Program Booklet

Midwest Geobiology Symposium 2023

~ at ~

University of Minnesota Twin Cities

Tate Hall

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Biological Sciences
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EARTH AND ENVIROMENTAL SCIENCES

COVID-19 safety precautions at Midwest Geobiology Symposium 2023

We strongly suggest wearing masks during the Oral and Poster sessions. Weather permitting, outdoor spaces for lunch and planned breaks will be available for attendees to foster social distancing. Masks will be made available for attendees during the day of the Symposium.

The official University of Minnesota policy regarding COVID-19 safety and precautions is outlined at:

https://safe-campus.umn.edu/personal-wellbeing/covid-19-response.

Thank you for attending this year's Midwest Geobiology Symposium.

As participants, we expect you to treat everyone with respect and maintain a professional demeanor throughout the conference. This includes treating all attendees, speakers, and organizers with dignity and courtesy. Please listen actively and respectfully during presentations and maintain a collegial atmosphere in all conference spaces. Unkind or disruptive behavior may result in removal from the event. Thank you for helping to create a positive experience for all attendees.

Welcome to MWGB 2023!

Greetings and welcome to the University of Minnesota, where we are proudly hosting the 11th annual Midwest Geobiology Symposium!

This meeting highlights all that spans the broad field of Geobiology – including everything from fundamental study to practical application research at the intersection of water-life-rock interactions. We are excited to provide a venue for early career researchers from across the Midwest to present their work in an environment that is constructive, friendly, and supportive. A primary goal of the Midwest Geobiology Symposium is to help build the geobiology community, so this is a great opportunity for emerging leaders (undergraduate students, graduate students, and post-doctoral researchers) to meet, share their research, foster connections, learn about research outside of their focus, and interact with established scholars in the field.

The Midwest Geobiology Symposium was first held at Washington University at St Louis nearly 11 years ago to the day – Sept 22, 2012 – with 50 people in attendance from 14 institutions and 28 abstracts. As a sign of the enthusiasm that this meeting tapped into, today we have over 100 registrants and 56 abstracts representing 22 institutions from Michigan, Ohio, Missouri, Indiana, Illinois, Wisconsin, Iowa, Nebraska, North Dakota, and Minnesota. Within UMN-Twin Cities we have ten different academic units represented, including: Plant and Microbial Biology; Earth and Environmental Sciences; Ecology, Evolution, and Behavior; The Biotechnology Institute; Civil, Environmental, and Geo-Engineering; Biochemistry, Molecular Biology, and Biophysics; Genetics, Cell Biology and Development; Soil, Water, and Climate; the Natural Resources Research Institute; and the Cedar Creek Ecosystem Science Reserve.

We would like to thank everyone who helped support this meeting through generous financial support, including the College of Biological Sciences, the College of Science and Engineering, the Department of Plant and Microbial Biology, the Department of Earth and Environmental Sciences, the Department of Ecology, Evolution, and Behavior, and especially the continued support of the Agouron Institute. We also want to thank all of the volunteers that helped to make this meeting happen. Finally thanks to all of you for bringing your excitement and enthusiasm, and for choosing to spend your weekend with us at this celebration of the future leaders of Geobiology.

Sincerely,

The Midwest Geobiology Symposium 2023 Organizing Committee

Hailey Sauer, Beatriz Baselga Cervera, Nahui Medina Chavez, Weiming Ding, Trinity Hamilton, and Jeff Havig.

