle coupled to Fe(III) reduction in the environment. Using saltmarsh sediment as inoculum, cultures were set up with hydrous ferrous oxides and exogenous thiol species to enrich for bacteria able to reduce Fe(III) utilizing disulfide species as terminal electron acceptors.

Amplicon sequencing of the 16S rDNA was used to determine the proportional abundances of microbial operational taxonomic units (OTUs) in the enrichment cultures over three time points spanning four months. The co-variance of the OTUs with chemical factors such as exogenous thiol addition or levels of Fe(II) produced was calculated via network analysis. The resultant networks indicated multiple bacterial OTUs capable of reducing disulfide species and thereby driving reduction of Fe(III); identifying both generalist OTUs growing with a variety of disulfide species as well as specialist OTUs enriched only with a specific disulfide species. Addition of exogenous thiols to enriched isolates and enrichment communities led to a faster rate and higher extent of Fe(III) reduction confirming a role for a cryptic sulfur component of Fe(III) reduction. These analyses unveiled novel microbial lineages associated with disulfide-driven reduction of Fe(III) and provide new insights into the role microbes play in the global iron, sulfur and carbon cycles.

1:30 PM

10. Evidence for Manganese(IV)-Coupled Anaerobic Nitrification in Marine Sediments

Shannon Owings*, Anthony Bertagnolli, Alex Price, Eryn Eitel, Joel Craig, Frank Stewart, Martial Taillefert

Georgia Institute of Technology

The biogeochemistry of continental slopes is generally poorly characterized worldwide. In this study, sediment cores were collected along a transect across the Louisiana shelf and slope in the Northern Gulf of Mexico to determine the role of manganese and iron in diagenetic processes. The cores were profiled for dissolved oxygen, Mn(II), Fe(II), dissolved sulfides, organic-Fe(III) complexes, and FeS(aq) using mercury/gold voltammetric microelectrodes. Pore waters were then extracted for the analysis of dissolved constituents (dissolved inorganic carbon, dissolved orthophosphates, nitrate, nitrite, and ammonium), and DNA recovered from sediment cores was analyzed using amplicon sequencing targeting the 16S rRNA gene. Dissolved oxygen was depleted within 5 mm below the sediment water interface across the entire transect, indicating that anaerobic respiration processes dominated in these sediments. Nitrate profiles revealed elevated nitrate concentrations near the sediment-water interface and only moderate decrease with depth. In addition, evidence for sulfate reduction was only found on the continental shelf, as already demonstrated in previous studies. Interestingly, pore water concentrations of reduced iron remained low across the transect. In turn, depth profiles of dissolved manganese displayed peaks in the shallow layers of the shelf sediment. The dissolved manganese peak migrated deeper in the sediment column along the transect from the shelf to the slope. The relatively moderate decrease in nitrate was mirrored by an increase in ammonium that coincided with the peak in dissolved Mn. These findings suggest a possible linkage between the nitrogen and manganese cycles via Mn(IV)-coupled anaerobic nitrification. Multivariate analyses of amplicon profiles revealed that site location and the main geochemical conditions were highly coupled to community structure. These findings demonstrate that a combination of chemical and genetic data collected with a high spatial resolution is needed to elucidate the main biogeochemical processes within distinct sedimentary environments.

* Indicates Presenting Author

1:45 PM

11. A New Way to Look at Soil Aggregation and Aggregating Particles: What Laser Diffraction Can Tell Us

Julio Pachon*, Allan Bacon, Dan Richter, Aaron Thompson, Madison K. Akers, Josh Cucinella, John M. Davis, Sabine Grunwald, Eric J. Jokela, Michael Kane, Marshall A. Laviner, Daniel Markewitz, Timothy Martin, Gary F. Peter, C. Wade Ross, and Jason G. Vogel

University of Florida

Particle aggregation exerts strong control on soil biogeochemical properties and processes. Soil macroaggregates have been extensively studied and are known to control soil interactions with the biosphere, hydrosphere, lithosphere, and atmosphere. Soil microaggregates (traditionally defined as aggregates <250 μm in diameter) are the building blocks of soil aggregation and have been found to be the largest repository of stable carbon in soil, but are difficult to study given the rudimentary methodologies that include stacked sieving, fractionation, and even selecting with tweezers. These traditional forms of characterization also impede the identification and study of the individual aggregating particles. Here we present results from two projects using laser diffraction to analyze Fine Earth Aggregates (aggregates <2,000 μm in diameter) and aggregating particles from soils in the southeastern United States.

Analysis of samples from the Calhoun Critical Zone Observatory show that both land use and depth have strong influence on Fine Earth Aggregates and aggregating particles properties such as size and abundance resulting from interactive effects of soil texture and organic matter. We also find that fine-silt have the strongest influence on Fine Earth Aggregates formation. Regional analysis of samples from the PINEMAP Tier II network reveal landscape scale controls on Fine Earth Aggregates and show a correlation between SOM concentration and Fine Earth Aggregates size. Our work using laser diffraction to analyze Fine Earth Aggregates and aggregating particles cracks an exciting door in the study of aggregation and its influence on soil biogeochemistry. Compared to traditional methods our analyses are more rapid and provide greatly enriched and higher resolution data.

2:00 PM

12. Assessing Petrocarbon Incorporation into Pelagic Food Webs in the Gulf of Mexico

Ana Clavere-Graciette*, Drake Lee-Patterson, Joseph.P. Montoya

Georgia Institute of Technology

The Deep Water Horizon (DWH) oil spill released massive amounts of oil and gas (838 kt of crude oil and 363 kt of methane and other gases) that affected the Gulf of Mexico (GoM) ecosystem and harmed a wide variety of organisms. Previous studies showed that hydrocarbons were incorporated into the planktonic food web following the DWH oil spill, and that petrocarbon remained in the system for at least 2 years after the wellhead was capped. However, it has been difficult to differentiate between incorporation of hydrocarbons from the DWH spill and from natural seepage, and few studies have assessed the possible long-term persistence of petrocarbon from the oil spill in offshore waters of the Gulf of Mexico. To address this issue, sites with different seepage activities, and situated at variable distances from the DWH wellhead were sampled at different time points from 2010 to 2016, and both carbon and nitrogen isotopic signatures were measured. The contrast in $\delta^{13}\text{C}$ between average marine organic matter (ca. -20‰), oil (ca. -27‰) and methane (ca. -57‰) provides a robust tool for exploring the pathways and mechanisms of assimilation of petrocarbon into both phyto- and zooplankton. Similarly, the differences in $\delta^{15}\text{N}$ between subsurface nitrate (ca. 4.5 ‰), and nitrogen fixation (ca. -2‰), help assess the different nitrogen sources being incorporated into biomass in the system. In this study, we document the presence of petrocarbon from the DWH spill in suspended particles up to 6 years after the explosion, as reflected in decreasing $\delta^{13}\text{C}$ through time at all stations. Interestingly, the $\delta^{15}\text{N}$ of suspended particles also decreased over time at most stations, suggesting a possible relationship between nitrogen fixation and the presence of petrocarbon. In contrast, zooplankton $\delta^{13}\text{C}$ values did not reflect persistent hydrocarbon incorporation, and increased over time suggesting a rapid movement of petrocarbon into the foodweb followed by recovery to apparent baseline conditions within several years. While $\delta^{15}\text{N}$ values in zooplankton followed a pattern similar to that in suspended particles, $\delta^{13}\text{C}$ values and zooplankton biomass showed opposite trends suggesting that zooplankton are selectively feeding on new primary production and avoiding petrocarbon-derived material.

* Indicates Presenting Author

Oral Session III
2:30 – 4:00 PM
Saturday April 1, 2017
Miller Learning Center

2:30 PM

**13. Oceanographic Redox Changes Associated
with the Late Silurian Lau Extinction Event:
New Geochemical Evidence from Central
Tennessee and Latvia**

Chelsie N. Bowman*, Seth A. Young, Jeremy D. Owens

Florida State University

The late Silurian is characterized by global oceanographic and biotic changes related to the Lau carbon isotope excursion (CIE). The Lau CIE is well documented in areas such as Sweden, Ukraine, Australia, and North America. This excursion is one of the largest positive carbon isotope excursions recorded in the Phanerozoic, +8‰ or greater in some localities. The associated Lau-Kozłowski extinction event (LKE), was initially discovered in conodonts and graptolites, but has since been documented in many other prevalent marine faunas, and is the most severe and widespread documented biotic event in the Silurian. Importantly, anachronistic sedimentary facies have also been associated with the LKE, which are comparable to those linked with larger mass extinction events such as the Permo-Triassic. The causes and consequences of this extinction event and the related CIE are not well understood with most work hypothesizing changes in the global carbon cycle, redox conditions and/or eustatic sea level. Here we report high-resolution paired $\delta^{34}\text{S}_{\text{CAS}}$ and $\delta^{13}\text{C}_{\text{carb}}$ analyses from the Brownsport Formation, central Tennessee; $\delta^{13}\text{C}_{\text{carb}}$ analyses from the Roberts Mountain Formation. Also, we report a new, multi-proxy data set for the late Silurian in the Priekule-20 drill core from Latvia, including $\delta^{13}\text{C}_{\text{carb}}$, $\delta^{13}\text{C}_{\text{org}}$, total organic carbon, trace metal enrichments, Fe speciation, and $\epsilon^{205}\text{Tl}$ analyses.

This data will help to elucidate the temporal variations of the global carbon cycle during such a perturbation though the use of multiple isotope systematics and redox proxies. This study begins to test, across multiple ocean basins, whether the Lau CIE was the result of the increased burial of organic carbon because of reducing conditions in the world's oceans or the weathering of a subaerial carbonate platform due to eustatic sea level fall. Coeval positive excursions in both the $\delta^{13}\text{C}$ and $\delta^{34}\text{S}$

data would suggest the carbon isotope excursion was caused by the global burial of organic matter and pyrite in euxinic (anoxic and sulfidic) waters. An expansion of wide-spread global euxinia would drive a dramatic $\delta^{34}\text{S}$ excursion and be detrimental to marine life which could serve as a mechanistic cause for the extinction event that occurs during the rising limb of the Lau CIE. Other proxies, such as Fe speciation, trace metal concentrations and Tl isotopes, will help determine local vs. global conditions and the global extent of anoxia and euxinia.

2:45 PM

**14. The Importance of Soil pH in Controlling
Organic Carbon Transformations in Arctic
Polygon Tundra**

Jianqiu Zheng*, Guoping Tang, Fengming Yuan, Peter Thornton, Boahua Gu, Stan Wullschlegel, David Graham

Oak Ridge National Laboratory

Accurately simulating CO_2 and CH_4 emissions from high latitude soils is critically important for reducing uncertainties in soil carbon-climate feedback predictions. The signature ice-wedge polygons in Arctic tundra have a high level of heterogeneity in soil thermal regime, hydrology and oxygen availability, which limits the application of current land surface models using simple moisture response functions. We synthesized data from incubations of Arctic soils across a wet-to-dry permafrost degradation gradient from low-centered to flat- and high-centered polygons to assess the Community Land Model Carbon Nitrogen (CLM-CN) decomposition cascade with extended anaerobic organic carbon transformations, including fermentation, iron reduction, and methanogenesis reactions. Modification of the Windermere Humic Aqueous Model (WHAM) enabled us to approximately describe the measured soil pH buffering capacity with model simulations. Separate parameterizations of pH response functions for fermentation, iron reduction and methanogenesis improved the simulation of pH evolution, including the initial pH drop due to organic acid accumulation caused by fermentation and then a pH increase due to iron reduction and methanogenesis. Accurate representation

* Indicates Presenting Author

of pH evolution also significantly improved CO₂ prediction as the speciation of CO₂ between gas, aqueous and solid (adsorbed) phases were better simulated under varying pH. These results provided critical insights into the process of soil decomposition, and demonstrated the importance of soil pH in controlling biogeochemical reactions in the Arctic.

3:00 PM

15. Metabolic Potential and *in situ* Activity of Marine Group A-SAR406 Bacteria in an Anoxic Water Column

Anthony D. Bertagnolli*, Cory C. Padilla, Jennifer B. Glass, Bo Thamdrup, Frank J. Stewart

Georgia Institute of Technology

Two near complete (94-97%) genomes from the PN262000N21 and ARCTIC96B-7 subgroups of MGA-SAR406, abundant members of oxygen minimum zones (OMZ), were assembled using metagenomes collected in the anoxic coastal OMZ of Golfo Dulce, Costa Rica. Genes for aerobic carbon monoxide (CO) oxidation, polysulfide metabolism, and hydrogen utilization were identified only in the PN262000N21 genome, suggesting a potential for lithotrophic metabolisms. Transcripts mapping to these genomes increased from <0.3% of total mRNA in metatranscriptomes from the oxic zone to a max of 22% under anoxia, with transcript pools of both taxa encoding dissimilatory nitrate reductase, implying contributions to OMZ nitrogen cycling by MGA-SAR406 lineages. PN262000N21 transcript representation was relatively constant throughout the anoxic zone, while ARCTIC96B-7 representation decreased by an order of magnitude from non-sulfidic to sulfidic depths. Transcripts mapping to PN262000N21 at sulfidic depths were enriched in thioredoxin (Trx)-containing negative regulators of GroEL and sulfur transferases harboring multiple rhodanese domains (thiosulfate sulfur transferase). Genes encoding a large protein with pectin and fibronectin domains similar to those in cellulosome-producing anaerobes were also abundant in PN262000N21. These data provide the first complete molecular description of any MGA-SAR406 subgroup, and provide evidence for niche

differentiation driven by local chemical conditions.

3:15 PM

16. Quorum Sensing in a Biofilm: Investigating How Interspecies Interactions Contribute to Biofilm Ecology

April Armes*, Nathan Cude, Alison Buchan

University of Tennessee

Heterotrophic marine bacteria play a central role in the recycling of carbon in the ocean. One group of heterotrophic marine alpha-proteobacteria, the Roseobacter Clade, dominates marine biofilms in coastal environments (Buchan 2014). Roseobacters have been shown to produce secondary metabolites with antimicrobial activities (Bruhn, 2007; Geng, 2008; Berger, 2011; Cude 2012). These antimicrobial agents inhibit growth of potential competitors, ultimately affecting carbon cycling within the biofilm. Density dependent cellular communication, in the form of quorum sensing (QS) molecules, play important roles in such relationships. The complex hierarchical regulation of antimicrobial production via QS in marine biofilms has not been fully explored. The roseobacter *Phaeobacter sp.* strain Y4I produces the blue antimicrobial indigoiodine, which has been shown to inhibit the growth of several marine bacteria, including *Vibrio fischeri* (Cude 2012, 2015). In Y4I, indigoiodine is under the regulation of two separate QS systems (Cude 2015). Current genetic investigations are underway to understand the contributions of each QS system to the genetic regulation of indigoiodine biosynthesis and how these systems affect the colonization success of Y4I. Elucidating the QS hierarchical regulatory network in relation to antimicrobial production will further our understanding of how antimicrobials are produced and how the production of antimicrobials alters the structure and function of marine biofilms.

3:30 PM

17. Structure and Function of the Sphagnum Phytobiome

Max Kolton*, Luis H. Orellana, Konstantinos T Konstantinidis, David Weston, Joel E. Kostka

Georgia Institute of Technology

Peat mosses of the genus *Sphagnum* are among the oldest of root-less terrestrial plants. *Sphagnum* dominates many peatland ecosystems and plays a crucial role in the

global nitrogen and carbon cycle. While the physiology and ecology of Sphagnum has been well-studied, the recruitment of specific microbial populations into the plant endosphere and their ecosystem function is poorly understood. We are applying a multi-omic approach to assess the role of plant species (*S. fallax* and *S. magellanicum*) and microhabitat in shaping phytobiome composition, metabolic potential, and photosynthetic production. In three independent microhabitats, *S. magellanicum* harbored a significantly higher phylosphere microbial diversity in comparison to *S. fallax*. Moreover, a significantly different taxonomic composition was observed between the two Sphagnum species hosts. While α -Proteobacteria were overrepresented in *S. fallax* phyto-biomes, delta- and gamma-Proteobacteria were more prevalent in the *S. magellanicum* phytobiomes. Genes involved in nitrogen metabolism were highly abundant in the *S. fallax* phytobiome, while genes for capsular and extracellular polysaccharide metabolism were relatively enriched in *S. magellanicum*, which usually colonizes dryer microhabitats. Interestingly, the nitrogen-fixing core-microbiome consisted of only 2 members, taxonomically affiliated with *Nostoc azollae* (symbiotic Cyanobacteria) and *Methyloferula stellate* (an obligate methanotroph). Finally, taxonomic and functional analysis indicated that the nitrogen-fixing cyanobacterial genus *Nostoc* represents 27% of total annotations in metagenomes sampled from the Sphagnum gametophyte. These results underlines a critical role of the nitrogen-fixing genus *Nostoc* in the Sphagnum phytobiome. Additionally we supported hypothesis that that both microhabitat and plant species collectively shaping phytobiome composition.

3:45 PM

18. Reductive Dechlorination of Vinyl Chloride to Ethene in the Absence of *Dehalococcoides mccartyi* and its Implication

Yi Yang*, Steven A. Higgins, Jun Yan , Burcu Simsir, Frank E. Löffler ; Karuna Chourey, Robert Hettich, Brett Baldwin, Dora M. Ogles

University of Georgia, University of Tennessee

Vinyl chloride (VC), a human carcinogen, is a daughter product of tetrachloroethene (PCE) and trichloroethene (TCE) reductive dechlorination, which are common groundwater contaminants. TCE and VC are ranked #16 and #4 on the Priority List of Hazardous Substances (SPL) and have been detected in 1,045 and 593 sites, respectively. The reductive dechlorination of chlorinated ethenes to non-toxic ethene has been attributed exclusively to *Dehalococcoides mccartyi* (Dhc) strains. Therefore, research has mainly focused on

characterizing Dhc cultures and a few functional reductive dehalogenase (RDase) genes implicated in the reductive dechlorination of chlorinated ethenes have been identified. Consequently, site assessment, bioremediation monitoring, and decision-making rely on the quantitative assessment of Dhc biomarker genes in groundwater. The goal of this study was to identify the population responsible for VC-to-ethene reductive dechlorination in an enrichment culture that tested negative for the presence of Dhc biomarker genes. The enrichment culture dechlorinated VC to ethene and the activity was maintained in transfer cultures in defined medium. Repeated efforts to detect Dhc biomarker genes failed suggesting that Dhc did not contribute to the VC reductive dechlorination in this culture. The 16S rRNA gene amplicon sequencing data indicated the dominance of a population phylogenetically related to the genus *Dehalogenimonas* (Dhgm) and corroborated the absence of Dhc. Metagenome sequencing of the enrichment culture enabled the assembly of a 2 Mbp Dhgm draft genome, and 52 putative reductive dehalogenase (RDase) genes were identified. A survey of 1,237 groundwater samples collected from 111 chlorinated solvent-contaminated sites revealed quantifiable Dhgm and Dhc 16S rRNA genes in 812 samples with a median Dhgm-to-Dhc ratio of 3.83. These findings demonstrate that the ability to grow with VC as respiratory electron acceptor is not limited to Dhc, and some members of the Dhgm genus can couple VC-to-ethene reductive dechlorination to growth. These findings impact site assessment, monitoring, decision-making and management, and are an important step toward implementing precision bioremediation (i.e., customized remediation with decisions and treatments being tailored to specific site conditions) at sites impacted with chlorinated ethenes.

* Indicates Presenting Author

Poster Session I
4:00 - 5:30 PM
Saturday April 1, 2017
Miller Learning Center

**1. Hydrologic Processes Determining
Porewater Salinity in a Southeastern Salt
Marsh**

David Miklesh*, Christof Meile

University of Georgia

Coastal wetlands provide many important ecosystem services, which include carbon and nitrogen sequestration and transformations, the provision of habitats, and the reduction of erosion by the vegetation. In coastal marsh ecosystems, porewater salinity strongly determines vegetation distribution and productivity. Therefore, as part of the Georgia Coastal Ecosystems Long Term Ecological Research project, an integrated modeling approach has been developed and applied to the Duplin River marsh, Sapelo Island, Georgia, which simulates porewater salinity and water content distributions in surface sediments across the entire Duplin River marsh domain. The development of the soil model is presented, which is based on mass conservation for water and salt and links physical, hydrological, and biological processes that determine porewater salinity, including precipitation, evapotranspiration, salt exchange between surface and subsurface, groundwater exchange, and tidal inundation, with the lateral exchange controlled by marsh topography. Model validation is performed by comparing model-estimated salinities to porewater salinity measurements of the same vegetation class and marsh elevation. To identify the environmental factors that control marsh salinities, a sensitivity analysis was carried out that assesses the effect of precipitation intensity, evapotranspiration, hydraulic conductivity, salt exchange, tidal salinity, and marsh elevation have on porewater salinities. Also, model-derived variability in porewater salinities was quantified over seasonal and interannual time scales, accounting for drought, normal conditions and years with excess rain. Annual simulations and the sensitivity analysis reveal that vegetation classes can be split up into two groups, low marsh plants—short, medium, and tall *Spartina alterniflora*—and high marsh plants—*Borrchia frutescens*, *Batis maritima*, *Juncus roemerianus*, and *Sarcocornia spp.* Initial results show that low marsh porewater salinity in our study region is sensitive to changes in the salinity of the flooding tide, which is strongly correlated with

Altamaha River flow, whereas the high marsh is sensitive to changes in precipitation and evapotranspiration.

**2. Temporal and Spatial Changes in Dissolved
Organic Matter Composition in a Marsh-
dominated Estuary: Insights from Optical and
FT-ICR MS Analyses**

Maria Letourneau*, V. Ruth Pannill, Patricia M.
Medeiros

University of Georgia

Bacterial transformations of dissolved organic matter (DOM) in a marsh-dominated estuarine system were investigated using bulk (DOC), optical (chromophoric DOM), and molecular (ultrahigh resolution mass spectrometry; FT-ICR MS) analyses. Monthly surface water samples were taken over a year (October 2015 – September 2016) covering different hydrological regimes at the Altamaha River (salinity $S = 0$ to 5; strong terrigenous inputs) and near the head of Sapelo Sound ($S = 7.3$ to 31.5; mixture of terrigenous, marine and salt marsh inputs). Samples were dark-incubated over short- and long-term intervals. Preliminary results show that increased river discharge resulted in higher DOC concentrations and increased average molecular size and aromaticity at both sampling locations. A clear microbial preference for degradation of compounds associated with marine DOM relative to those of terrestrial origin was observed, especially during low river discharge. Understanding transformations of the DOM pool in estuaries is important in order to constraint the characteristics of DOM introduced to the coastal zone that may ultimately reach the deep sea.

* Indicates Presenting Author

3. Dimethylsulfoniopropionate Degradation in the Coastal Ocean: Gene- and Taxon-Centric Approaches

Brent Nowinski*, Christina M. Preston, Ronald P. Kiene, Christopher A. Scholin, James M. Birch, William B. Whitman, Mary Ann Moran

University of Georgia

Dimethylsulfoniopropionate (DMSP) is an abundant organic sulfur and carbon compound produced by marine phytoplankton. Marine bacteria transform DMSP via two pathways: the demethylation pathway retains DMSP-derived sulfur in the cell where it can be incorporated into biomass or oxidized, while the cleavage pathway releases volatile DMS with potential implications for cloud formation. The prominent hypothesis explaining differential regulation of these pathways poses that demethylation is favored when DMSP dominates the organic sulfur pool, while cleavage is favored when other organic sulfur compounds can substitute as the cellular sulfur source. Marine phytoplankton groups differ in their production and release of DMSP and other organic sulfur compounds, so shifts in phytoplankton community composition alter sulfur source availability. We tracked bacterial DMSP gene abundance in Monterey Bay surface waters during a 21-day study in which the Environmental Sample Processor (ESP) autonomously filtered and archived the seawater microbial community.

Sequencing of twelve metagenomes during the ESP deployment showed taxa known to carry DMSP genes made up 23-39% of the bacterial community, with SAR11-like cells representing the most abundant DMSP degraders, followed by Roseobacter-, SAR116-, and marine gamma proteobacterium HTCC2080-like cells. Placement of metagenomic reads to reference, assembled, and single-cell genomes revealed nine major clades of DMSP demethylation (*dmdA*) genes, with SAR11-like cells the source of 53%. Roseobacter-like cells were the source of most of the DMSP cleavage genes, averaging 63% of *dddP*, *dddK*, *dddQ*, and *dddD* genes.

Over the ESP deployment, chlorophyll *a* measurements remained relatively low for this coastal system (~1-7 $\mu\text{g L}^{-1}$). The abundance of picoeukaryotes and the diatom *Pseudo-nitzschia* was elevated at the end of the deployment, co-occurring with low DMSP concentrations and consumption rates. However, dynamics in the phytoplankton community were not associated with changes between the four major groups of the bacterial DMSP degrading community. DMSP

degraders compose a large fraction of the bacterial community in this coastal ecosystem, and changes in the relative abundance of these cells may not be closely connected to the phytoplankton community in the absence of blooms of DMSP-producing phytoplankton.

4. Potential for the Microbially-driven Fenton Reaction in Subsurface Environments

Nan Xie*, Martial Taillefert

Georgia Institute of Technology

The “Fenton reaction” or the oxidation of ferrous iron (Fe(II)) by hydrogen peroxide (H_2O_2) to form reactive oxygen species (ROS) is well known to promote the degradation of organic substrates and currently accepted as one of the most effective methods for the degradation of organic pollutants. The conventional Fenton reaction presents the disadvantage that Fenton reagents (i.e. H_2O_2 and Fe(II)) must be continuously supplied to drive the chemical degradation of contaminants. In recent studies, a microbially-driven Fenton reaction system (driven by the Fe(III)-reducing facultative anaerobe *S. oneidensis*) was designed to produce H_2O_2 via microbial respiration under aerobic conditions and Fe(II) via microbial Fe(III) reduction under anaerobic conditions. Alternating between aerobic and anaerobic conditions periodically produced both H_2O_2 and Fe(II) and alleviated the need for continuous addition of Fenton reagents. The Fenton reaction promoted by these conditions generated ROS to degrade source zone levels of TCE, PCE, and 1,4-dioxane as single contaminants or as binary and ternary mixtures. As iron oxyhydroxides are ubiquitous reactive constituents of soils and sediments, the metabolic activity of iron reducing bacteria may contribute to a significant fraction of organic matter degradation in subsurface environments. Upon reoxidation during rain events, the microbially-driven Fenton reaction may degrade various organic contaminants in subsurface environments. The objective of this project is to reconfigure the microbially-driven Fenton reaction in flow-through columns and develop reactive transport models to characterize and predict the role of ROS in the transformation of organic contaminants. In this study, the concentration of Fe(II) and H_2O_2 was monitored at the output of flow-through columns loaded with ferrihydrite-coated sand and *S. oneidensis* to determine the potential for sustained ROS production under periodic aerobic and anaerobic conditions.

* Indicates Presenting Author

5. The Potential Growth Regulating Function of Extracellular Superoxide Production by Phytoplankton

Sydney Plummer*, Julia M Diaz, Elizabeth Harvey

University of Georgia

Phytoplankton serve critical ecosystem roles in primary production, oxygen generation, and carbon dioxide uptake, impacting climate and marine food webs. Therefore, mechanisms that regulate phytoplankton blooms have profound global effects. Biological production of extracellular Reactive Oxygen Species (ROS), such as superoxide, by phytoplankton may be a widespread growth regulating strategy, as evidenced by the role of ROS in growth regulation in some phytoplankton species, as well as other eukaryotes, and prokaryotes. Here, we measured the net superoxide production rates and steady state superoxide concentrations at increasing cell densities of phytoplankton during exponential and stationary growth phase to help elucidate the potential growth regulating function of extracellular superoxide production by phytoplankton. Net superoxide production rates and steady state superoxide concentrations were obtained by detecting chemiluminescence emitted through the reaction of superoxide and the superoxide specific probe methyl Cypridina luciferin analog (MCLA) at increasing cell densities and at different stages of growth. Our results demonstrate higher rates of superoxide production during exponential phase than at stationary phase in *Emiliana huxleyi* CCMP 374. These results render further studies on the effects of extracellular superoxide production during different growth phases of model phytoplankton to elucidate its potential mechanism of growth regulation in these organisms.

6. Microbial Community Changes and Crude Oil Biodegradation in Global Deep Oceans

Jiang Liu*, Stephen M. Techtmann, Hannah L. Woo, Daliang Ning, Julian L. Fortney, Terry C. Hazen

University of Tennessee

Many studies have shown that microbial communities can play an important role in oil spill cleanup. However, very limited information is available on the oil degradation potential and microbial community response to crude oil contamination in deep oceans. Therefore, we investigated the response of microbial communities to crude oil and dispersant in various deep-sea basins around the world where oil exploration

is anticipated (Eastern and Central Mediterranean Sea, Great Australian Bight and Caspian Sea). In-lab microcosm experiments were set up aerobically to study the microbial respiration, community changes and oil biodegradation.

Microbial respiration followed a similar pattern in all of these basins. The treatment of oil and dispersant had the highest CO₂ production. The amendment of oil lead to a higher CO₂ accumulation compared to control. However, they were all much lower than the Gulf of Mexico (GOM). What's more, oil biodegradation occurs in all of the sites. The total organic carbon revealed that a big portion of oil was degraded in the first several days, which was consistent with the GC-MS results.

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. Oil and dispersant can simplify the community and speed up the oil biodegradation. In particular, the relative abundance of Proteobacteria increased drastically while the relative abundance of archaea decreased. In addition, although oil and dispersant drive the community into a similar endpoint, different bacterial groups were found associating with oil and dispersant.

7. Transcriptomic Characterization of *Vibrio vulnificus* Viable-But-Nonculturable (VBNC) Dormancy Dynamics

Tiffany Williams*, Seongwon Kim, Gary Vora and James D. Oliver

University of North Carolina, Charlotte

The viable but nonculturable (VBNC) state is a well-recognized form of bacterial dormancy, in which exposure to stressful environmental conditions cause populations to cease growth and to escape detection using culture-based methods. At least 105 bacterial species have been reported to enter the VBNC state in response to environmental stress. *Vibrio vulnificus*, a global estuarine bacterium and opportunistic pathogen, enters the VBNC state when exposed to low temperature (<10° C). This dormancy mechanism is presumed to act as a survival mechanism allowing populations to persist in the environment throughout seasonal transitions. Little is known regarding the molecular mechanisms of VBNC cell formation and resuscitation, thus the objective of the current study was to obtain a comprehensive understanding of the mechanisms facilitating VBNC dormancy mechanisms.

* Indicates Presenting Author

To do this, we performed temporal transcriptomics of *Vibrio vulnificus* in seawater microcosms placed at 4° C. Entry into the VBNC state was monitored by measuring culturability over time. Once the entire population was non-culturable, resuscitation was induced by incubation at 22° C. Samples were harvested from log phase cells and on days 0 (pre-VBNC), 2 (early VBNC), 14 (late VBNC), and after resuscitation. Samples were subjected to RNA extraction, rRNA depletion, and Illumina transcriptome sequencing. Pairwise comparisons revealed a substantial transition in gene expression during early VBNC formation followed by fewer changes as time passed. Resuscitation resulted in a significant burst in the gene expression profile distinct from pre-VBNC populations indicating that resuscitated populations take on a unique physiology. Currently, we are investigating specific differentially expressed genes to pinpoint mechanisms underlying the dormancy process. This temporal study will allow for a more resolved investigation into the complex dynamics involved in VBNC cell formation and resuscitation.

8. A Bottom-Up Method to Estimate Species-Specific Primary Production Rates on Coral Reefs

Daniel P. Owen*, Brian M. Hopkinson, William K. Fitt

University of Georgia

Coral reefs are known to have extremely high rates of primary production, but the methods used to obtain these rates cannot distinguish which primary producers are responsible. Corals visually dominate the landscape on pristine reefs, but primary producers on coral reefs are diverse and include corals (through their symbiotic algae), fleshy algae, turf algae, and gorgonians. Here we present an approach to estimate the contribution of different types of primary producers to total primary production on coral reefs. First, photographic 3D mapping is employed to build high resolution 3D images of the benthic ecosystem. Next, primary producers are identified in the 3D reconstruction using machine learning tools. Chamber measurements of photosynthetic rates of the major sessile components of a reef benthic community are then obtained as a function of irradiance, the primary short-term driver of photosynthesis. The metabolic rates of individual reef community members, together with the surface areas obtained from the 3D benthic maps, will allow for a bottom up estimate of total reef metabolism and partitioning of total reef productivity among community members. Our primary study site is Little Grecian Reef in the Florida Keys where we have obtained preliminary measurements of

photosynthetic rates on the dominant primary producers and have generated 3D reconstructions of sections of the reef.

9. A Transcriptional Analysis of Anaerobic Respiration in the Dissimilatory Metalloid-Reducing Bacterium *Desulfuribacillus stibiiarsenatis* MLFW-2

Christopher A. Abin*, James T. Hollibaugh

University of Georgia

Bacteria and archaea are known to exploit a wide range of environments characterized by extremes of redox conditions. This metabolic versatility has largely arisen out of a capacity to produce enzymes capable of catalyzing a remarkable range of energy-conserving substrate interconversions. Complex iron-sulfur molybdoenzymes (CISMs) are a group of ancient enzymes that play important roles in electron transport by catalyzing redox reactions involving oxyanions of nitrogen, arsenic, selenium, tellurium, chlorine, and sulfur. Based on phylogenetic analyses of the catalytic subunits, a total of at least 15 different clades comprise the CISM superfamily. However, our knowledge of these enzymes is incomplete and there exist several clades for which the biological function(s) remain undefined. Therefore, our goal is to derive a function for these unknown CISMs using physiological experiments coupled with transcriptional analyses such as RT-qPCR. Recently, we isolated and described an obligately anaerobic bacterium, *Desulfuribacillus stibiiarsenatis* MLFW-2, capable of using nitrate, nitrite, DMSO, As(V), Se(VI), Se(IV), and Sb(V) as terminal electron acceptors for growth. The genome of *D. stibiiarsenatis* MLFW-2 encodes 17 putative CISMs, the majority of which may be involved in anaerobic respiration. We are gaining a better understanding of CISM function in *D. stibiiarsenatis* MLFW-2 by measuring their relative gene expression during growth on specific electron acceptors. Of particular interest is the terminal reductase responsible for the conversion of Sb(V) to Sb(III), for which no data currently exist in the literature.

* Indicates Presenting Author

10. Location and Continuity of the Annual Hypoxic Zone Influences Microbial Diversity in the Gulf of Mexico

Lauren E. Gillies*, J. Cameron Thrash, Nancy N. Rabalais, and Olivia U. Mason

Florida State University

The world's second largest coastal hypoxic (≤ 2 mg of O_2 L⁻¹) zone (HZ) occurs annually in the northern Gulf of Mexico (nGOM). As part of a multi-year time series characterizing the microbial community in this HZ, water column samples were collected at both the surface and oxygen minimum of 52 sites, 27 of which were hypoxic. In 2014, the HZ was discontinuous, shallow and primarily located at the Mississippi River (MR) mouth, which contrasts with the continuous and deeper 2013 HZ. Thaumarchaeota, closely related to *Nitrosopumilus maritimus* were dominant in both years as were archaeal ammonia-monooxygenase (amoA) genes (16S rRNA gene iTag sequencing and quantitative polymerase chain reaction (qPCR) of Thaumarchaeota 16S rRNA genes). In both years these genes had a significant inverse correlation with dissolved oxygen (DO) concentrations. However, the abundance of the dominant Thaumarchaeota Operational Taxonomic Unit was lower in 2014 than 2013, yet the absolute abundances (qPCR) of Thaumarchaeota were higher in 2014 than 2013. Further, the 2014 qPCR data revealed that Thaumarchaeota were highest at the mouth of the MR. These datasets exhibited that low DO adapted Thaumarchaeota may be composed of sub-populations with higher abundances when conditions with a strong riverine influence prevail, as they did in 2014. Oligotyping analysis of *Nitrosopumilus* 16S rRNA gene sequences (iTag) revealed that one oligotype was significantly inversely correlated with DO in both years, suggesting an oligotype adapted to low DO conditions. Patterns of microbial co-occurrence emerged between *Nitrosopumilus*, MGII Euryarchaeota and Nitrospina that varied with biogeochemical conditions, where co-occurrence was statistically stronger between these species in 2014 HZ, when Thaumarchaeota abundance was lower. Taken together, the data suggested the location and continuity of the nGOM HZ influenced the spatial extent of the nGOM ammonia-oxidizing archaeal hotspot, the abundance of a low DO adapted oligotype and the co-occurrence patterns of specific microorganisms.