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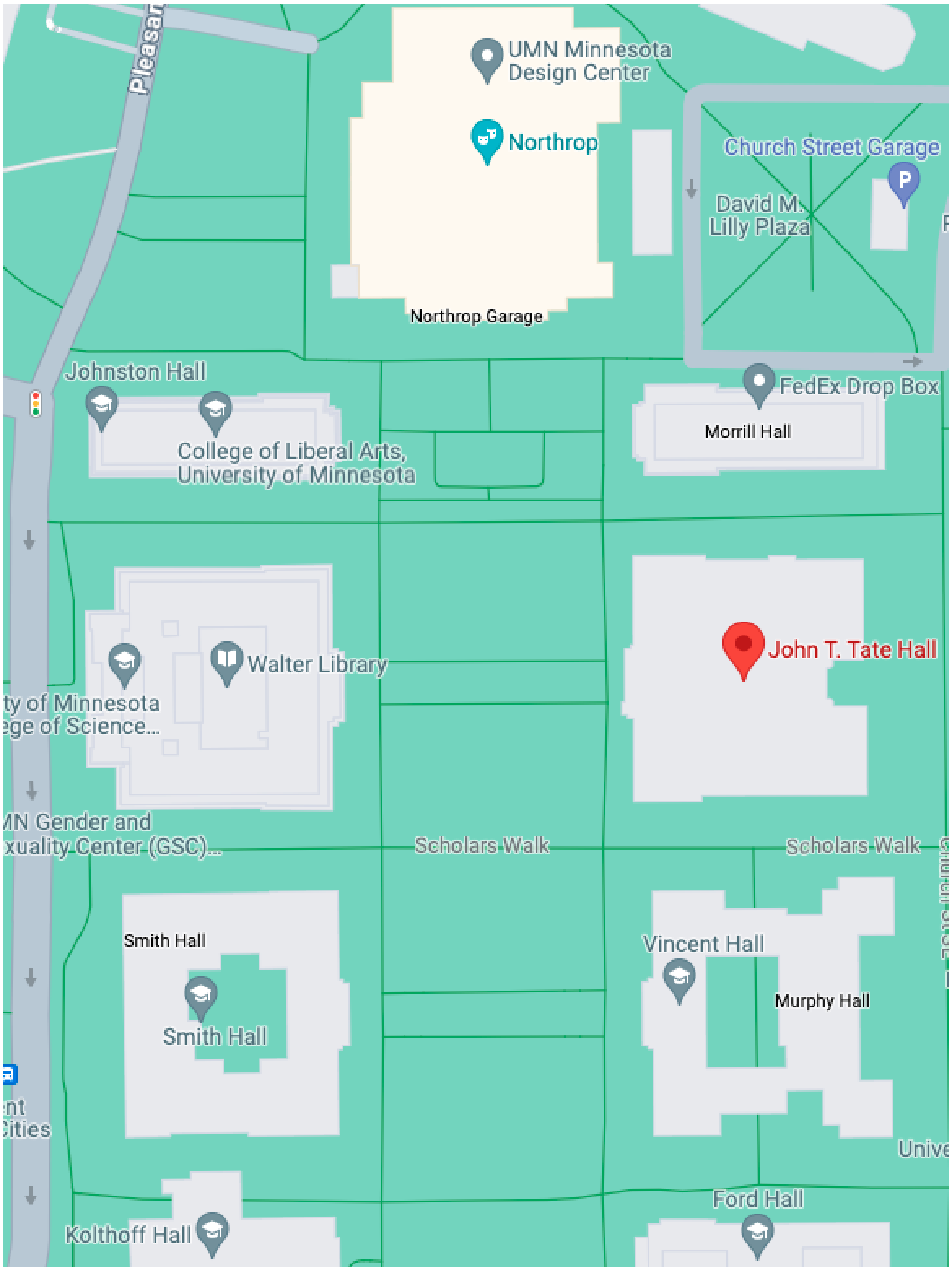
Orientation information



Schedule

FRIDAY (9/22)

5:30 – 8:30	**Inauguration**

SATURDAY (9/23)

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8:35 – 10:00	**Breakfast/ Posters-Session 1**
10:00 – 10:10	**Coffee Break**
10:10 – 11:30	**Talks-Session 1**
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Midwest Geobiology Symposium 2023
Oral Presentations Schedule

Session #1-Topic: Deep Time

10:10 Ashika Capirala (Purdue University):
Geophysical Controls on Ocean Dynamics Shape Spatiotemporal Patterns of Marine Oxygenation

10:25 Marcelo Prianti (Central Michigan University):
Can we trust the current methods to assess the chrome authigenic fractionation? Implications for the chrome isotopes.

10:40 Viktor J. Radermacher (University of Minnesota, Twin Cities):
The Macroevolution of the Ornithischian Dentary Battery - preliminary results

10:55 Émilie Laflèche (Purdue University)
Impacts of Oxygen Seasonality on the Neoproterozoic Biosphere

11:10 Maggie Hinkston (Washington University in Saint Louis)
Estimating the maximum size of planetary biospheres from energy fluxes

Session #2 – Topic: Modern Systems/Ancient Analogs

11:45 Amanda Patsis (University of Minnesota, Twin Cities):
Organic sulfur fuels the terrestrial deep biosphere: evidence from a novel candidate bacterial order inhabiting an oxic-anoxic transition zone

12:00 Christopher Schuler (University of Minnesota, Twin Cities):
Fracture-scale alteration processes impact habitability of the continental deep biospherehic methanogenesis