11. Alternative Molecules for the Imaging of Carbohydrates

Max Lowman*, Carol Arnosti

University of North Carolina, Chapel Hill

Polysaccharides are major constituents of marine organic matter, fueling considerable heterotrophic production. Investigating the dynamics of carbohydrates in marine systems is difficult, however, because carbohydrates lack the chemical characteristics that would allow them to be readily quantified or extracted from the water column or sediments. New advances in imaging techniques – as well as new insights into the mechanisms by which carbohydrates are processed by marine microbes - offer the opportunity to design novel probes which can more be used to investigate the bioavailability of carbohydrates to microbial communities. We focused on the synthesis and characterization of alternative molecules for use in measuring the carbohydrate processing in marine systems. Our objectives were to label the disaccharide sucrose with an established fluorophore which fluoresces in the 530nm range, and to test the efficacy of a new fluorophore that fluoresces in the 615nm range.

Fluoresceinamine has been successfully used to label larger polysaccharides for studies of hydrolysis rates in marine systems, but its usefulness in tagging smaller carbohydrates, including the disaccharide sucrose, was unknown. Sucrose is an important plant-sourced nutrient in saltmarsh ecosystems, and could be useful in studies of a variety of bacterial communities if appropriate imaging techniques were developed. Using a carbodiimide coupling reaction, the activated sucrose was reacted with the primary amine on the fluorescent tag to form a stable covalent linkage. We are investigating strategies to separate labeled sucrose from unreacted tag, and will use NMR to characterize the reaction products.

The new fluorescent tag chosen was Texas Red cadaverine which also had a primary amine and minimal functional groups that could facilitate unwanted side reactions. Similarly to fluoresceinamine, its primary amine was used to form a stable covalent linkage to chondroitin-6-sulfate through a carbodiimide based coupling reaction. TR cadaverine's utility was also tested with laminarin. A gel permeation column was used to separate the unreacted tag from the labeled polysaccharide and a stability test was carried out to measure shelf life of the labeled product over the span of 1 week at 70°C. For the tests with chondroitin-6-sulfate, a 30 kD filtration cartridge was used to wash unreacted tag off by centrifugation because the gel permeation

* Indicates Presenting Author

column proved to be inefficient. Unreacted tag was then collected and concentrated using solid phase extraction for possible reuse.

Having a diverse selection of distinct fluorescent tags is desirable because it allows the measurement of multiple carbohydrates in the same experiment. It also facilitates investigations using advanced microscopic techniques that are optimized for specific fluorescence characteristics.

12. The Impact of Saharan Dust Deposition on Bacterioplankton in Marine Surface Waters

Trace Borchardt*, Elizabeth Ottesen, Erin Lipp

University of Georgia

Each year dust storms in the Middle East, North-China, Australia, and North-Africa lift ~1,700 Tg of dust into the atmosphere where it is globally transported by wind. The transportation and deposition of this dust affects global biogeochemical cycles, climate change, and human health. The North African Saharan Desert contributes 69% of this atmospheric dust, most of which settles in the tropical North Atlantic. A number of studies have suggested that dust deposition has large impacts on marine microbial community structure and function. However, most published work has been carried out using experimental microcosms and simulated dust events. In the summer of 2016, we collected daily snapshots of microbial (bacterial and archaeal) community composition using high-throughput 16S rRNA gene amplicon sequencing. During this time series, we captured multiple in situ dust deposition events. The depositions caused large changes in microbial community composition, resulting in significant changes in the abundance of major marine bacterial lineages such as *Prochlorococcus*, *Synechococcus*, and *Pelagibacter*. In addition, less abundant, opportunistic taxa such as *Vibrionales*, *Cryomorphaceae* and members of the *Rhodobacteraceae* showed significant changes in abundance. Experimental incubations of unamended seawater collected immediately following a dust deposition event showed similar shifts in community composition as the in situ community after 24 hours. However, similar shifts were not observed when seawater unaffected by dust was amended with similar quantities of nutrients typically found in dust, including iron, carbon, and phosphorus. Together, these results suggest that 1.) Saharan dust deposition events can stimulate large shifts in marine surface water microbial communities, and 2.) these responses are not easily simulated through the

addition of individual dust constituents.

13. Study of Orange Guaymas *Beggiatoa Spp.* Recombinant Proteins Involved in the Nitrite Reduction Pathway

Andrew Buckley*, Barbara MacGregor, Luke McKay, Andreas Teske

University of North Carolina, Chapel Hill

Members of the *Beggiatoaceae* family are generally characterized as sulfide-oxidizing bacteria that form large, filamentous microbial mats in freshwater or marine environments. Representative taxa contain a large central vacuole that accumulates nitrate that could be used to oxidize sulfide for energy. The Guaymas Basin in the Gulf of California is replete in hydrothermal vents and sulfide-rich seeps that support polymicrobial mat communities that volumetrically consist of mainly *Beggiatoa Spp.*, and may reach several meters in diameter. The Orange Guaymas *Beggiatoa Spp.* (BOGUAY), like most marine *Beggiatoaceae*, remain unculturable and must be procured by submersible from the seafloor. Primary sample material subjected to physiologic and enzymatic procedures result in sample destruction, and therefore limits the amount of physiologic studies that can be performed. Amplified BOGUAY genomic DNA was used to create recombinant-proteins in *E. coli* for use in cell-free enzymatic studies, to reduce the initial amount of sample material used. Three genes currently targeted are BOGUAY_0691, BOGUAY_2386, and BOGUAY_2967, which putatively code for secreted orange nitrite reductase, periplasmic *NirS*-like nitrite reductase, and membrane associated octaheme nitrite reductase respectively. The classified enzymatic function of the named proteins is to reduce nitrite to either nitric oxide or ammonia. The enzymes represent parts of a proposed nitrate reduction pathway in BOGUAY. The project objective is to generate a cell-free physiologic characterization of *Beggiatoa* nitrogen metabolic pathways.

14. What makes a bloom in the Amundsen Sea Polynya? A 1-D biogeochemical modeling perspective

Hilde Oliver*, Pierre St-Laurent, Rob Sherrell, Patricia Yager

University of Georgia

The Amundsen Sea Polynya (ASP) is the most productive

* Indicates Presenting Author

(per square meter) region in the Southern Ocean. Both increased glacial melt and sea ice decline have affected the ASP over the past few decades, and processes underlying the intense phytoplankton blooms are not yet fully understood. Here we use a 1-D biogeochemical model (ROMS “Bio-toy”) to identify the importance of various processes to the inception, rise, and decline of the bloom. Model runs are compared to conditions observed during ASPIRE 2010-11 at thirteen stations that ranged from early bloom to high bloom conditions. We use the 1-D model to estimate how the initial water column stratification and lateral iron inputs cause important differences in the bloom’s development. The relative importance of these two factors vary according to distance from the ice sheet (a key iron input) and distance from the Thwaites Ice Tongue, where mixed layers are thickest. We specifically focus on the bloom timing, chlorophyll, primary productivity, nitrate drawdown, iron concentrations, light/nutrient limitation, and export at each station. This work is part of the NSF-funded INSPIRE project.

15. Nitrogen Fixation Dynamics During Ecosystem Recovery in Longleaf Pine Savannas

Julie Tierney*, Nina Wurzburger

University of Georgia

Biological nitrogen fixation (BNF) is a critical source of new N for disturbed terrestrial ecosystems, yet how BNF is regulated and organized over time remains unclear. Here, we investigated how BNF dynamics change throughout ecosystem development in restored longleaf pine savannas, and how BNF responds to fire. We examined BNF in 59 1-ha plots of longleaf pine distributed across gradients of age and fire frequency at two sites (Fort Benning and Eglin AFB) in the southeastern US. We determined plot-level BNF contributions by three functional groups of N-fixers (herbaceous legumes, biological soil crusts, and heterotrophic N-fixing bacteria) by quantifying their abundances and assessing nitrogenase activity. We also estimated the balance of available N in each plot as the difference between N supply (mineralization and deposition) and N demand from biomass growth. We fit linear models to evaluate the effects of stand age and fire disturbance on BNF and N demands throughout stand development. We found that the three taxonomic groups of N fixers differed in the magnitude and timing of BNF over stand age, and that fire frequency had differential effects on BNF. Legumes contributed the most to ecosystem BNF, and rates remained constant

over time, which challenges the expectation that BNF peaks in early stages of development in temperate terrestrial ecosystems. Soil crusts, however, fixed the most N in the youngest stands. Both fire return interval and months since fire negatively correlated with legume BNF, indicating that fire promotes N-fixation on annual and decadal time scales. Soil N availability did not influence patterns of BNF in any group, suggesting that obligate fixation strategies prevail in longleaf pine savannas. In total, site difference explained the most variation in BNF rates where Fort Benning supported more BNF than Eglin AFB, raising questions about landscape-level drivers of BNF in these ecosystems.

16. Oxidation of Polyamine Nitrogen by Marine Thaumarchaeota in the Coastal Ocean and the Laboratory

Julian Damashek*, Natalie J. Wallsgrove, Barbara Bayer, Gerhard J. Herndl, Brian N. Popp, James T. Hollibaugh

University of Georgia

Dissolved organic nitrogen (DON) is a substantial fraction of the total nitrogen (N) pool in the coastal ocean, but little is known about DON biogeochemical cycling compared to well-studied inorganic N. Polyamines, aliphatic compounds consisting of a carbon chain with two or more amine substitutions, represent only a small fraction of the marine DON pool, yet high polyamine turnover rates (comparable to dissolved free amino acids) have suggested polyamines can account for a significant fraction of microbial DON cycling in the coastal ocean. In addition to bacterial assimilation, recent field measurements suggested oxidation of polyamine N to nitrite by marine Thaumarchaeota, suggesting polyamines may be a potential alternative substrate for these abundant ammonia-oxidizing archaea. However, it remains unknown whether these archaea can directly oxidize polyamine N to nitrite, or whether precursory N remineralization to ammonium is required. Here we present field and culture data on thaumarchaeal polyamine N oxidation to determine the biogeochemical impact of this process. ¹⁵N oxidation rates of multiple polyamines in Thaumarchaea-rich Sapelo Island waters were lower than ammonium oxidation but higher than glutamic acid N oxidation rates (e.g., excluding remineralization followed by ammonium oxidation), and polyamine N oxidation rates increased with the length of the carbon skeleton of the polyamine substrate. We also assessed the ability of two marine Thaumarchaea strains (*Ca. Nitrosopumilus piranensis* D3C and *Ca. N. adriaticus* NF5), as well as an enrichment

* Indicates Presenting Author

culture from Sapelo Island waters, to oxidize polyamine N in the laboratory. When co-cultured heterotrophs were inhibited with streptomycin, polyamine N oxidation rates were far slower than ammonium oxidation, suggesting these archaeal strains may rely on bacterial activity to access polyamine N. The metabolic pathway responsible for polyamine N oxidation remains unclear, precluding conclusions about whether N oxidation is direct or mediated by bacterial remineralization to ammonium.

17. Biology Meets Subduction: Exploration of Microbial Diversity of Costa Rican Convergent Margin

Katherine Fullerton*, Peter Barry, Angelo Battaglia, Patrick Beaudry, Giulio Bini, Monserrat Cascante, Maarten de Moor, Donato Giovannelli, Gino Gonzalez, Daniel Hummer, Kayla Iacovino, María Martínez, Heather Miller, Steve Turner, Katie Pratt, Carlos Ramirez, Yemerith Alpizar Segura, Karen Lloyd

University of Tennessee

Geological, geochemical, and biological processes drive the cycling of carbon on Earth, both in surface and subsurface environments. Subduction represents a critical link between the shallow and deep carbon cycles where crustal carbon is transported into the mantle. Along the Costa Rican convergent margin, the Cocos Plate actively subducts beneath the Caribbean Plate, where shallow dewatering processes allow for carbon-containing fluids to be released into the overlying forearc, much of which is subaerial. These shallow subduction fluids may transport microbes from oceanic sediments to the forearc under non-lethal conditions to some extremophiles. While extensive research has been invested in quantifying abiotic volcanic carbon fluxes, the influence of biological processes on the deep carbon budget is not well understood. In February 2017, an expedition to Costa Rica allowed for the collection of biological samples from 25 geochemically diverse sites including hot springs, mud pots, and volcanic lakes in parallel with geochemical and gas flux measurements along the convergent margin. Water and sediment samples will be analyzed for methane, sulfate, and sulfide to characterize biologically relevant geochemical properties of these sites in parallel with biological measurements. Single cell amplified genome (SAG) analysis will allow for determination of individual organisms present in these environments to complement metagenomic and metatranscriptomic data generated by our collaborators. Through the synthesis of the aforementioned biological parameters with geological and gas flux analyses, we can begin to tease apart the

biological and abiotic processes driving carbon cycling and gain a more holistic understanding of deep carbon on Earth.

18. Rapid Nitrous Oxide Production from Hydroxylamine Oxidation by Birnessite

Amanda R. Cavazos*, Yuanzhi Tang, Martial Taillefert, Jennifer B. Glass

Georgia Institute of Technology

Nitrous oxide (N_2O) is a potent greenhouse gas that depletes stratospheric ozone. In marine N_2O production models, it is assumed that N_2O originates from enzymatic processes of nitrification, denitrification, and nitrifier denitrification. However, N_2O can also be produced abiotically when nitrification intermediate hydroxylamine (NH_2OH) is oxidized by the manganese mineral birnessite ($Mn(IV)O_2$), which is thermodynamically favorable in circumneutral pH. For this reaction to be considered in marine N_2O production models, the kinetics must be understood. We found that the reaction has a first-order rate dependence on NH_2OH concentrations with a rate constant (k) of $0.002 \pm 0.0005 s^{-1}$. The age of $Mn(IV)O_2$ affected its reactivity; fresh $Mn(IV)O_2$ resulted in N_2O yields of 12-88%, whereas aged $Mn(IV)O_2$ resulted in yields of 22-29%. Because NH_2OH conversion to N_2O was incomplete, we measured other possible dissolved N products, which appeared to be minor (<5% and <2% consumption of NO_3^- and NO_2^- , respectively). It is assumed that the remaining NH_2OH was converted to N_2 . Our proposed mechanism begins with the removal of the H^+ from the hydroxyl group of NH_2OH to the $Mn(IV)O_2$ surface, creating a nitroxyl radical that decomposes to nitroxyl (HNO). An electron from the N in HNO breaks the double bond on the O, allowing reaction with another HNO to form hyponitrous acid which dissociates to N_2O . In oceanic oxyclines, where ammonia- and manganese-oxidizing organisms tend to proliferate, NH_2OH and $Mn(IV)$ can potentially accumulate and produce large quantities of N_2O .

19. Bacterial Lignin Degradation via the Phenylacetyl-CoA Pathway in the Eastern Mediterranean Sea

Hannah Woo*, Terry Hazen

University of Tennessee

The degradation of allochthonous terrestrial organic

* Indicates Presenting Author

matter, such as recalcitrant lignin and hemicellulose from plants, occurs in the ocean. We hypothesize that bacteria instead of white-rot fungi, the model organisms of aerobic lignin degradation within terrestrial environments, are responsible for lignin degradation in the ocean due to the ocean's oligotrophy and hypersalinity. Warm oxic seawater from the Eastern Mediterranean Sea was enriched on lignin in laboratory microcosms. Lignin mineralization rates by the lignin-adapted consortia improved after two sequential incubations. Shotgun metagenomic sequencing detected a higher abundance of aromatic compound degradation genes in response to lignin, particularly phenylacetyl-CoA, which may be an effective strategy for marine microbes in fluctuating oxygen concentrations. 16S rRNA gene amplicon sequencing detected a higher abundance of Gammaproteobacteria and Alphaproteobacteria bacteria such as taxonomic families Idiomarinaceae, Alcanivoraceae, and Alteromonadaceae in response to lignin. Meanwhile, fungal Ascomycetes and Basidiomycetes remained at very low abundance. Our findings demonstrate the significant potential of bacteria and microbes utilizing the phenylacetyl-CoA pathway to contribute to lignin degradation in the Eastern Mediterranean where environmental conditions are unfavorable for fungi. Since very little is known about the biodiversity of bacterial lignin degraders, they may yield efficient lignin degrading enzymes for lignocellulosic biofuels.

20. Downward Transport of Dissolved Black Carbon from Shelf Region to the Deep Ocean: A Case Study from Prydz Bay, Antarctica

Ziming Fang*, Weifeng Yang, Min Chen, Aron Stubbins, Haoyang Ma, Renming Jia, Qi Li, Qianna Chen

University of Georgia

Dissolved black carbon (DBC) makes up ~10% of the global flux of riverine dissolved organic carbon (DOC) to oceans. Part of the riverine DBC is degraded in the ocean surface due to solar radiation while the other part can survive long distance transport from river mouth to abyssal seas and increase the deep ocean refractory carbon pool. In the Antarctica, the downward transport of dense shelf waters (DSW) from shelf regions to deep Southern Ocean may serve as a short-cut for DBC to escape from the sunlit ocean surface and play an important role on the biogeochemical cycle of DBC and marine carbon cycle. Here, we chose Prydz Bay as a case study to figure out this issue. We found that DBC and DOC concentrations of DSW in the Prydz Bay

were ~139% and ~38% higher than the circumpolar deep water (CDW), respectively. Moreover, DBC/DOC ratio was higher in DSW ($1.8 \pm 0.4\%$) than the CDW ($1.1 \pm 0.1\%$), which suggested DOC in DSW may have older bulk ^{14}C age than CDW (DBC has much old ^{14}C age than bulk DOC). Using sea water oxygen isotopes ($\delta^{18}\text{O}$), we confirmed that the down-flow DSW could entrain DBC, as well as DOC, from the shelf region to the deep Southern Ocean. Basing upon a two end-member mixing model, the downward transport of DBC and DOC from Prydz Bay could increase DBC and DOC concentrations of Antarctica Bottom Water by $0.02 \sim 0.04 \mu\text{mol L}^{-1}$ (4~9%) and $0.7 \sim 1.5 \mu\text{mol L}^{-1}$ (2~4%), respectively. This result indicated that DBC and DOC exported from shelf regions may account for the observed increase and aging of DOC in the deep Southern Ocean. Thus, we highlight the downward transport of DBC, as well as DOC, from Antarctic shelf regions should have profound influence on the biogeochemistry of DBC and deep ocean carbon cycle.

21. Methanethiol Concentrations in the Northeast Subarctic Pacific Ocean and its Relationship with Dimethylsulfoniopropionate and Dimethylsulfide

Tara Williams*, Ron Kiene, Kaitlin Esson, John Dacey, Philippe Tortell

University of South Alabama, Dauphin Island Sea Lab

The majority of sulfur supplied to the atmosphere comes from exchange with the ocean. Dimethylsulfoniopropionate (DMSP) is an abundant, rapidly cycled algal osmolyte that is used as a source of carbon and sulfur by bacterioplankton. DMSP undergoes two different degradation pathways: cleavage (by DMSP lyase), which gives rise to dimethylsulfide (DMS) and acrylate; or demethylation, which ultimately can lead to production of methanethiol (MeSH). MeSH is the major sulfur gas product of dissolved DMSP degradation but is usually found in lower concentrations than DMS because of its high biological and chemical reactivity. In the past, it has been difficult to measure MeSH and, as a result, few data are available. In July 2016, discrete samples were obtained with Niskin bottles and CTD casts from the northeast subarctic Pacific Ocean and analyzed for MeSH by purge-and-trap gas chromatography with flame photometric detection. Surface waters (5 m depth) had an average MeSH concentration of 0.75 nM with concentrations reaching up to 3 nM. MeSH was correlated with total DMSP ($r = 0.93$) and dissolved DMS ($r = 0.63$). The data show that surface water MeSH concentrations can be significant

* Indicates Presenting Author

relative to DMS, with MeSH:DMS concentration ratios averaging 0.19 and ranging up to 0.50. This suggests that fluxes of MeSH-sulfur to the atmosphere can be significant relative to DMS, and thus are important for estimates of atmospheric sulfur inputs.

22. Hydroxyl Radicals May Help Heterotrophic Microbes Mineralize Recalcitrant Organic Matter

Robert E. A. Souder*, Lauren A. Mullen

University of Tennessee

Heterotrophic microbes at the edge of our biosphere mineralize recalcitrant organic matter as a food source. The mechanisms of this mineralization are not yet entirely understood. This investigation aims to determine the effect that hydroxyl radicals have on the lability, and in turn the bioavailability, of recalcitrant dissolved organic matter. Fenton chemistry was used to produce unnaturally high levels of hydroxyl radicals in the presence of recalcitrant natural organic matter from the Suwannee River. The bioavailability was measured by comparing the oxygen consumption rates observed in this organic matter after it had been inoculated with microbes (≤ 2.2 μm) from the Tennessee River. The mean oxygen consumption rate of samples exposed to hydroxyl radicals (29.1 nM/min) was observed to be 5.5 times higher than that of samples which were not exposed (5.26 nM/min). This suggests that hydroxyl radicals are capable of converting organic matter from recalcitrant to labile, and thereby increasing the food supply for microbial communities in aphotic systems.

23. Microbial Communities from Gill Tissues and Patchy Seagrass Habitat of a Chemosymbiotic Bivalve, *Stewartia floridana*

Sam Scheffler*, Audrey Paterson, Brooke Long, Laurie Anderson, Annette S. Engel

University of Tennessee

Lucinids are a taxonomically diverse family of bivalve marine mollusks that possess chemosymbionts. These endosymbionts, typically classified as sulfur-oxidizing Gammaproteobacteria, can vary among lucinid species and/or their habitat. Lucinids acquire endosymbionts from the environment, and previous work indicates that *Stewartia floridana* shell morphology is affected by the duration of time a clam lives in seagrass or bare sand, likely due to distinct biogeochemical and sedimentological

conditions established by the different coverage regimes, including porewater pH, grain size, oxygen and sulfide flux, etc. For this study, we hypothesized that coverage type (e.g., bare sand or 100% seagrass coverage) produces distinctly different bacterial microbiomes associated with *S. floridana* habitat sediment and porewater, and differences in habitat microbiomes results in lucinid endosymbiont genetic diversity. Four transects in Bokeelia, Florida, were established perpendicular to the shoreline, and live *S. floridana* and excavated sediment samples were collected every five meters, from 5 m - 50 m. Porewater samples were collected from 14 of the transect sites. Total nucleic acids were extracted from gill tissue, sediment, and porewater, and bacterial 16S rRNA genes were amplified and sequenced using 454 tag pyrosequencing. Amplicons were analyzed using mothur, classified using the Silva reference database, and binned into operational taxonomic units (OTUs) based on sequence identity (96%). Gill tissues from 25 specimens were analyzed from a subset of seven sites, each representing distinct types of subtidal vegetative cover (*Halodule wrightii*, *Syringodium filiforme*, *Thalassia testudinum*, or bare sand). Two OTUs dominated the gill tissues, both classified to the genus *Sedimenticola* (from 90-99% of amplicons from any individual). There were subtle distinctions between the sediment bacterial compositions associated with homogeneous *H. wrightii* or *S. filiforme* seagrass cover, but there were no statistical differences between sediment and porewater bacterial diversity from the different coverage types or bare sand. Implications of this study include the highlighted importance of seagrass stability on benthic infaunal ecology. Future work includes incorporation of geochemical analyses to help resolve the relationship between seagrass habitats and lucinids that will test hypotheses generated from shell morphology results.

24. Biodegradation of Ferrihydrite-Humic Acid Co-precipitates

Nadia Noor*, Chunmei Chen and Aaron Thompson

University of Georgia

The association of organic matter (OM) with Iron (Fe) minerals is an important mechanism for the preservation of carbon in soils and sediments. The short-range-ordered Fe minerals, (e.g., ferrihydrite (Fh)) are particularly important sorbents of organic matter and often form co-precipitates if when formed in OM-rich solutions. In the presence of O_2 , degradation of OM in Fh-OM co-precipitates can be inhibited leading to long-term stabilization of C in soils. However, in anoxic conditions, dissimilatory Fe reduction could

* Indicates Presenting Author

drive the release and decomposition of Fh-associated OM. The aim of the present study is to perform microbial incubation experiments to determine the fate of OM that is coprecipitated with Fh -under both oxic and anoxic conditions. We have synthesized OM-Fh coprecipitates using humic acid and are currently performing aerobic and anaerobic incubations with two microbial systems: a microbial consortium extracted from soil and a pure culture of the iron reducing bacteria *Shewanella oneidensis* MR-1. During the incubation, we will track Fe (II), DOC and CO₂ production to quantify Fe reduction, and OC mobilization and mineralization rates. The results of this study will help elucidate the importance of OM-Fh coprecipitation on soil C stabilization.

25. Effects of Salinity and Steel Type on Microbiologically Influenced Corrosion in North Carolina Estuarine River Systems

Cody E. Garrison*, Erin K. Field

East Carolina University

Iron-oxidizing bacteria (FeOB) play a large role in the biogeochemical cycles of iron in the environment, and recent advancements in culturing methods have shed new light on their role in steel colonization and corrosion. Steel structures in marine environments naturally corrode through chemical oxidation of iron via the formation of rust. Biological oxidation of iron can increase the rate of corrosion via FeOB colonizing the surfaces of steel structures. Differences in susceptibility to corrosion can be assessed via a colonization study on two stainless steel types that vary in composition (304 and 316L) to identify distribution and abundances of FeOB along a salinity gradient in two separate North Carolina estuarine river systems (Neuse River and Pamlico River). Differences in colonization between steel types of varying composition may further reveal implications on heavy metal resistance in FeOB. Stainless steel coupons were deployed at five sites on each river along a salinity gradient for a period of six weeks to ensure adequate time for colonization. A most probable number (MPN) method is being used to estimate abundances for each site. Preliminary results from two deployments show that FeOB colonization has been influenced by both salinity and steel type. FeOB attachment to stainless steel coupons has been observed at salinities ranging from 0.1-16.1 ppt, and 316L stainless steel has exhibited greater abundances of FeOB. Ongoing studies will aim to reveal differences in susceptibility and implications for the long-term preservation of commercial and private property in coastal environments characterized

by tidally influenced estuarine systems.

26. Salinity-Structured and Particle-Associated Variations in Bacterial Communities and Enzymatic Activities in the Coastal North Atlantic

Karylle Ervinne G. Abella*, John Paul Balmonte, Carol Arnosti

University of North Carolina, Chapel Hill

Marine microbes secrete enzymes to initiate the degradation of organic matter, but the extent to which compositional differences of bacterial communities correspond with differences in enzymatic potential are poorly understood. The manner in which these relationships vary along salinity gradients and with particle association is understudied, despite important implications for river-to-ocean transfer of organic carbon. Here, we build on a previous study that investigated microbial enzymatic activities across different salinities and organic matter sources between the South Atlantic Bight and Mid-Atlantic Bight: at the mouth of Chesapeake Bay (CBM), Cape Lookout Nearshore (CLN), and Cape Hatteras Offshore (CHO). To investigate the relationship between bacterial community composition and enzymatic potential, we coupled 16S rRNA gene sequencing analyses with previously measured enzymatic activities. Our results demonstrate that salinity differences underlie patterns of dissimilarity in both bulk and particle-associated communities at all sites, and these patterns parallel substantial variations in enzymatic activities at CBM (freshwater-influenced) versus CLN and CHO (marine), in bulk seawater as well as on particles. Additionally, taxonomic analyses reveal the enrichment of specific taxa on particles; these taxa differ at CBM versus CLN and CHO. In particular, select members of Comamonadaceae, Alcaligenaceae, and Cryomorphaceae, are enriched on CBM surface and bottom water particles, and reflect the influence of riverine runoff at this station. In contrast, a more diverse range of marine taxa, including members of Planctomycetales, Alteromonadaceae, and Rhodobacteraceae, are enriched on CHO and CLN particles. The narrower subset of taxa enriched on particles from CBM, in contrast to the greater diversity of particle-enriched bacteria at CHO and CLN, correlates with the lower enzymatic activities previously measured on CBM versus CHO and CLN particles. Thus, congruence in bacterial community composition differences and enzymatic activities suggest a link between structure and function—a relationship evident along salinity gradients and with particle-association.

* Indicates Presenting Author

27. Genomic Insights into a Coastal Marine Sediment Mesocosm Incubation

Richard Kevorkian*, Karen Lloyd

University of Tennessee

Difficulty measuring growth and diversity of microbes in marine sediment limits our ability to assess competition/mutualism, in situ growth rates, and niches of uncultured taxa. We present evidence supporting the possible metabolic strategies of several microbial taxa found in methane-producing environments, are capable of growth under methanogenic conditions in anoxic long term incubations of marine sediments from Cape Lookout Bight, NC. Using a novel method of calculating generation time for slow-growing microbial taxa measured from the change in the product of relative read abundance and cell counts we were able to determine that uncultured members of Methanomicrobiales and Methanosarcinales increased at the onset of methanogenesis with doubling times of 9.4 ± 5.8 and 9.2 ± 3.5 days, respectively. Uncultivated Syntrophaceae, which are related to fermentative syntrophs of methanogens, and the uncultivated Kazan-3A-21 archaea also increased at the onset of methanogenesis with doubling times of 14.7 ± 6.9 and 10.6 ± 3.6 days, respectively. Supplementing this data with a single metagenome from these incubations we hope to suggest metabolic strategies for several uncultured and slow growing microbes.

28. Using Chromophoric Dissolved Organic Matter (CDOM) to Predict Dissolved Black Carbon (DBC) Distributions in South Atlantic Bight Estuaries and Adjacent Sea

Lixin Zhu*

University of Georgia

Dissolved black carbon (DBC), which leached from soil to rivers, has been realized as an important component in global carbon cycle. However, still few DBC studies were conducted in South Atlantic Bight area where the complex biogeochemical process, the increased pressure of storm and human activities made it a needed area for research. In this study, Samples were collected from 12 cruises in SBA area, including three major estuaries and coastal ocean (Salinity range is 0 – 37) in different seasons between August 2014 and May 2016. Overall, DBC concentration decreased from the river end to the sea water end because of the dilution effect of seawater. But in the river end, the DBC concentration

was not consistent. The Ogeechee Estuary always had much higher DBC concentration than Altamaha and Wilmington Estuary. This difference combined with the complex hydrology condition made the DBC distribution hard to predict in the SAB coastal ocean just using simple mixing model. Despite the concentration difference in different area, we found a strong linear relationship ($R^2 = 0.96$) between chromophoric dissolved organic matter (CDOM) absorption coefficients at 254 nm (a_{254}) and DBC in the 89 paired samples we collected. This gave us a strong confidence to use the CDOM which is easy to obtain as a proxy to predict more detailed distribution patterns of DBC in a large area. So, we further got a larger distribution pattern of DBC in SAB area based on the underway S::CAN UV-Vis spectrometer probe and satellite derived CDOM data.

29. Hydrocarbon Biodegradation Affected by Dispersant in the Gulf of Mexico Coastal Seawater

Xiaoxu Sun*, Lena Chu, Isabel Romero, David Hollander, and Joel Kostka

Georgia Institute of Technology

During the Deepwater Horizon oil spill, a large amount of released oil contaminated beaches along the northern Gulf of Mexico. Oil contamination not only affects tourism, but also may adversely impact coastal ecosystems. To protect shorelines, an extensive amount of chemical dispersant was applied to reduce oil droplet size and enhance the bioavailability of discharged oil. This study investigates the effectiveness of dispersant application to stimulate biodegradation as well as the influence of dispersant on metabolically active microbial communities in coastal seawater. Dispersant and weathered oil concentrations were representative of concentrations and ratios expected during active response efforts. Preliminary results show that the application of dispersant decreased the half-life of most compound classes in 2 ppm weathered oil, even under relatively low mixing conditions in a 40-day-incubation. Alkanes up to C15 were completely removed in treatments with or without dispersant. For alkanes between C15 – C20, dispersant treatment significantly enhanced degradation. PAHs naphthalene and its homologs as well as phenanthrene approached complete removal, while the degradation of phenanthrene homologs decreased with an increase in alkyl groups. Elevated oxygen consumption and respiration also suggests application of dispersant facilitates biodegradation. Currently, experiments are being repeated under conditions of elevated mixing and microbial community analysis is

* Indicates Presenting Author

underway.

30. Deep-Water Sediment Resuspension in the Northern Gulf of Mexico and the Effect of Bottom Topography

Yu Wang*, Christof Meile

University of Georgia

Sediment resuspension occurs when sediment that has been deposited at the seafloor is moved back into the benthic boundary layer, resulting in lateral transport of particulate and dissolved matter. This redistribution of sedimented particles can affect sediment accumulation patterns at the seafloor and biogeochemical transformations by exposing the resuspended material to the water column.

In this study, we focus on the seep site Green Canyon 600 (GC600) in the northern Gulf of Mexico at a water depth of approximately 1250 m. GC600 is characterized by several active seeps and has been studied extensively. Here, we combine multiple datasets including high-resolution bathymetry, ADCP current measurements and Mola-Mola imagery data with results from resuspension experiment in a numerical model.

The research goal is to investigate under what conditions and at which frequencies sediment resuspension at GC600 occurs, and whether there is an indication of spatial heterogeneity in sediment resuspension. To assess whether sediments get resuspended, we quantify near-bottom flow across a spatial domain at the seafloor of GC600, and then compare the flow velocity with experimental critical shear velocity. The near-bottom flow model uses bathymetry data to define the bottom boundary, and ADCP data is used to force the flow dynamics at the upper boundary. Equations solved in the model are Navier-Stokes equations for conservation of momentum, continuity equation for conservation of mass, and two equations of k- ϵ turbulent model.

To estimate resuspension, we extract simulated flow velocities of the lowest layer in the mesh. We then calculate the percentage of time when the flow velocity is higher than an experimentally determined critical shear velocity, to assess the resuspension probability for each point in the model mesh. Comparing modeled velocities at the ocean bottom to this threshold indicates where resuspension is likely to happen and the spatial pattern affected by sediment surface topography.

31. Gene Expression Patterns in Natural Bacterioplankton Communities as Biosensors of High-flux Dissolved Organic Matter

Alexey Vorobev*, Mary Ann Moran

University of Georgia

Microbial communities of coastal ocean ecosystems process Dissolved Organic Matter (DOM) from both marine and terrestrial sources. The interplay between this dynamic DOM pool and diverse bacterioplankton communities remains a major challenge to understand. This study characterizes the active microbial community processing coastal ocean DOM and identifies the key enzymes involved in its degradation during 24 h incubations, comparing between two seasons and two tidal stages. The community transcriptome from coastal water was dominated by transcripts from Gammaproteobacteria representatives of the OM60/NOR5 clade, and Alphaproteobacteria representatives of the SAR11 and the Roseobacter clades. Microbial taxa that contributed significantly but less consistently to the metatranscriptomes included the Actinobacteria, Planctomycetes, Bacteroidetes, and uncultured Marine Group II Euryarchaeota. Transcriptome composition following a 24 h dark incubation (T24) was compared to the initial seawater sample (T0) for four experiments conducted in July and October 2014. The analysis focused on transport and metabolism related genes, representing catabolic pathways, upregulated at T24 as the most informative for identifying biologically labile organic compounds sustaining bacterial growth. Gene expression analysis indicated the importance of carboxylic acids, polyamines, and amino acids as highly labile compounds at this coastal site. High expression of metabolic genes also demonstrated the importance of fatty acid degradation. Our data suggest that Alphaproteobacteria representatives of the SAR11 and Roseobacter clades operate as generalists in this coastal system with many transporters being highly expressed simultaneously. On the contrary Gammaproteobacteria strains HTCC2148, HTCC2080, and NOR5 from the OM60/NOR5 clade and strain SAR86E, as well as Marine Group II Euryarchaeota appear to function as specialists with only a few transporters being expressed under given conditions.