Midwest Geobiology Symposium
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Oral Presentations Schedule

Session #2- Continuation

12:15 Michelle Chamberlain (Iowa State University): Quantifying primary productivity and intracellular iron among phytoplankton in Brownie Lake

12:30 Joe Rabaey (University of Minnesota Duluth, Large Lakes Observatory): Mixing regime drives seasonal greenhouse gas fluxes in ponds

12:45 Nicole Fiore (University of Nebraska, Lincoln)
Preference of calcium carbonate minerals for hydrogenotrophic methanogenesis

Session #3 – Topic: Impacts and Mediation

3:10 Jack Hutchings (Washington University in St. Louis):
Towards Removal of Spectral Inference from Volatile Organics on a Picarro L2140-i Cavity Ringdown Spectrometer

3:25 Fernando Medina Ferrer (University of California, Berkeley):
An unknown archaeal sensing pathway that blocks biogenic methane production

3:40 Debasis Golui (North Dakota State University):
Arsenic in soil-plant-human continuum: exposure and risk assessment

3:55 Saurabh Singh (North Dakota State University):
Predicting pollutant removal in constructed wetlands by employing machine learning

4:10 Anand Gupta (North Dakota State University):
Phosphate Removal from Aqueous medium with Agricultural Waste based Nanocellulose

4:25 Taylor Rosso (University of Nebraska, Lincoln):
Iron Reduction in Unsaturated Soils Following Perturbations of Nitrate

ABSTRACTS

ORAL PRESENTATIONS

Geophysical Controls on Ocean Dynamics Shape Spatiotemporal Patterns of Marine Oxygenation

Ashika Capirala, Stephanie Olson, Camilla Liu

Department of Earth, Atmospheric, and Planetary Sciences, Purdue University

Planetary oxygenation is crucial to the evolution and survival of aerobic life on Earth. However, our knowledge of Earth's oxygenation is incomplete: in particular, our understanding of the landscape of marine oxygen before the oceans achieved complete ventilation roughly 400 Myr ago. Alongside metabolic and biogeochemical evolution, Earth experienced a slowing rotation rate and a diversity of continental distributions through time. These geophysical controls significantly affected ocean circulation and mixing, potentially altering nutrient supply to the biosphere and the transport of oxygen to the deep ocean. Present oxygenation timelines lack consideration of marine O2 in this evolving oceanographic context. We use a sophisticated 3D Earth system model (cGEnIE) to explore the impact of changing continental distribution and rotation rate on marine oxygenation. We find that continents drastically change the spatial patterns of upwelling and deepwater formation, and in turn control surface primary productivity and dissolved O2 in the deep ocean. However, our results also show productivity and ventilation are strongly influenced by rotation rate. Faster rotation rates simulating early Earth produce weakened overturning circulation, limiting nutrient recycling, marine O2 production, and ventilation even at present-day levels of atmospheric oxygen. We will discuss how this oceanographic evolution may have affected surface oxygen and the development of aerobic life through time.

Can we trust the current methods to assess the chromium authigenic fraction? Implication for the chromium isotopes

Marcelo T. A. Prianti, Mahsa Tashakor, Anthony Chappaz

Department of Earth And Atmospheric Sciences, Central Michigan University

Examining redox-sensitive trace elements in sedimentary records is crucial for paleo-reconstructions, specifically for studies aiming to investigate the Earth's oxygenation. Chromium (Cr) isotopes have emerged as a powerful paleo-redox proxy for tracking the presence of oxygen in the ancient atmosphere, mainly because the oxidation of Cr(III) to Cr (VI) induced significant isotopic fractionation that can be measured and preserved in sedimentary settings. For paleo-redox reconstruction purposes, only the authigenic fraction of Cr holds significance. Currently, methods used to assess the Cr authigenic fractions rely mostly on Cr/Ti ratio or leaching techniques. However, these two approaches may induce some bias resulting in significant miscalculations of the d53Crauthigenic. Our objective was to determine the Cr speciation to properly assess the authigenic fraction by using a combination of synchrotron based absorption techniques. Samples from three different formations were selected for this study: Demerara Rise, Peru Margin and Cariaco Basin. As expected, two Cr species were identified in all samples: Chromite (detrital) and (Fe,Cr)(OH)3(s) (authigenic). Surprisingly, our quantification of the authigenic fractions differs significantly with the published ones. Our new results question the current methods applied for determining the authigenic fraction and highlight the importance of determining the Cr speciation for paleo redox reconstructions.

The Macroevolution of the Ornithischian Dentary Battery - preliminary results

Viktor J. Radermacher, Peter J. Makovicky

Department of Earth & Environmental Sciences, University of Minnesota

The ability to process and digest plant matter has independently evolved countless times among vertebrates. The constraints herbivory places on organisms often necessitates a stereotypical cascade of analogous bauplan modifications between even distantly related groups. While their origins were humble, ornithischian dinosaurs would eventually become the most conspicuous, speciose, and diverse large-bodied herbivores by the Late Cretaceous. Elaborating on the plesiomorphic condition, two ornithischian lineages, Ornithopoda and Ceratopsia, both independently evolved dental batteries. Dental batteries are generally characterised as mosaics of multiple tooth families uniformly worn to produce a single grinding surface. We have devised a novel method for quantifying a suite of orodental proxies sampled from species spanning derived and early diverging members of ornithopods and ceratopsians. Using a combination of μCT and laser surface scan data, we quantify the volume of worn dental material as well as the surface areas of the resultant triturating surface in the dentary and maxillary toothrows. These metrics can then be scaled against relevant measures of skull and body size as well as biodiversity, to investigate the macroevolutionary implications of dental battery evolution. We present preliminary results of this method that elucidate the trade-offs involved in individual tooth size, dental battery surface area, and masticatory efficiency.

Impacts of Oxygen Seasonality on the Neoproterozoic Biosphere

Émilie Laflèche, Jonathan Jernigan, Stephanie Olson

Purdue University

Earth's seasons affect a number of fundamental processes in the biosphere, including oxygenic photosynthesis and aerobic respiration. The relative rates of these reactions fluctuate over the seasonal cycle in response to changes in insolation and surface temperature. However, the implications of seasons for the co-evolution of life and its environment on early Earth remain unclear. For instance, seasonality in O2 would be more dramatic during the Proterozoic than on present-day Earth due to lower pO2 conditions, leading to rapidly changing environmental conditions and potentially biological stress. Importantly, the extent to which this stress could have also affected the rise of animals towards the end of the Proterozoic is unknown. We use cGENIE, a 3D marine biogeochemical model, to quantify environmental seasonality under a range of estimates for Neoproterozoic (~540 Ma) pO2 conditions (~0.001% PAL to ~0.1% PAL) and continental configurations. We then describe the corresponding seasonal patterns in primary productivity, surface ocean oxygenation, and nutrient availability in the marine biosphere. Finally, we discuss the potential consequences of oxygen seasonality for the earliest marine animals.

Estimating the maximum size of planetary biospheres from energy fluxes

Maggie Hinkston, Alexander S. Bradley

Earth and Planetary Sciences, Washington University in Saint Louis

Life, as defined by Schrödinger [1] encompasses (i) the conservation and replication of heritable information and (ii) metabolism, which require energy derived from environmental sources. On Earth, the biosphere is dependent on solar energy, with minor contributions from other sources. However, the relative significance of various sources of energy will differ among planetary bodies. To assess habitability of planets beyond the Earth the possibility of diverse methods for the capture of environmental energy must be considered, invoking the need for an inventory of all potential energy supplies. On some planetary bodies, energy availability may constrain the maximum size of the biosphere. We calculated energy fluxes for 28 planetary bodies in the solar system. We considered the energy fluxes from (i) solar radiation, (ii) radioactive decay, (iii) accretion, (iv) differentiation, (v) tidal forces. The probable minimum energy requirements of biology are based on the requirements for information storage as derived from information theory [2], and the mass-normalized energy utilization rates for various forms of life on Earth [3]. These comparisons provide a starting point for understanding the likely maximum size of the biosphere on a range of planetary bodies in the solar system and may also be useful in assessing habitability of extrasolar planets.