32. Rates of Benthic Metabolism in an Intertidal Marsh Throughout a Diurnal Oxygen Cycle

Kara Gadeken*, Kelly Dorgan

Dauphin Island Sea Lab

Oxygen availability is a critical factor affecting metabolic processes and organic matter remineralization in marine sediments. Hypoxia (dissolved oxygen concentrations below 2 mg L⁻¹) decreases macrofaunal bioturbation and bioirrigation activity and lowers sediment metabolism rates. Shallow water oxygen patterns often follow a diurnal cycle as dissolved oxygen drops to hypoxic levels at night due to respiration and then increases during the day with photosynthesis, creating a recurring, potentially stressful suboxic benthic environment. Sediment metabolism is known to depend on ambient dissolved oxygen concentration, but responses of organisms to hypoxia are more complex and likely contribute to variability in sediment metabolism. In this study, sediment oxygen consumption rates were measured in a salt marsh via metabolism chambers throughout a diurnal cycle in natural and artificially oxygenated sediments. We hypothesize that varying responses of macrofauna to hypoxia result in a time lag between the diurnal oxygen cycle and the corresponding diurnal cycle in sediment oxygen consumption that prevents sediment metabolism from attaining fully oxic rates, even at peak daily ambient dissolved oxygen concentrations. The multiple potential responses of macrofauna to short-term oxygen variability may be an important factor driving shallow sediment metabolism rates and macrofaunal behavior.

33. Investigating the Linkage of Increasing Oxygen to the Great Ordovician Biodiversification Event Using Geochemical Fingerprints in the Appalachian Basin

Nevin Kozik*, Seth Young, Jeremy Owens

Florida State University

The Ordovician is a dynamic period in terms of paleoclimate, with large epeiric seas and greenhouse climates that eventually give way to icehouse conditions and lowered sea level. Additionally, the Paleozoic's largest bio-diversification event has been documented, the Great Ordovician Biodiversification Event (GOBE), and is followed by the first of the "Big 5" mass extinctions. The GOBE is a globally recognized, roughly threefold increase in family and twofold increase in genera diversity, whose causal mechanisms

are poorly understood. One explanation for this bio-diversification is an increase in the oxygenation of the deeper portions of the oceans. This study will focus on two stratigraphic sections in the Middle-Late Ordovician that overlap with pulses of the GOBE and an associated globally documented 2-3‰ positive carbon excursion called the mid-Darriwilian carbon isotope excursion (MDICE). These two sections are located in Tennessee and Virginia, the first being a shallow water carbonate dominated sequence representing a continental shelf environment, while the section in Virginia, being predominantly a black shale lithology represents a slope environment both having been studied biostratigraphically to create high resolution for the timing of these events. To elucidate the causal mechanisms of the GOBE, this study focuses on paired stable carbon and sulfur isotopes, as well as iron speciation and trace metal concentrations in these two sections. $\delta^{13}\text{C}$ will be used as a global proxy for burial of organic matter while $\delta^{34}\text{S}$ will be used as a proxy for oxygen dynamics during this time. To directly test the paleoredox conditions throughout the Darriwilian and Sandbian, two new shale-proxies will be investigated which have never been used in this period of the Ordovician. Iron (Fe) speciation and trace metal concentrations will be used as a local and global proxy, respectively, to elucidate how the biosphere may have responded to potential changes in the redox state of the deep oceans. This study hopes to test the hypothesis that portions of Ordovician ocean basins cycled from oxic to anoxic/euxinic conditions, and that these intervals of increased oxygenation are coincident with pulses of the GOBE. With the data collected, this study will greatly improve the understanding of the Ordovician period and how the changing climate system affects the biogeochemical cycling of key elements and their impacts on the global biosphere. The data generated from this study will help to create a better understanding on how the global redox state of the oceans may be related to faunal diversification and/or extinctions.

34. Anaerobic Acetate Oxidation Coupled to Metal Reduction in *Shewanella* Algae

Nadia Szeinbaum*, Nadia Szeinbaum, Hui Lin, Jay A. Brandes, Martial Taillefert, Jennifer B. Glass, and Thomas J. DiChristina

Georgia Institute of Technology

Introduction: Manganese(III) (Mn(III)) is a newly identified oxidant in anoxic marine and terrestrial environments. Acetate is a naturally abundant substrate that fuels microbial activity in the modern biosphere, and likely on early Earth. *Shewanella* respire a variety

* Indicates Presenting Author

of anaerobic extracellular electron acceptors, including transition metals such as Mn, and thus play important roles in metal and carbon cycling in the environment. *Shewanella* is thought unable of complete lactate oxidation to CO₂ under anaerobic conditions, producing acetate in the process.

Results: We isolated a *Shewanella* algae strain from an enrichment with acetate and Mn(III). Unlike other metal-reducing members of the *Shewanella* genus, isolate MN-01 and phylogenetically related strains *S. algae* BrY and ACDC, and *S. haliotis* were able to oxidize acetate to CO₂ anaerobically with Mn(III)-pyrophosphate, and Fe(III)-citrate as electron acceptors. Genomic analyses with other acetate-oxidizing, metal-reducing gamma and delta proteobacteria uncovered four genes that may be involved in acetate oxidation in *Shewanella* and other Gammaproteobacteria: Succinate-semialdehyde dehydrogenase, NADHP oxidoreductase, AcnA and a distinct fumarase.

Methods: Whole genome sequences of isolate MN01 and *Shewanella* algae BrY were obtained using an Illumina sequencing platform and assembled using CLC genomic workbench V8. All other proteobacterial genomes were downloaded from the NCBI database. Whole genome sequences were compared using RAST (12) together with KEGG, BioCyc, and NCBI databases for ORF completeness, protein sequence similarity and domain analysis, and tested for phylogenetic relationships using MEGA. In anaerobic incubations, Mn(III) and Fe(III) reduction were monitored spectrophotometrically and acetate concentrations were measured by HPLC.

Conclusions: *Shewanella* algae are the first members of the genus reported to couple anaerobic acetate oxidation to metal reduction thus expanding their known ecological niche. Based on genomic differences, metal reduction under oxygen sensitive and insensitive central carbon metabolism may have emerged under different oxygen regimes in ancient ecosystems.

35. Reduced growth of a Key N₂-fixing Tree Under Drought May Decrease Soil N Availability and Inhibit Forest Productivity

Jeffery Minucci*, Cheley Ford Miniat, Nina Wurzburger

University of Georgia

Global climate change is leading to more arid growing seasons and increased frequency of severe drought events, which may directly reduce forest productivity by imposing water stress on trees. However, drought

can also indirectly affect productivity through its impact on the nitrogen (N) cycle. This may be of particular importance in early successional forests, where productivity is strongly N limited and a large proportion of ecosystem N inputs come from symbiotic N₂-fixing trees. N₂-fixers differ from other trees in that they can access an unlimited N supply, given sufficient water and carbon. Thus, N₂-fixers may be water limited while non-fixers are primarily N limited. As a result, the growth of N₂-fixing trees may decline more strongly in response to decreased moisture than non-fixers, leading to a long-term reduction in soil N availability. Here we assessed direct and indirect effects of drought on Southern Appalachian early successional forest recovery by diverting 0, 20, or 40% of growing season precipitation to 18 forest plots for 3 years. We found that growth of the N₂-fixing tree *Robinia pseudoacacia* was limited by soil moisture and not light or N availability, while three non-fixing species were mainly limited by N. We also observed that *R. pseudoacacia* plot biomass fraction decreased through time in the driest plots, but increased through time in the wettest plots. Finally, we found that plots with greater *R. pseudoacacia* biomass had significantly increased soil N mineralization rates, N pool sizes, and relative growth rate of non-fixing trees. Our findings suggest that decreased soil moisture could impact forest productivity indirectly through its effects on N₂-fixing plants and thus, soil N availability.

Oral Session IV
9:00 - 10:30 AM
Sunday April 2, 2017
Miller Learning Center

19. Modelling Ecosystem Metabolism in Coastal Estuaries

Annette M. Hynes, Brian M. Hopkinson, Joan E. Sheldon, Joseph J. Vallino, and Charles S. Hopkinson

University of Georgia

Concentrations of dissolved oxygen (DO) result from the combined effects of photosynthetic production, respiration, and air-water gas exchange, and time series of DO can be used to calculate ecosystem metabolism. We are adapting a nonlinear inverse model to estimate spatially explicit ecosystem metabolism in the Sapelo Island Estuary (Duplin River, GA) using DO measurements from high-speed transects along the river. This work in progress modifies a model developed to measure gross primary production (GPP), community respiration (CR), and net ecosystem production (NEP) in the Plum Island Estuary, MA. We are also using harmonic analysis of long-term DO time series from stationary sondes to calculate temporal estimates of GPP, CR, and NEP. These long-term studies can examine the effects of nutrient loading, sediment loading, river discharge, sea level rise, and temperature on estuarine community metabolism.

20. Functional Redundancy Versus Functional Dissimilarity Among Distinct Marine Microbial Assemblages in the North Atlantic

John Paul Balmonte*, Andrew Buckley, Adrienne Hoarfrost, Sherif Ghobrial, Kai Ziervogel, Andreas Teske, Carol Arnosti

University of North Carolina, Chapel Hill

The relative importance of functional redundancy versus functional dissimilarity, which underlie microbial community structure-function relationships, is poorly understood for marine microbial communities. These relationships, however, have implications for microbial responses to environmental perturbations and consequently affect ecosystem processes. We investigated whether distinct microbial communities from hydrographically-varying water masses exhibit

functional redundancy or functional dissimilarity in their enzymatic responses to the addition of high molecular weight (HMW) organic matter. We collected surface and bottom water samples from the coastal and open North Atlantic, and set up triplicate mesocosms with (amended) and without (unamended controls) HMW extracts of *Thalassiosira weissflogii*. Over a 69-day incubation period, we sub-sampled six times to track the following: 1) changes in bacterial production, cell counts, and dissolved organic carbon concentrations; 2) bacterial community succession using 16S rRNA gene sequencing; 3) functional shifts as represented by measurements of peptidase, glucosidase and polysaccharide hydrolase activities. Our results demonstrate that community succession in amended mesocosms was coincident with cell growth, increased bacterial production, and most notably in substantial shifts in enzymatic activities. In all amended mesocosms, phylogenetically-related bacterial taxa, dominated by conditionally rare taxa, emerged from initially distinct communities. Nonetheless, distinct differences in the specific taxa that were enriched, and in the changes in enzymatic activities, were clearly apparent among the different water masses. These results suggest that while phylogenetically-related, copiotrophic taxa recruited from the rare biosphere drive similar response patterns among initially distinct communities, unique responses of water-mass specific taxa provide evidence for functional dissimilarity.

21. Characterizing the Relationship Between Iron-Oxidizing Bacteria and Sulfate-Reducing Bacteria in Estuarine Environments

Chequita Brooks*, Erin Field

East Carolina University

Microbes are actively involved in the cycling of many elements such as iron and sulfur. Among the microbial drivers present are iron-oxidizing bacteria (FeOB) and sulfate-reducing bacteria (SRBs) which can be found co-occurring in a variety of environments such as sediment, microbial mats, and in the water column. This co-occurrence suggests the possibility that these organisms may participate in a relationship, such as syntrophy, where these microbes are mutually beneficial to one

* Indicates Presenting Author

another through interrelated redox reactions. If this is the case, then the relationship between SRBs and FeOB could connect the global cycling of sulfur and iron. The purpose of this study is to assess whether FeOB and SRBs are involved in a syntrophic relationship. Samples were collected from estuarine sediments in North Carolina and a method of growing the organisms in co-culture was developed. The oxygen levels of the lab cultures were measured in order to begin assessing the oxygen concentrations throughout the growth media. Results from this analysis suggest that oxygen levels determine where in the media FeOB can grow (4mg/L to anoxic boundary). However, results indicate that the SRBs do not necessarily begin growing at the anoxic boundary, suggesting that there are other factors involved in the niche separation of these bacteria. Studies are ongoing to elucidate what factors are influencing the niche separation of FeOB and SRBs. Developing an understanding of how these organisms interact will deepen our knowledge of how microbial community function could influence cycling of geochemically important elements in aquatic systems.

22. Microbial Response to Weathered Oil Buried in Submerged Coastal Sands

Will Overholt*, Elisa Mercado, Xiaoxu Sun, Kostas Konstantinidis, Markus Huettel, Joel E. Kostka

Georgia Institute of Technology

An estimated 22,000 tons of weathered crude oil from the Deepwater Horizon blowout contaminated Gulf coast beaches in 2010 and deposited an unknown amount into nearshore environments, which so far has received little attention. In this study, we employ advective-flow chambers that simulate in-situ pressure gradients found in saturated coastal sediments to test hypotheses generated from field studies of Gulf beaches. Our objectives are to (1) determine the acute impacts of weathered crude oil on carbon and nitrogen cycling processes, (2) directly link the metabolic pathways of biodegradation to specific microbial groups, and (3) examine the controls on biodegradation activity and community succession. Incubations were conducted over a 3-month period and oxygen consumption rates as well as nutrient concentrations were monitored. At regular intervals, oil chemistry, viable cell counts, microbial metabolisms, and specific metabolic rates were determined. Initial results indicate sustained and increasing rates of respiration in oiled chambers 2 times higher than observed in controls. Viable counts indicate a significant increase in bacterial abundances that increase with time. Ammonium, nitrite, and nitrate

concentrations remain depleted in oiled chambers while in the controls ammonium is rapidly released into the overlying water, followed by a transient increase in nitrite, and finally a large increase of nitrate up to 60 $\mu\text{mol/L}$. This can potentially be explained by a high potential for nitrification observed in the control chambers and not in the oiled chambers. Furthermore, a similar succession in microbial populations is observed as to what was seen in the field, although the overall response is not as severe and a sharp reduction in richness and evenness was not observed. Overall, our results will contribute to a comprehensive prediction on the fate, impacts, and microbial community response to buried oil in sandy subtidal coastal sediments under a “no hydrocarbon transport” regime.

23. Ground-Truthing Novel Paleoredox Isotope Proxies: The Good, Bad, and Ugly

Kyle S. Rybacki*, Noah J. Planavsky, Xiangli L. Wang, Christopher T. Reinhard

Georgia Institute of Technology

Much of what we know about the environmental conditions on early Earth is inferred from a sparse geological record. In an attempt to improve the temporal resolution of deep-time geochemical studies, researchers have recently begun using the Cr-isotope ratios of ancient carbonate sequences as a proxy for tracking the paleo-atmospheric oxygen levels during the ‘Great Oxidation Event’ (GOE) between 2.45 and 2.06 billion years. There are two key issues associated with this approach. First, it is not well understood how the Cr-isotope composition of carbonate rocks is linked to the redox state of the modern ocean, let alone the atmosphere. Second, nearly all Precambrian carbonate sequences have had their primary calcite/aragonite mineralogy altered to dolomite.

In order to assess the effect secondary processes, including dolomitization, have on the Cr-isotope composition of carbonates, we have conducted a detailed geochemical study on the two drill cores from the Bahama’s Drilling Project (Clino and Unda Cores) that were used to demonstrate the effects of marine and meteoric diagenesis have on carbonate sediments. Our research has demonstrated that: (1) the measured Cr-isotope values of modern platform carbonates are not representative of modern seawater, and (2) secondary processes, including meteoric diagenesis and dolomitization, do not alter the measured Cr-isotope values of carbonates in a systematic way. These results show that we still do not fully understand the Cr-isotope

* Indicates Presenting Author

systematics with respect to secondary alteration, and more work is needed before attempting to use the system in deep time.

24. Constraining the Relationships Between Methanogenesis, Sulfate Reduction and the Anaerobic Oxidation of Methane in Marine Sediments

Guangchao Zhuang*, Vladimir Samarkin, Samantha Joye

University of Georgia

Methane is a potent greenhouse gas, and marine sediment is the largest global reservoir of methane. Anaerobic production and oxidation of methane are important microbial metabolism in the global carbon cycle, while the metabolic dynamics and mechanisms of those processes, in particular under *in situ* condition, remains largely unconstrained. Here, we seek to quantify the rates of methanogenesis, anaerobic oxidation of methane (AOM), and sulfate reduction with radiotracers under *in situ* pressure and methane concentration, and further detangle the relationships among those processes in cold seep sediments. Specifically, we found that methanogenesis and AOM occurred simultaneously, and methylotrophic methanogenesis might be a possible driver of AOM as it was the dominant methanogenic pathway in the surface sulfate-reducing sediment. Hydrogen-based methanogenesis was significantly stimulated with increasing methane concentrations under high pressure, which could be attributed to a back reaction of AOM. AOM rates strongly exceed those of sulfate reduction when high pressures and methane concentrations are applied, suggesting that AOM and sulfate reduction were not necessarily coupled, and AOM might be supported by other terminal processes. Those field observations provided evidence for the possible decoupling of AOM and SR under *in situ* conditions, and this decoupling might be widespread in those methane rich marine sediments. Our study improved our understanding on the metabolism and dynamics of dominant microbial processes in the cold seeps environments.

* Indicates Presenting Author

Poster Session II
10:30 AM - 12:00 PM
Sunday April 2, 2017
Miller Learning Center

36. Seasonal Variation in the Potential for Iron Reduction in Soils of the Southeastern Piedmont

Caitlin Hodges*, John Mallard, Daniel Markewitz, Aaron Thompson

University of Georgia

Soil iron reduction influences ecosystem form and function by altering the cycling of carbon, nutrients, and trace elements in both the aqueous and solid (or particulate) phases. Nearly all of our understanding of soil iron reduction comes from work on saturated soils (wetlands). However, recent work shows iron reduction can be a pivotal process in upland soils that experience dynamic redox conditions. We hypothesized that in upland soils, iron reduction intensity and prevalence would be affected by seasonal variations in soil moisture. We tested this by delineating the spatial and temporal distribution of upland soil iron reduction to 70 cm depth in a sub-tropical forested watersheds using in situ, rusted steel Indicator of Iron Reduction in Soil (steel IRIS) probes, and non-invasive moisture sensing over the course of a year. Steel IRIS probes were deployed and soil moisture and water depth were recorded three times throughout the year: (a) after an extreme rainfall event in October 2015; (b) during the end-of-winter warming in March 2016; (c) and during a period of high evapotranspirational demand in June 2016. Our results indicate that the potential for iron reduction varied with depth and intensity over the year. Iron reduction was greatest at depth (40 – 60+ cm) following a rainfall event that generated prolonged subsurface soil saturation; iron reduction was greatest near the surface (0 – 30 cm) in late winter/early spring when biological oxygen demand was likely high due to labile carbon and soil warming. We found low potential for Fe reduction across all depths in June of 2016. Our results indicate that Fe reduction in the soils of the Southeastern Piedmont occurs both seasonally and periodically in response to environmental factors, pointing towards a need to restructure our understanding of anaerobic processes in upland soils.