Organic sulfur fuels the terrestrial deep biosphere: evidence from a novel candidate bacterial order inhabiting an oxic-anoxic transition zone

Amanda Patsis, Cara Santelli, Cody Sheik

Earth and Environmental Sciences, University of Minnesota

While inorganic sulfur reduction and oxidation are well documented in deep subsurface microbial communities, the utilization of organic forms of sulfur remains poorly explored. Organosulfur, however, is abundant in biomass, occupies a range of oxidation states, and can serve as an important source of inorganic sulfur in oligotrophic settings. Thus, organosulfur compounds are predicted to play a central role in deep biosphere sulfur cycling. To investigate this hypothesis, we mined shotgun metagenomic datasets from Soudan Underground Mine, MN, a 2.7 Ga hematite iron formation hosting isolated hypersaline groundwater. We identified two novel metagenome assembled genomes inhabiting the drainage channels that collect outflowing brines. These reconstructed genomes are 83.6% and 97.8% complete, and represent a candidate novel bacterial order in the class Gammaproteobacteria. Protein annotations confirm these organisms have the genetic potential for organosulfur cycling, with the gene encoding sulfoacetaldehyde acetyltransferase (xsc) promoting sulfoacetaldehyde mineralization to sulfite. Additionally, these organisms have the capacity for dissimilatory sulfite oxidation. The coupling of these two pathways would allow organosulfur mineralization to supply electron donors for dissimilatory sulfur metabolisms. Thus, the metabolic capacity of this lineage supports the potential for cryptic organosulfur cycling as a key source fueling oligotrophic deep subsurface microbial communities.

Fracture-scale alteration processes impact habitability of the continental deep biosphere

Christopher J. Schuler, Sarah L. Nicholas, Cara M. Santelli, Brandy M. Toner

Department of Earth & Environmental Sciences, University of Minnesota Twin Cities

Fracture-scale mineralogy plays an essential role in the continental deep biosphere. Most microorganisms in deep crustal environments reside within communities attached to rock surfaces, and rock-water interactions source the nutrients and substrates necessary to fuel subsurface life. To better understand weathering and alteration processes impacting fracture mineralogy, we characterized thin sections prepared from cores from the Soudan formation, a 2.7 Ga banded iron formation in the southern Canadian Shield. Thin sections were characterized via petrographic microscopy, electron probe microanalysis, and X-ray fluorescence microprobe. These analyses revealed that the Soudan formation contains minerals relevant to subsurface life, such as S-bearing pyrite, P-bearing fluorapatite, and Fe(III)-bearing hematite. However, fractures are preferentially lined with phyllosilicate chlorite minerals. These chlorites have less immediate relevance to microbial life, but their dissolution controls microbial access to more essential mineral phases. A poorly crystalline Ca-bearing phase was also found on many fractures and was characterized via Ca XANES spectroscopy. These spectra suggest that the Ca-rich phase is likely a mixture of the carbonate minerals calcite, dolomite, and ankerite. The presence of these carbonates can reveal important details about fracture-scale processes impacting pH and alkalinity, shedding more light on microbial and geochemical dynamics in the subsurface.

Quantifying primary productivity and intracellular iron among phytoplankton in brownie lake

Michelle Chamberlain, Kaleigh Block, Elizabeth Swanner

Department of Geological and Atmospheric Sciences, Iowa State University

Subsurface chlorophyll maxima layers (SCML) are regions of maximum abundance of the photosynthetic pigment chlorophyll a in phytoplankton. SCML often occur in meromictic lakes because the subsurface environments remain stable due to a lack of mixing, resulting in nutrient-rich ecological hotspots. Although iron (Fe) is often a limiting nutrient among marine phytoplankton, the role of Fe in SCML formation and primary productivity in these lakes remains unclear. Brownie Lake (BL) in Minneapolis, Minnesota is both meromictic and ferruginous, or iron-rich, with a consistently observed SCML, representing an ideal study site for these investigations. We have developed methods to estimate gross primary productivity (GPP) in Brownie Lake using rapid light curves and photosynthetic irradiance (PE) models. Rapid light curves measured with the PHYTO-PAM II (Walz) instrument were used to determine taxon-specific electron transport rates across an in-lake gradient of Fe and light. These were then fit to PE models to generate both depth-specific and whole lake estimates of GPP within the lake. Additionally, we have developed methods to concentrate cells from Brownie Lake water and separate them from particulates for single-cell elemental analysis using sp-ICP-ToFMS . This will allow comparisons of intracellular Fe concentrations among SCML and epilimnion phytoplankton. These methods can be used in long-term monitoring of GPP and Fe uptake BL and other ferruginous, meromictic lakes.