37. Expansion of Anoxia/Euxinia as Driver for Early Silurian Extinction Events: New Geochemical Proxy Data from Sweden

Emily Benayoun*, Seth Young, Jeremy Owens

Florida State University

The early Silurian was characterized by oceanographic and biotic change associated with survival/recovery from one of the largest mass extinctions in the Phanerozoic. Lower Silurian (Llandovery) strata contain evidence for widespread anoxia, continued glaciation, and three positive carbon ($\delta^{13}\text{C}$) isotope excursions: Early Aeronian, Late Aeronian, and Valgu. However, mechanisms capable of causing widespread climatic and oceanographic changes that can be linked to biotic events are not well understood. Previously documented Silurian episodes of biotic extinction are coincident with major perturbations in the carbon cycle. These previous studies have proposed major oceanographic circulation and climatic changes as the driver for these marine extinction events and changes in marine lithofacies patterns. This study presents new geochemical data using redox proxies such as iron speciation and trace metal geochemistry along with pyrite-sulfur ($\delta^{34}\text{S}_{\text{pyr}}$) and organic carbon ($\delta^{13}\text{C}_{\text{org}}$) from a Llandovery deeper water shale sequence within the Baltic Basin. Preliminary results record positive shifts in $\delta^{13}\text{C}_{\text{org}}$ ranging from +2‰ to +4‰, in magnitude, for three globally recognized carbon isotope excursions through the Hirnantian (latest Ordovician stage) to the Telychian as well as positive shifts in corresponding $\delta^{34}\text{S}_{\text{pyr}}$ during these carbon cycle perturbations. In conjunction, preliminary iron speciation and trace metal geochemistry data present implications for local water column and global oceanographic conditions. Results thus far link several Llandovery moderate extinction events, in many marine taxonomic groups, to evidence for a local water column that was predominantly anoxic and intermittently euxinic, and a possible global expansion of euxinia during the early Silurian. Expansion of this basinal to global pool of sulfidic waters into shallow shelf settings provides a unique mechanism to tie biotic turnover events to perturbations of the global C and S cycles.

38. Biogeochemistry of Vertebrate Decomposition in a Forest Ecosystem

Sarah W. Keenan*, Sean M. Schaeffer, Virginia L. Jin,
Jennifer M. DeBruyn

University of Tennessee

Decomposing plants and animals provide critical nutrients for ecosystems, including forests. The cycling of plant-derived organic matter released during decay is widely studied, and is known to stimulate soil micro- and macro-fauna. By comparison, the cycling of animal-derived soft and hard tissues is less well-resolved. During vertebrate decay, the rapid release of limiting nutrients, including N, P, C, and S fundamentally transforms the soil environment by stimulating endogenous organisms. The goal of this study was to evaluate the release and cycling of N and C compounds in soil beneath decomposing vertebrates in a forest, results that will be used to quantify the rates and fluxes of decay-derived compounds. Five 10-20 kg beavers (*Castor canadensis*) were placed in scavenger-exclusion cages in a temperate forest in Oak Ridge, TN, and allowed to decompose on the soil surface starting 29 July 2016. Soil beneath each beaver as well as control soils were collected during key phases of decay: initial placement, early, active, and advanced decay, skeletal exposure, and four months post decay. Soils were analyzed to measure pH, conductivity, moisture, ammonium content, bulk C and N, and $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ composition. The release of CO_2 , N_2O , and CH_4 from soil was measured adjacent to each carcass.

The internal carcass temperatures reached a maximum of $\sim 50^\circ\text{C}$ during active decay before returning to ambient conditions after 1 week. Soil pH significantly increased during active and advanced decay up to pH 9.0 before returning towards an initial pH of 6.8 after 4 months. Electrical conductivity demonstrated a similar pattern, reaching a maximum of $3500 \mu\text{S}/\text{cm}$ during active decay. Ammonium concentrations significantly increased, reaching a maximum concentration of 137 ppm/gram dry weight soil during active decay. CO_2 release significantly increased during decay, with an average of 1000 ppm above background observed during active decay. N_2O and CH_4 release also significantly increased, releasing a maximum of 0.45 ppm and 0.15 ppm, respectively, during the skeletal stage. Soil C:N decreased significantly during active decay from ~ 17 to 12, and persisted around 12 after 4 months. The $\delta^{15}\text{N}$ of bulk soil significantly increased from $<2\text{‰}$ up to 12‰ during advanced decay, with values ranging from ~ 8 to 10‰ after 4 months. In contrast, there was no significant change to soil $\delta^{13}\text{C}$, with values ranging from -27.2 to -28.2‰ .

These results demonstrate the significant and long-lasting contributions of vertebrate decomposition to ecosystem functioning. In particular, decay results in a net release of CO_2 , N_2O , and CH_4 , reflecting rapid nutrient cycling by gut- and soil-derived microorganisms. $\delta^{15}\text{N}$ enrichment after 4 months suggests that carrion decay significantly alters surface soil isotopic composition, and that carcass derived N persists in these ecosystems.

39. Geochemical and Mineralogical Analysis of Kashmir Cave and Isolation of Bacteria Having Antibacterial Activity

Sahib Zada*, M. Rafiq, Imran Khan, Abbas Ali
Naeem, Fariha Hasan

Georgia Institute of Technology

Bacterial strains having the ability to inhibit the growth of other bacteria were isolated from soil samples collected from Kashmir Smast (smast is Pushto for cave), Khyber Pakhtunkhwa, Pakistan. The study includes mineralogical and geochemical analyses of soil sample collected from the cave, so as to describe the habitat from which the microorganisms have been isolated. Total bacterial count of the soil sample was $5.25 - 3 \times 10^4 \text{ CFU mL}^{-1}$. Four bacterial isolates having activity against test organisms *Micrococcus luteus*, *Klebsiella sp.*, *Pseudomonas sp.*, and *Staphylococcus aureus* were screened out for further study. Two of the isolates were found to be Gram-positive and the other two Gram-negative. The four isolates showing antibacterial activity were identified as *Serratia sp.* KC1-MRL, *Bacillus licheniformis* KC2-MRL, *Bacillus sp.* KC3-MRL, and *Stenotrophomonas sp.* KC4-MRL on the basis of 16S rRNA sequence analysis. Although all isolates showed antibacterial activity, only *Bacillus licheniformis* KC2-MRL was selected for further study due to its large zone of inhibition. Anti-bacterial activity of *B. licheniformis* KC2-MRL was optimum when grown in nutrient broth adjusted to pH 5 and after 24 hours of incubation at 35°C . The extracted antibacterial compound was stable at pH 5–7 and 40°C when incubated for 1 hour. The strain was found resistant against cefotaxime (ctx). Atomic-absorption analysis of the soil sample collected from the cave showed high concentrations of calcium ($332.938 \text{ mg kg}^{-1}$) and magnesium ($1.2576 \text{ mg kg}^{-1}$) compared to the control soil collected outside the cave. FTIR spectrum of the concentrated protein showed similarity to bacitracin. The antibacterial compound showed activity against both Gram-negative and positive test strains. Mineralogy of Kashmir Smast is diverse and noteworthy. Different

* Indicates Presenting Author

geochemical classes identified by X-ray diffraction were nitrates, oxides, phosphates, silicates, and sulfates. Weathered cave limestone contributes notably to the formation of these minerals or compounds. FTIR spectroscopic analysis helped to identify minerals such as quartz, clinocllore, vermiculite, illite, calcite, and biotite.

40. Metabolites of Bacterial-Phytoplankton Interactions in the Surface Ocean

Courtney M. Thomas*, Shalabh Sharma, Mary Ann Moran

University of Georgia

Marine dissolved organic matter (DOM) is a mixture of thousands of molecules that impact ocean life and the cycling of all major elements on Earth. Characterization of the most rapidly-cycling subset of DOM will enhance our understanding of the fate and flux of recently-fixed marine carbon and reveal interactions occurring between members of the ocean microbiome. Operons hypothesized to transport organic compounds based on up-regulation by marine bacterium, *Ruegeria pomeroyi*, when grown in a co-culture system with marine diatom *Thalassiosira pseudonana* were previously identified. However, most of the up-regulated transporter systems are poorly annotated and their substrates unverified. Transcriptomic analysis was performed to begin the experimental verification of predicted substrates. An analysis of these transporter systems in the Tara Oceans data set characterized the abundance of these systems in the global ocean microbiome and the potential ecological significance of the substrates they transport.

41. (Bio)chemical Weathering of Chromium Containing Minerals

Emily M. Saad*, Yuanzhi Tang

Georgia Institute of Technology

Because of its utility in many industrial processes, chromium (Cr) has become the second most abundant metal contaminant in the United States. Additionally, Cr isotopes have recently emerged as a potential proxy for tracking redox processes at the Earth's surface. The current paradigm for Cr cycling suggests that Cr mobilization is redox dependent. However, very few studies have examined the effect of environmentally relevant organic molecules on the complexation and solubilization of Cr(III) from its solid phase hosts (i.e.

a redox independent mechanism). We investigated the stability of Cr(III)-Fe(III)-(oxy)hydroxides in the presence of the common microbial exudates, siderophores and small organic acids. We found that microbial exudates promoted the release of Cr(III) from solid phases via both ligand complexation and increased solid solubility (i.e. after solid transformation). Furthermore, exudate-promoted dissolution induced a Cr isotope fractionation that may interfere with redox-sourced isotope signatures. Understanding the potential reaction kinetics and pathways of Cr in the presence of microbial activities is necessary to assess the long-term stability of Cr sinks as well as to establish a more robust framework for using Cr isotopes to track Earth's oxygenation.

42. Anaerobic Digestion Combined with Hydrothermal Pretreatment for Further Energy and Nutrient Recovery from Organic Wastes

CI FANG*

Georgia Institute of Technology

For improving organic wastes management and further strengthening the phosphorus recovery ratio by follow-up struvite crystallization technology, anaerobic digestion combined with hydrothermal pretreatment were investigated for release and transformation of organic compounds and phosphorus from activated sludge and swine manure. Meanwhile, total biogas production and chemical oxygen demand (COD) reduction were explored. The results indicated that with hydrothermal pretreatment, much more soluble chemical oxygen demand (SCOD) and phosphorus could be released from activated sludge because of the breakdown of extracellular polymeric substances (EPS), and almost all the organic phosphorus could be transformed to inorganic phosphorus from swine manure. With lower hydrothermal temperature (398K), more total biogas and methane could be produced from both activated sludge and swine manure in a shorter time. However, higher hydrothermal temperature (498K) made them more difficult for biogas production because of more stable carbon forms. Therefore, anaerobic digestion combined with low-temperature hydrothermal pretreatment can facilitate the recovery of energy and phosphorus from activated sludge and swine manure.

* Indicates Presenting Author

43. Antibiotic Resistance Patterns in Mallard and Sugar Creek Wastewater Treatment Plants

Alicia Sorgen*, Molly Redmond

University of North Carolina, Charlotte

This study assesses antibiotic resistance in wastewater treatment plants and the surrounding environment using culturing and culture-independent techniques. We sampled upstream water, residential and hospital sewage influent, sewage throughout the treatment process, and downstream effluent from the Mallard and Sugar Creek Wastewater Treatment Plants in Charlotte, NC from February to April 2016.

We cultured bacteria resistant to ampicillin, ciprofloxacin, doxycycline, and sulfamethoxazole from each location, incubating under high and low nutrient conditions and at room temperature and at human body temperature. Plate counts show that more bacteria grow under low nutrient conditions at room temperature. Additional testing was conducted to eliminate the salt concentration bias between the two media types. The salt concentration was observed to have an effect on bacterial growth; however, nutrient concentration was concluded to be the main factor in determining growth on the different media types.

Colonies from each treatment condition were isolated in order to obtain pure cultures for further community characterization. Water samples were filtered in triplicate using 0.45 μm filters to concentrate the microbial communities within each sample for DNA extraction and sequencing. Genome sequences from the isolated cultures will be used to identify antibiotic resistance genes in combination with characterization of antibiotic resistance patterns throughout the wastewater treatment process and within environmental communities.

44. Using Continuous *in-situ* Measurement of Fluorescence to Inform Dissolved Organic Matter Dynamics in River Systems

Kevin Ryan*, Sasha Wagner, Aron Stubbins, Karla Haiat, Camisha Few, Peter Raymond, Jacob Hosen

University of Georgia

Dissolved organic carbon (DOC) is a key component of aquatic ecosystems where it fuels the food web and shades organisms from harmful UV radiation. River systems act as a link between the major stores of terrestrial and aquatic carbon, serving as a net exporter from land to

the ocean. Along the way, physical and biogeochemical processes actively modify DOC, changing its composition and reactivity. Fluorescence signatures of river water, a proxy for DOC, is most commonly measured in the laboratory using a fluorometer under controlled conditions. However, sample collection and analysis is limited and exposure to contamination is possible. In situ measurement of fluorescence using fifteen-minute interval data logging allows higher temporal resolution, but raw data must be corrected for temperature, absorbance and turbidity interferences occurring in the field. Multiple Eureka Manta water quality sondes recording fluorescence, temperature, conductivity, pH, dissolved oxygen and turbidity were installed in nested streams in a Connecticut River subwatershed to measure changes in fluorescence from headwater streams to a 6th order river. The nested data loggers observed fluorescence peaks responding to discharge events and traced fluorescence changes occurring from upstream to downstream. In addition, loggers recorded a diurnal fluorescence pattern during base flow conditions which we hypothesize is influenced by photochemical degradation of DOC by sunlight. We conclude that continuous in-situ records of river water fluorescence can be used to inform organic matter dynamics in watersheds to characterize DOC sources, composition, and reactivity to improve our understanding of aquatic biogeochemical processes.

45. Process Simulation and Modeling: Electron Transport Between Anaerobic Methanotrophic Archaea and Its Bacterial Partner

Xiaojia He*, Christopher Kempes, Grayson Chadwick, Shawn McGlynn, Yimeng Shi, Victoria Orphan and Christof Meile

University of Georgia

We aim to expand our understanding of the key microorganisms, metabolic strategies, and interspecies relationships involved in the formation and oxidation of methane in the environment. To study methane-cycling archaea, their syntrophic partners, and their ecophysiological properties across a range of spatial scales we use single cell/single consortia targeted approaches combined with characterizations of field samples, geochemically- characterized laboratory microcosms, environmental bioreactors, and defined syntrophic co-cultures, and utilize novel meta-omics strategies, state-of-the-art analytical imaging methodologies and stable isotope geochemistry. Ultimately, our goal is to develop and refine predictive models of the larger scale biogeochemical processes mediated by methane-

* Indicates Presenting Author

metabolizing microorganisms.

46. Bacterial Community and Resistome Compositions in Urban Streams and Wastewater Reclamation Facilities - The Urban Environmental Genomics Project (UEGP)

Kevin Lambirth*, Abrar Al-Shaer, Orion Wynblatt, Molly Redmond, Cory Brouwer, Cynthia Gibas

University of North Carolina, Charlotte

Wastewater treatment plants (WWTPs) are increasingly thought to be potential incubators of antibiotic resistance. In these environments, a wide variety of bacterial species from the microbiota of healthy and unhealthy individuals are brought into close and prolonged contact, along with native environmental strains endemic in soils and sediments. It has been shown that pharmaceuticals including metformin, caffeine, reproductive hormones, muscle relaxants and antidepressants persist through the wastewater treatment system and into surface waters, in some cases resulting in detectable biological effects on unintended species targets. Persistence of commonly used antibiotics in wastewater may increase the potential for survival and horizontal transfer of adaptive genes, some of which may pose a threat to human health. In this study, we have assayed the concentrations of ten common antibiotic compounds in wastewater influents, effluents, and associated up and downstream surface waters from two Charlotte area wastewater plants, including residential and hospital trunkline locations. We then performed Illumina 16s and shotgun sequencing to assay the taxonomic and resistome compositions at each of these sites across four time points, spaced approximately 30 days apart, during early to mid-2016. Antibiotic compounds are present throughout the wastewater lifecycle, and significantly increase between sites upstream and downstream of effluent release. Persistence of the WWTP core microbiome and antibiotic resistance elements outside the plants is remarkably consistent, with little variation in community structure due to effluent discharge. Numerous antibiotic resistant genes (ARGs) were detected in all samples, with the highest abundance in the less processed influents. Most ARG abundances and pathogenic taxa were drastically reduced in the treatment process, though a few were able to proceed seemingly unaffected and were discharged into environmental streams. While we do see an increase in abundance of ARGs within the plants themselves, this may simply be due to the concentration of large volumes of waste, rather than WWTPs being

genuine antibiotic resistance “hotspots”. In general, the reduction in ARGs as a result of the treatment process was highly effective, indicating that while treatment systems may not be infallible, they are efficient in significantly reducing potential microbial threats.

47. In Situ Genetic Responses by Distinct Genotypes of *Vibrio vulnificus* Experiencing Oxygen Limitation in Oysters and Water, and Parallel Bacterial Community Analyses

Britney L Phippen*, James D Oliver

University of North Carolina, Charlotte

Human infections caused by *Vibrio* species are rising, and factors associated with global climate change have been suggested to impact their abundance and geographical range. One such species, *Vibrio vulnificus*, is globally distributed and can be isolated from various sources. Genetically diverse, it is divided into three biotypes, of which biotype 1 strains are typically associated with human disease. We divide those strains into environmental (E) and clinical (C) genotypes, with the latter being primarily associated with septicemia. Importantly, this bacterium is frequently exposed to hypoxia in both the environment and the host, however few studies have investigated this factor as it impacts gene expression of *V. vulnificus*. Furthermore, the composition of pathogenic species in the environment might be impacted by this hypoxia, making describing these communities a necessity. Thus, we investigated the role of oxygen on in situ gene expression in both genotypes of *V. vulnificus*, in planktonic cells as well as those seeded in oysters, using novel in situ modified membrane chambers. Simultaneously, by comparing 16S ribosomal RNA we determined bacterial community compositions during cyclical hypoxia, while concurrently recording abiotic profiles. Briefly, genes involved in virulence, environmental survival, and stressosome production, were negatively correlated with oxygen in planktonic cells. Comparisons of the expression of these genes in *V. vulnificus* isolated from oyster tissue has shown distinctive profiles. We found similar community compositions during both hypoxia and normoxia, however, unweighted beta analyses revealed a potential for shifts in lower abundant species, which may be important for areas that are becoming increasingly more hypoxic. This study emphasizes investigating hypoxia as a trigger for gene expression by marine *Vibrio* species, highlights the need to study this bacterium during its life in an oyster, and stresses the need for more in depth community analyses during estuarine hypoxia.

* Indicates Presenting Author

48. Organic Fertilizer Improves Revegetation of Roadside Soils

Evan Barnard*, Carly A. Phillips, Nina Wurzburger

University of Georgia

Urbanization and road construction affect the global carbon cycle by releasing carbon from soil and reducing carbon inputs into soil from plant productivity. Revegetation of areas disturbed by construction can replenish soil organic matter, thereby increasing plant productivity and soil carbon storage. Plant restoration of disturbed roadsides can be facilitated by the application of fertilizers. However, fertilizers (i.e., organic or inorganic) vary in their effectiveness and carbon footprint. We conducted a plant growth experiment using *Elymus virginicus* and soils sampled along roads in Atlanta, GA to investigate how fertilizer treatments affect plant growth. We performed a two-way factorial experiment, with two factors (inorganic and organic fertilizers) each with two levels (with or without), that were crossed to create four experimental treatments. We hypothesized that both inorganic and organic fertilizers would increase plant growth, but that plants grown with organic fertilizer would produce more biomass compared to those receiving inorganic fertilizer. Following twelve weeks of growth, we quantified plant growth, root:shoot ratios, soil microbial biomass, and soil nutrient and pH pools. We found that both inorganic and organic fertilizers increased plant biomass and decreased the root:shoot ratio, however addition of organic fertilizer increased plant biomass more than the addition of inorganic fertilizer. Our findings suggest that the addition of organic fertilizer is an effective management tool for revegetating disturbed roadsides, thereby promoting greater carbon sequestration in urbanized areas and counteracting the rise in atmospheric greenhouse gases.

49. Compartmental Biogeochemical Process Model for Estimating Emission of Ammonia from Stored Liquid Dairy Manure

Sampath A. Karunarathne*, Jactone A. Ogejo

Virginia Tech

Processed-based biogeochemical models are used to estimate production and emission of ammonia from liquid dairy manure storage. The biogeochemical processes responsible for these gaseous emissions are governed by environmental factors and manure characteristics. Manure is a heterogeneous material and the environmental factors and manure characteristics

vary spatially in the stored manure. Existing process-based models consider stored manure as a homogeneous system and do not consider these spatial variations leading to inaccurate estimations. In this study, a compartmental biogeochemical model is used to (i) estimate spatial variation of temperature and substrate concentration (ii) incorporate these spatial variations to estimate occurrence and rates of biogeochemical processes, and (iii) estimate production and emission of ammonia from stored manure. A compartmentalization approach is used whereby; manure storage is partitioned into several sections in vertical domain assuming that the conditions are spatially uniform within horizontal domain. Spatial variation of temperature and substrate concentration are estimated using principles of heat and mass transfer. Biogeochemical processes are assigned to each compartment to estimate the production and emission of ammonia. We anticipate that the integration of spatial heterogeneity of environmental factors and manure characteristics will better represent the natural processes occurring in stored manure and improve accuracy of emission estimates. Model performance was evaluated and sensitivity analysis was performed to identify the model parameters that have greater impact on model outputs. The model was simulated for different scenarios to estimate ammonia emission from a hypothetical dairy farm located in Virginia using historical and forecast weather data.

50. Mapping Depth to Argillic Horizon Using Electromagnetic Induction on Historically Farmed Soils within the Piedmont Region of the United States

Rachel Ryland*, Daniel Markewitz, Aaron Thompson

University of Georgia

Historic agricultural practices have led to accelerated erosion throughout the Piedmont region of the southeastern United States. Practices, such as tilling, degraded soil quality altering hydrologic processes of the landscapes by limiting infiltration leading to overland flow and erosion. Erosion due to these practices has substantially redistributed sediment from upper to lower landscape positions, causing a shallower depth to argillic horizon along ridges. By mapping the depth to argillic horizon within watersheds that have a history of farming and watersheds with little evidence of agricultural disturbance, a better understanding of the effects of farming practices on erosion and sediment redistribution can be made. This study uses extensive soil sampling within historically farmed and unfarmed watersheds to map spatial variations in the depth to argillic horizon.

* Indicates Presenting Author

In addition to sampling, the electrical conductivity of the soil was tested by electromagnetic induction and calibrated to clay content and other topographic characteristic (i.e. landscape position, aspect, percent slope) from which the depth to argillic horizon can be predicted. The results from this study will improve understanding of erosion on sediment redistribution and the use of electromagnetic induction as an accurate and efficient means to predicted depth to argillic horizon. This information can be applied to hillslope hydraulic model that rely on a quick and noninvasive mean to determine soil texture for parameterizing.

51. Enhanced Enzymatic Response of Pelagic Microbial Communities to Additions of High Molecular Weight Substrates

Sarah Brown*, A. Hoarfrost, J.P. Balmonte, S. Ghobrial, C. Arnosti

University of North Carolina, Chapel Hill

Heterotrophic microbial communities play a central role in carbon cycling in the ocean, repackaging, respiring, and transforming a considerable fraction of organic matter. The remineralization of high molecular weight (HMW) organic matter by heterotrophic bacteria is initiated by structurally specific extracellular enzymes. We investigated the range of extracellular enzymes used by heterotrophic microbial communities in response to an addition of complex HMW organic matter at two stations in the Northeast Atlantic Ocean, measuring peptidase and polysaccharide hydrolase activities in surface, mesopelagic, and bottom waters at each station. To prepare a HMW substrate, *Thalassiosira* was homogenized, dialyzed in a 10kd membrane, and lyophilized. Moderate concentrations (25 mg/L) of the HMW *Thalassiosira* extract were added to seawater in replicate 20 L carboys. Potential hydrolysis rates of α - and β -glucosidase, leucine aminopeptidase, and trypsin and chymotrypsin endopeptidases were measured in each carboy, and then periodically over a month-long timecourse. Triplicate amended mesocosms had higher hydrolysis rates and an increase in the spectrum of substrate utilization than unamended mesocosms. Surface water samples had the broadest spectrum of substrate utilization and the highest potential hydrolysis rates; the response in mesopelagic mesocosms (water depth ca. 800-900 m) were fairly similar to surface waters, while deep waters were considerably lower and later in response. Measurements of polysaccharide hydrolase activities with fluorescently labeled polysaccharides (pullulan, laminarin, xylan, fucoidan, arabinogalactan, chondroitin, alginic acid, and lambda-carageenan) were

initiated 15 days after *Thalassiosira* addition; analysis of these samples is still ongoing, but in surface water, all 8 polysaccharides were hydrolyzed in the amended carboys, while only 4 polysaccharides were hydrolyzed in the unamended carboys. Next generation (Illumina) sequencing of samples from these carboys will enable us to determine the extent to which changes in the spectrum and rates of enzyme activities correlate with changes in microbial community composition compared to unamended carboys.

52. Shifting Microbial Communities Sustain Multi-Year Iron Reduction and Methanogenesis in Ferruginous Sediment Incubations

Marcus S. Bray*, Jieying Wu, Benjamin C. Reed, Cecilia B. Kretz, Keaton M. Belli, Rachel L. Simister, Cynthia Henny, Frank J. Stewart, Thomas J. DiChristina, Jay A. Brandes, David A. Fowle, Sean A. Crowe, Jennifer B. Glass

Georgia Institute of Technology

Reactive Fe(III) minerals can influence methane (CH_4) emissions by inhibiting microbial methanogenesis or by stimulating anaerobic CH_4 oxidation. The balance between Fe(III) reduction, methanogenesis, and methane oxidation in ferruginous Archean and Paleoproterozoic oceans would have controlled CH_4 fluxes to the atmosphere, thereby regulating the capacity for CH_4 to warm the early Earth under the Faint Young Sun. We studied CH_4 and Fe cycling in anoxic incubations of ferruginous sediment from the ancient ocean analogue Lake Matano, Indonesia over three successive transfers (500 days total). Iron reduction, methanogenesis, methane oxidation, and microbial taxonomy were monitored in treatments amended with ferrihydrite or goethite. After three dilutions, Fe(III) reduction persisted only in bottles with ferrihydrite. Enhanced CH_4 production was observed in the presence of goethite, highlighting the potential for reactive Fe(III)-oxides to inhibit methanogenesis. There was limited evidence for Fe(III)-dependent CH_4 oxidation, although some incubations displayed CH_4 -stimulated Fe(III)-reduction. 16S rRNA profiles continuously changed over the course of enrichment, with ultimate dominance of unclassified members of the order Desulfuromonadales in all treatments. Microbial diversity decreased markedly over the course of incubation, with subtle differences between ferrihydrite and goethite amendments. These results suggest that Fe(III)-oxide mineralogy and availability of electron donors could have led to spatial separation of Fe(III)-

* Indicates Presenting Author

reducing and methanogenic microbial communities in ferruginous marine sediments, potentially explaining the persistence of CH₄ as a greenhouse gas throughout the first half of Earth history.

53. Downward Transport of Dissolved Black Carbon from Shelf Region to the Deep Ocean: A Case Study from Prydz Bay, Antarctica

Ziming Fang*

University of Georgia

Dissolved black carbon (DBC) makes up ~10% of the global flux of riverine dissolved organic carbon (DOC) to oceans. Part of the riverine DBC is degraded in the ocean surface due to solar radiation while the other part can survive long distance transport from river mouth to abyssal seas and increase the deep ocean refractory carbon pool. In the Antarctica, the downward transport of dense shelf waters (DSW) from shelf regions to deep Southern Ocean may serve as a short-cut for DBC to escape from the sunlit ocean surface and, thus, play an important role on the biogeochemical cycle of DBC and marine carbon cycle. Here, we chose Prydz Bay as a case study to figure out this issue. We found that DBC and DOC concentrations of DSW in the Prydz Bay were ~127% and ~37% higher than the circumpolar deep water (CDW), respectively. Moreover, DBC/DOC ratio was higher in DSW than the CDW, which suggested DOC in DSW may have older bulk ¹⁴C age than CDW (DBC has much old ¹⁴C age than bulk DOC). Using sea water oxygen isotopes (δ¹⁸O) and salinity, we confirmed that the down-flow DSW could entrain DBC, as well as DOC, from the shelf region to the deep Southern Ocean. Basing upon a two end-member mixing model, the downward transport of DBC and DOC from Prydz Bay could increase DBC and DOC concentrations of Antarctica Bottom Water by 3.8~8.8% and 1.7~3.7%, respectively. This result indicated that DBC and DOC exported from shelf regions may account for the observed increase and aging of DOC in the deep Southern Ocean. Thus, we highlight the downward transport of DBC, as well as DOC, from Antarctic shelf regions should have profound influence on the biogeochemistry of DBC and global deep ocean carbon cycle.

54. Effects of State Change on Shallow Lake Nutrient Sediment Fluxes

Olivia Torano*, Suzanne Thompson, Mike Piehler

University of North Carolina

Shallow lake ecosystems generally persist in one of two alternative stable states. These states can be distinguished by the dominant primary producer present, submerged aquatic vegetation (SAV) or phytoplankton. The transition between these stable states is a function of numerous variables including nutrient levels, depth, PAR, and fish communities. The largest natural lake in North Carolina, Lake Mattamuskeet, is a shallow lake that was divided by a road into two basins. For much of its recent history, the west basin was dominated by phytoplankton and the east basin was dominated by SAV. In 2013 the east basin lost much of its vegetation and quickly shifted to mirror the west basin. Subsequent work on the lake has been aimed at determining why the lake persisted in different states, what caused the 2013 shift, and how this shift is altering the material cycling and biodiversity of the lake. In this study we measured how the loss of vegetation has impacted nutrient cycling at the sediment water interface. To do so, triplicate sediment cores were collected in vegetated, recently unvegetated, and historically unvegetated areas of the east and west basins. These cores were incubated in a continuous flow through system. Flow through water was collected and analyzed for N₂ gas, phosphate, and ammonium fluxes using a membrane inlet mass spectrometer and flow injection analyzer. The percent organic matter of the sediment surface within each core was then measured by loss on ignition. Nutrient fluxes and percent organic matter varied between basins and vegetative histories of the collection site. Cores taken from recently and historically unvegetated areas in the west basin were the only to show any denitrification, but these fluxes were small.

55. Temperature Sensitivity of Biodegradable Plastic Mulches to Microbial Decomposition

Marie English*, Sreejata Bandopadhyay, Douglas G. Hayes, Jennifer M. DeBruyn, Larry C. Wadsworth, Sean M. Schaeffer

University of Tennessee, Knoxville

In the production of many specialty crops, plastic mulch films are employed to provide benefits such as moisture retention, soil temperature optimization, and weed control. Biodegradable plastic mulches (BDMs) are a

* Indicates Presenting Author

more sustainable alternative which, after being tilled into the soil subsequent to service life, biodegrade into carbon dioxide, water, and microbial biomass as part of the soil carbon (C) cycle. However, the role of temperature in biodegradation of BDMs is not well known. Diverse soil conditions across the US present a challenge in attempts to develop durable mulches that will biodegrade after being tilled into soil. An incubation experiment was conducted under controlled conditions to investigate biodegradation of two BDMs, a poly lactic acid/polyhydroxyalkanoate experimental product (PLA/PHA) and a commercially available starch/polyester blend (BioAgri, BioBag Americas, Palm Harbor, FL), and a cellulosic paper mulch (the latter serving as a control), at three different temperatures (10, 20, and 30°C). The evolution of carbon dioxide was measured biweekly over 16 weeks. Total organic carbon, dissolved organic carbon, and stable isotope ($\delta^{13}\text{C}$) measurements provided insight into the transport and accumulation of plastic mulch-derived C in the soil. Cumulative carbon dioxide produced was greater at 30°C incubation for the BDMs when compared to the no mulch control (536 ± 13 , 510 ± 35 , and $344 \pm 33 \text{ ug C g}^{-1}$ dry soil for PLA+PHA, BioAgri, and the paper mulch, respectively) indicating microbial assimilation of the mulch. When comparing biodegradation at 20°C to 30°C, temperature sensitivity of decomposition (Q10) was highest for the PLA/PHA treatment (Q10 value of 1.85 ± 0.32 compared to the control value of 1.42 ± 0.28). For most treatments, the addition of BDMs led to a higher Q10 value than the no-mulch control, indicating that mulches affected the temperature sensitivity of the microbial metabolism. A deeper understanding of the influence of temperature on biodegradation of BDMs will help determine the optimal conditions for conducting biodegradation in the field.

56. Hierarchical Classifiers in Transcription Reveal Responses of Extreme Microbial Communities to Oil and Dispersant Exposure.

Tito D. Peña-Montenegro*, Sara Kleindienst, Andrew E Allen and Samantha B Joye

University of Georgia

Chemical dispersants are used commonly in response to oil spills. However, the impacts of dispersants on microbial community composition and activity are poorly understood. We simulated the deep water conditions that prevailed following the 2010 BP/Deepwater Horizon oil spill and evaluated the response of the microbial community to elevated levels of oil, chemical dispersants and dispersed oil using metatranscriptomics.

Clustering factors were compared across levels of a hierarchical annotation system to increase the power of prediction and contrast in our datasets. We found significant dispersant-driven changes in terms of diversity and abundance of microbial composition and activity, shifting the dynamics from one dominated by oil biodegradation in oil-only treatments to those dominated by dispersant biodegradation in dispersant-amended treatments. These results have important implications for understanding the impacts of chemical dispersants on the ability of microbial communities to efficiently degrade oil in the environment.

57. Serpentinization and Synthesis: Can Abiotic and Biotic Non-Volatile Organic Molecules Be Identified in the Subsurface of the Atlantis Massif?

Katherine Hickok*, Tran Nguyen, Beth Orcutt, Gretchen Früh-Green, IODP Expedition 357 Science Party, Susan Q. Lang

University of South Carolina

The high concentrations of hydrogen created during serpentinization can promote the formation of abiotic organic carbon molecules such as methane, formate, short chain hydrocarbons and, in laboratory experiments, larger molecules containing up to 32 carbon atoms. Subsurface archaeal and bacterial communities can use these reduced compounds for metabolic energy. International Ocean Discovery Project Expedition 357 drilled into the Atlantis Massif with the goals of investigating carbon cycling and the presence of life in a zone of active serpentinization. The expedition recovered multiple rock lithologies including gabbros, basalts, carbonate sands, and serpentinites. A subset of these samples are being analyzed to determine if non-volatile organic molecules are produced abiotically in serpentinizing environments and to identify 'hot spots' of microbial life in the subsurface.

Rock samples of contrasting representative lithologies are being analyzed for the presence of n-alkanes and fatty acids. Preliminary results have so far indicated the presence of alkanes in some samples. The isotopic (^{13}C , ^2H) characteristics of these compounds are being compared to a suite of oils, greases, and drilling fluids used during sample collection to distinguish in situ abiotic and biotic signatures from contaminant compounds. Other initial results have shown the efficacy of various sample-handling procedures designed to reduce surface contamination. This study will contribute to the overall understanding of the role serpentinization plays in the

* Indicates Presenting Author

global carbon cycle and its implications for pre-biotic chemistry.

58. Spatial Variability in Carbon Export in the California Current Region

Thomas Bryce Kelly*, Michael R Stukel

Florida State University

Within the upper water column, phytoplankton fix inorganic carbon into biomass which then enters into the ecosystem. The vast majority of this organic carbon is respired back into CO₂ on short timescales, yet a small fraction does escape into the deeper water column (export production) where it may remain for years to centuries. Thorium-disequilibrium profiles are a geochemical tracer for carbon export. Here I analyze a suite of thorium-derived export measurements collected during the November CalCOFI cruise of 2016 with emphasis on the spacial variability and the ecosystem drivers that underpin the variability.

59. High Resolution Microbial Community Analysis of Sediments from the High Arctic, Kongsfjorden and Van Kuelenfjorden, Svalbard

Joy Buongiorno*, Karen Lloyd

University of Tennessee

As global temperatures continue to rise in response to atmospheric greenhouse gas concentrations (IPCC, 2007), polar regions are experiencing tangible environmental alterations. Most noticeably, calving of iceshelves in the Antarctic and glacial retreat in the Arctic have been observed, leaving the question of what impact these processes will have on ecosystem biodiversity and element cycling. In the high Arctic, which is the most sensitive to a warming climate, glacial retreat has the potential to disrupt biogeochemical cycles. This is because shrinking glaciers will no longer act as conduits of turbid sediment, which in turn will enhance penetration of sunlight into the fjord and foster blooms of phytoplankton that feed benthic microbial communities. In this way, increased organic matter delivered to sediments may induce a positive feedback of increased greenhouse gas emission as this organic matter is degraded. Here, we investigate the current microbial community structure of sediments underlying glaciers within Kongsfjorden and Van Keulenfjorden, Svalbard (79°N). Kongsfjorden sediments are deposited under Kongsbreen and Kronebreen, which are retreating at a

rate of 0.5 km yr⁻¹ (Lefauconnier et al., 1994). Runoff from these hematite-rich glaciers feeds iron into the fjord, which collects in the anoxic sediments and drives a unique subsurface geochemical profile where sulfate becomes reoxidized as far down as 20 centimeters below the surface. In order to characterize the microbial community in these sediments, we created 16S rRNA gene libraries of DNA extracted at 1 cm intervals as deep as 20 centimeters into the sediment. In addition, we performed quantitative PCR (qPCR) to quantify the abundance of bacteria and archaea. Finally, we place these data into the context sulfate concentrations to observe any shift in community composition or abundance with geochemistry.

60. Dissolved and Particulate Trace Elements in Arctic Melt Ponds

Chris Marsay*, William Landing, Peter Morton, Brent Summers, Jessica Fitzsimmons, Nathan Lanning, Clifton Buck

University of Georgia

Melt ponds on polar sea ice represent a potentially important but poorly understood intermediary step between high latitude atmospheric deposition of trace elements and their delivery to the surface ocean. The seasonal rise in temperature during spring and summer leads to melting of sea ice and of snow that has accumulated on the ice during the previous winter, resulting in pooling of melt-water in depressions upon the sea ice. As a result, trace elements within the snow/ice collect in the relatively fresh water of these melt ponds, before being released to the surface ocean by rapid drainage or by gradual mixing with the underlying seawater.

Here we present dissolved and particulate trace element concentrations measured in five melt ponds during the US Arctic GEOTRACES cruise of summer 2015. Salinity measurements of the melt ponds indicated varying degrees of seawater influence. Dissolved trace element concentrations ranged from 1 – 33 picomolar (Pb) to 3 – 24 nanomolar (Mn), while particulate trace element concentrations ranged from sub-picomolar (Pb, Co) to 4 – 124 nanomolar (Al). We also compare trace metal/aluminum ratios of melt pond particulate material to those in precipitation samples collected during the same GEOTRACES cruise and use them to identify possible sources of the particulate material collected.

* Indicates Presenting Author

61. Fungal Extraction of Rare Earth Elements from Coal Fly Ash

Pan Liu*, Yuanzhi Tang

Georgia Institute of Technology

Rare earth elements (REEs) are critical for a wide range of high-technology applications due to their unique magnetic, phosphorescent, and catalytic properties. Discrepancy between the increasing global demands for REE production and deficiency of natural REE deposits has intrigued extensive researches on alternative REE resources. Coal fly ash is recently proposed to be a promising REE resource because of its high REE concentration (e.g. ~800 ppm La) after coal burning process. In this study, we propose to extract REEs from coal fly ash using microbes, which is low-cost and environmental friendly. Two types of fly ashes from a local coal fire plants were reacted with different fungi species isolated from acid mine drainage system that are capable of tolerating high metal concentrations. Preliminary chemical leaching experiments using nitric acid showed that REEs were readily extractable from the fly ashes, and the recovery rate (%) increased with decreasing pH. However, biotic leaching experiments at pH 2, 4, and 7 displayed initially increasing then decreasing REE concentrations in the leachate after 4 week incubation. This is likely due to the high alkalinity of fly ashes (beyond the buffering capacity of growth medium), which possibly caused secondary precipitation of the extracted REEs. Future biotic experiments will focus on fungal reactions with pre-acidified fly ashes and kinetics and extent of REE leaching. Results from this study can provide important insights for the feasibility and efficiency of fungal bioleaching for REE recovery from coal fly ash.

62. Riverine Microbial Community Assembly in the Upper Oconee Watershed

Morgan Teachey*, Normal Hassell, Elizabeth Ottesen

University of Georgia

Stream networks play key roles in global carbon and nutrient cycles, connecting terrestrial and marine environments and determining the quality and quantity of carbon and nutrients transferred between these biomes. Because microbes are vital to nutrient cycling within the moving water column, understanding the make-up of stream microbial communities and their contribution to riverine stream metabolism is key to watershed health. In an initial study, water samples

were collected from streams across the Upper Oconee watershed in Athens, GA on a quarterly basis for a year. 16S rRNA gene analysis of the extracted bacterial DNA for five consecutive seasons revealed a recurring trend in which microbial diversity (richness and site-to-site variation) was negatively correlated with upstream dendritic distance. Interestingly, the relative abundance of soil and sediment-associated microbial taxa also declined with increasing dendritic distance, while the relative abundance of freshwater taxa increased. These patterns, however, were disrupted at a landscape scale for two out of five seasonal collections, potentially as a result of temperature and rainfall fluctuations. To investigate short-term variability in these assembly patterns, a lower-order creek in the watershed that consistently exhibiting similar trends in population succession was selected for a multi-day high-resolution study. We collected water at three locations within this stream daily for 11 days, and used these samples for high-throughput 16S rRNA gene amplicon sequencing. This time series revealed similar, highly consistent longitudinal trends in microbial community diversity and taxonomic representation, with the upstream sampling site exhibiting the highest temporal variability in community composition. Continuing studies are underway to determine how this community assembly process impacts microbial community metabolism and ecosystem function.

63. Elucidation of Anaerobic Aromatic Hydrocarbon Degradation Pathways in *Geobacter daltonii* Strain FRC-32

James Bullows*, James Dulaney, William Furin, Natalie Pain

Georgia State University

Fe(III) and U(VI)-Reducing bacterium *Geobacter daltonii* strain FRC-32 is capable of oxidizing various petroleum hydrocarbons anaerobically using a host of unique enzymatic mechanisms, all of which are pertinent to the degradation of crude oil and its components. Annotation of the *G. daltonii* genome revealed many duplicates and homologs of known genes from various anaerobic aromatic degradation pathways. One of these genes, mbs, encodes for m-hydroxybenzylsuccinyl-CoA synthase, while a homologous gene, bss, encodes for the radical forming, toluene activating enzyme benzylsuccinate synthase. Certain proteins integral to various degradation pathways utilized by other aromatic degrading bacteria are not present in *G. daltonii*, indicating the bottlenecking of multiple substrate pathways into a single, unified pathway. After

* Indicates Presenting Author

growing *G. daltonii* anaerobically on various petroleum hydrocarbons including toluene and benzene as the sole electron donors, total cell RNA was isolated during the mid-log stage of growth. Quantitative real-time RT-PCR was used to measure the transcript level of the key functional genes bamR, bamY, bss, and mbs. The bss transcript level was significantly higher during oxidation of toluene, a substituted aromatic, while the mbs transcript level was higher during oxidation of benzene, an unsubstituted aromatic. SDS-PAGE of total cell lysate analysis from cells grown on benzene and toluene confirmed the same gene product expression profiles, demonstrating expression of Bbs, an enzyme constituent of the toluene degradation pathway, in both. Our study aims to elucidate the novel pathways taken during anaerobic oxidation of a diverse array of aromatic carbon sources in *G. daltonii*. We hypothesize that *G. daltonii* methylates benzene to toluene to continue down the toluene degradation pathways via the Mbs activating subunit MbsD, and that the first step of unsubstituted aromatic degradation after methylation utilizes Mbs, while substituted aromatics utilize Bss instead. Such a versatile bacterium represents an almost unprecedented adaptability in anaerobic degradation, and this study could harness new methods of oil spill bioremediation otherwise unfeasible in anaerobic environments. Further studies comparing the structure of each of these proteins are underway.

64. Hydrocarbon and Fluid Transport in Surficial Cold Seep Sediments

Jurjen Rooze*, Leigha Peterson, Richard N. Peterson,
Christof Meile

University of Georgia

Hydrocarbon seepage from cold seeps provides energy to cold seep biota, stimulates carbon cycling in the water column, and serves as a natural analogue to anthropogenic hydrocarbon discharge in deep-water environments. To study the fate of these hydrocarbons and to assess their ecological impact it is important to constrain benthic hydrocarbon fluxes. The flux of hydrocarbons from cold seeps to the overlying water is dependent on the efficiency of hydrocarbon removal in surface sediment, which in turn is contingent on the upward fluid flow velocity and downward diffusion of oxidants.

Fluid and hydrocarbon fluxes have been constrained in the past by fitting transport models to measured salt and temperature profiles, yet strong salt gradients at the sediment-water interface only develop in brine

seeps. We instead fitted profiles of the radioactive decay of radium - a method applicable to any cold seep. In addition, we used measured sulfate reduction rates in combination with sulfate profiles to estimate fluid fluxes. The reliability of the methods was analyzed in detail by performing parameter identifiability analysis and constraining confidence intervals with Monte Carlo simulations. Finally, the validity of the commonly made assumptions of steady-state and unidirectional flow was evaluated by developing a biogeochemical reaction-transport model that simulates the effect of gas hydrate and calcium carbonate formation on the permeability field, and the emergent spatiotemporal flow patterns.

65. Assessing the Export of Terrigenous Dissolved Organic Matter in the South Atlantic Bight using CDOM Analysis: 2014 and 2016 Cruises

V Ruth Pannill*, Maria L. Letourneau, Patricia M.
Medeiros

University of Georgia

The Altamaha River in Georgia drains one of the largest basins on the U.S. eastern seaboard and is the third largest contributor of freshwater to the Atlantic Ocean on North America's eastern shore. Surface water samples collected during two surveys in the central South Atlantic Bight (SAB) in April 2014 and April 2016 were analyzed for DOC contents and chromophoric DOM (CDOM). Specific absorption ratios (SUVA: a₂₅₄/DOC) indicate higher aromaticity in the South Atlantic Bight close to the shore; spectral slope coefficient of CDOM in the 275-295 nm band (S₂₇₅₋₂₉₅) had the lowest values along the coastal region and progressively increase off shore. Terrigenous organic matter was a major contributor to total DOM in a relatively thin band close to shore, peaking near the mouth of the Altamaha River and Sapelo Sound. As the low salinity plume was transported across the shelf, wind-driven mixing and entrainment of marine water resulted in the progressive dilution of the terrigenous DOM signature.

66. Microbial Community Profiles and Microbial Carbon Cycling in Orca Basin

Andrew Hyde*, John Paul Balmonte, Mandy Joye,
Andreas Teske

University of North Carolina, Chapel Hill

Orca Basin is the largest seafloor brine pools in the world,

* Indicates Presenting Author

covering over 400 km² and reaching brine layer depths of 200 m. The brine pool contains water 8 times denser than the overlying seawater and is separated from the overlying water column by a sharp pycnocline that prevents vertical mixing. The transition from ambient seawater to brine occurs over 100 m [2150 to 2250 m] and is characterized by distinct changes in temperature, salinity, chemical conditions, oxygen, and organic matter concentration. The sharp brine-seawater interface results in a sharp pycnocline, which serves as a particle trap for sinking marine organic matter. Previous studies have used lipids to show that this organic-rich interface is host to an active microbial community which is potentially involved in deep-sea carbon remineralization and metal-cycling. Additionally, previous work on methane, ethane, and propane concentrations and ¹³C-isotopic signatures has also implicated the brine pool as well as the interface as sources for biogenic low-molecular weight hydrocarbons, resulting from the high concentration of suspended organic matter above and within the brine pool. Here we investigate the profiles of microbial community composition and metabolic potential in Orca Basin, ranging from seawater through the Orca Basin chemocline and into the deep Orca Basin brine. To characterize the microbial community and stratification, we used high-throughput bacterial 16S rRNA gene sequencing of filtered water above, within, and below the Orca Basin chemocline. Our sequence data shows that three distinct and unique communities exist in the Orca Basin water column with varying potential for carbon cycling along this steep environmental gradient.

67. Endosymbiont Diversity and Shell Morphology Differences for *Ctena orbiculata* (Lucinidae: Bivalvia)

Zackary Payne*, Broc Kokesh, Audrey Paterson,
Laurie Anderson, Annette S. Engel

University of Tennessee

All known extant lucinids harbor endosymbionts within their gills that are capable of oxidizing hydrogen sulfide, and are lucinids are thought to play a key role in shallow marine ecosystems where they can burrow up to 50 cm beneath the rhizosphere of various seagrasses. The removal of sulfide facilitates seagrass productivity, thus forming a three-way symbiotic system. Based on 16S rRNA genes sequences and metagenomics, genetic and functional differences among the endosymbiotic bacteria are apparent. The role of geography and clam age in explaining these genetic differences have not been considered, however. The goal of this study was

to evaluate endosymbiont diversity from one lucinid host, *Ctena orbiculata*, retrieved from geographically and geochemically distinct locations, and to combine these data with shell geometric morphometrics to determine if there were distinct differences in shell morphology among the locations. The study site included an open ocean location and two inland marine ponds on the island of San Salvador, The Bahamas. Total nucleic acids were extracted from the gills and foot, and bacterial 16S rRNA gene amplicons were analyzed using MOTHR and taxonomically classified using the Silva and Ribosomal Database Project (RDP) reference databases. Analysis of operational taxonomic units (OTUs) indicated three dominant endosymbiont OTUs. One OTU abundant in three specimens from X Pond, was closely related to the putative sulfide-oxidizing genus *Sedimenticola*, which has been previously detected from lucinids in other seagrass beds in Florida. All other analyzed specimens had more abundant OTUs closely related to an unclassified Gammaproteobacteria, best identified as Milano WF1B-44 (according to the Silva database), which has no known metabolism, or as *Methylococcus* (RDP database), which is associated with methanotrophy. Shell morphologies of the three *Sedimenticola*-harboring specimens were compared to the other clams found in the pond; no apparent correlation between shell morphology and OTU distribution was found, but the sizes of these three clams were particularly small, suggesting that clam age may affect endosymbiont diversity. The combination of bacterial diversity analysis and shell morphology provides unique information about lucinid diversity and intraspecific morphologic variation that may help in reconstructing environmental variation in coastal paleoenvironments over time.

68. Zooplankton C and N Stable Isotopes in the Wake of the Deepwater Horizon Oilspill

Drake Lee-Patterson*, Ana Clavere Graciette, Dr.
Joseph P. 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 from April to July of 2010. This event discharged an unprecedented volume of petrocarbon into pelagic waters, an environment with distinctive redistribution of materials throughout the water column. We collected zooplankton and water samples from the Northern Gulf one month after the DWH wellhead was sealed and have resampled the system annually to monitor carbon and nitrogen stable

* Indicates Presenting Author

isotope signatures across animal biomass and suspended particles. We use stable isotope measurements of $d^{13}C$ and $d^{15}N$ to quantify the incorporation of low $d^{13}C$ material from petrocarbon and low $d^{15}N$ material from nitrogen fixation into the marine food web. By taking diel pairs of samples at a multitude of sites and depth intervals and repeating this sampling annually we can compare $d^{13}C$ and $d^{15}N$ values from areas suspected to have heavy input from the DWH spill to later time points taken at the same sites.

69. The Genome Sequence of *Nitrosococcus wardiae* Strain D1FHST Reveals the Archetypal Metabolic Capacity of Ammonia-Oxidizing Gammaproteobacteria.

Lin Wang*, Chee Kent Lim, Molly C. Redmond,
Martin G. Klotz

University of North Carolina, Chapel Hill

Strain D1FHS of a new species classified as “*Nitrosococcus wardiae*” in the genus *Nitrosococcus*, family Chromatiaceae, order Chromatiales, class Gammaproteobacteria, was isolated into pure culture by enrichment from a sediment sampled from Jiaozhou Bay. Here we report the complete genome sequence of type strain D1FHS and provide insight into the molecular mechanisms leading to its distinct physiology enabling it to grow as an ammonia-dependent chemolithotroph in the marine environment. The *Nitrosococcus wardiae* D1FHS genome sequence was analyzed in context with the genomes of the other type strains in the *Nitrosococcus* genus: *Nitrosococcus oceani* C-107 (=ATCC19797), *Nitrosococcus halophilus* Nc4 and *Nitrosococcus watsonii* C113. Surprisingly, the genome of D1FHS revealed the presence of a cyanase gene (*cyn*), thereby making *Nitrosococcus wardiae* D1FHS the first AOB with the genetic potential to encode cyanate hydratase (EC 4.2.1.104).

70. Sorption, Degradation and Transformation of Polyphosphates – Implications for Understanding the Biogeochemical Cycling of Polyphosphate

Rixiang Huang*

Georgia Institute of Technology

Synthesized and accumulated by a vast variety of bacteria and planktons, polyphosphates (polyP) constitute a significant portion of phosphorus (P) in dissolved phase, sinking particulates and sediments in

aquatic environment, making it a key player in global P cycling. Despite its environmental significance, little is known about its transport and fate. This work investigated the mineral adsorption, enzymatic hydrolysis and transformation of linear polyP with different chain lengths. The adsorption of these polyP onto iron and aluminum oxide minerals was studied by quartz crystal microbalance with dissipation (QCM-D) and ^{31}P solid state nuclear magnetic resonance spectroscopy (NMR). Results suggested that polyP were irreversibly adsorbed with a “side-on” configuration on the minerals, and the adsorption amount was dependent on chain length and pH. The polyP can be catalytically hydrolyzed by alkaline phosphatase, and most likely through the terminals, as supported by ^{31}P liquid NMR. In the presence of Ca^{2+} , calcium phosphate precipitate formed and was identified to be amorphous, as suggested by X-ray diffraction and scanning electron microscopy with X-ray microanalysis. Effects of mineral sorption and solution chemistry on polyphosphate transformation are being conducted and will be characterized by P K-edge X-ray absorption spectroscopy. Results from this study provide a mechanistic understanding of reactions governing the mobility and transformation of polyP in aquatic environment, therefore, improves our understanding of the P cycle.

71. Dissolved Organic Carbon Analyzer

Max Liao*

University of Georgia

Design, construction, and testing of an instrument for dissolved organic carbon. This device will seek to expand precision on current devices using a combination of wet chemical oxidation and ultraviolet radiation. The goal is to create a system that can produce sub-micromolar precision with higher sensitivity than currently available commercial instruments in order to quantify small differences in DOC caused by microbial respiration, photochemical oxidation, and the mixing of water masses.