Mixing regime drives seasonal greenhouse gas fluxes in ponds

Joseph S. Rabaey, James B. Cotner

University of Minnesota Duluth, Large Lakes Observatory

Inland waters are important sources of the greenhouse gases carbon dioxide (CO2) and methane (CH4). Ponds have amongst the highest CO2 and CH4 fluxes of all aquatic ecosystems, yet measured fluxes from ponds are highly variable, creating challenges for accurately estimating emissions. Little is known about the seasonality of greenhouse gas fluxes from ponds, which may contribute to the large observed variation in annual flux estimates. Ponds can exhibit a range of mixing regimes which may influence seasonal fluxes of CO2 and CH4, yet the effect of mixing regimes on greenhouse gas dynamics in ponds is unknown. Here, we assessed yearly dynamics of CO2 and CH4 in four temperate ponds (Minnesota, USA) that varied in mixing regimes. The ponds ranged from annual sinks to sources of CO2 and were all significant sources of CH4, with annual fluxes of 0.7 – 1.5 kg C m-2 yr-1 in CO2 equivalents. Mixing regimes greatly impacted seasonal patterns of fluxes, and in ponds with longer stratified periods there was more anoxia, greater accumulation of gases in the bottom waters, and higher diffusive fluxes of CO2 and CH4 that contributed most of the annual fluxes relative to ebullition (81-91%). The more frequently mixed ponds had less anoxia, little to no gas accumulation, and ebullitive CH4 fluxes were the dominant flux pathway (76-81%). Overall, the two ponds with stronger stratification had higher annual fluxes compared to the two ponds that more frequently mixed.

Preference of calcium carbonate minerals for hydrogenotrophic methanogenesis

Nicole A. Fiore, Karrie A. Weber

University of Nebraska-Lincoln

Most of the carbon on Earth is sequestered in the form of sedimentary carbonates. Under alkaline conditions, carbonate minerals are often considered metastable and inaccessible for microbial metabolism. Here, we compare several natural and synthetic carbonate minerals as sole inorganic carbon sources for hydrogenotrophic methanogenesis under alkaline conditions. An anerobic enrichment culture (containing a Methanobacterium sp.) maintained on H2 and synthetic calcium carbonate served as an experimental inoculum. The enrichment was cultivated in minimal, alkaline medium with H2 and either calcite, aragonite, dolomite, siderite, or synthetic calcium carbonate as sources of inorganic carbon. After a three-week incubation, headspace methane increased considerably in cultures amended with calcium carbonates (3407, 2800, and 3412 umol L-1 for calcite, aragonite, and synthetic calcium carbonate respectively). Methane concentrations did not differ significantly among the calcium carbonates ($p = 0.2198$). Low levels of methane were measured in dolomite and siderite containing cultures (370 and 143 umol L-1), with no methane detected in heat-killed controls. These results demonstrate that calcium carbonate polymorphs are a preferential source of inorganic carbon for hydrogenotrophic methanogenesis. As such, of the minerals tested, calcium carbonates have the greatest potential to sustain past or present methanogens on Earth or on other carbonate-bearing planets or moons.

Towards Removal of Spectral Inference from Volatile Organics on a Picarro L2140-i Cavity Ringdown Spectrometer

Jack A. Hutchings, Tyler E. Huth, Bronwen L. Konecky

Earth, Environmental, and Planetary Sciences, Washington University in St. Louis

Water isotope measurements are routinely made using isotope ratio infrared spectroscopy (IRIS). IRIS measurements are desirable as minimal sample preparation is generally necessary for traditional water isotope measurements (i.e., δD and δ18O). However, natural water samples can contain dissolved volatile organic compounds that interfere with the spectral peaks associated with water isotopologues and are particularly problematic for accurate analyses of water triple oxygen isotope composition. Post-correction is generally not a viable option, so the contaminant must be eliminated before analysis or the sample must be analyzed by other means (e.g., mass spectrometry). Critically, the spectral interference can be small enough to be undetected by the analyst but still able to compromise the data. In these cases, only removal of the contaminant would yield a valid IRIS measurement. This challenge is at least partly understood by the scientific community and, in the case of Picarro instruments, an on-line catalytic combustion peripheral is sold by the manufacturer to eliminate contaminants causing spectral interference. Here, we explore alternatives to the rhodium catalyst used in Picarro's peripheral, as on-going supply issues have made replacement prohibitively expensive. We present a variety of alternative on-line removal techniques and find that, currently, all alternatives have undesirable shortcomings and should be generally avoided until a suitable replacement is developed.

An unknown archaeal sensing pathway that blocks biogenic methane production

Fernando Medina Ferrer, Dipti D. Nayak

Molecular and Cell Biology, University of California, Berkeley

A large fraction of the potent greenhouse gas methane is generated by methanogenic archaea that are prevalent in modern anoxic environments. These microorganisms produce methane via methanogenesis, an ancient metabolism that originated ~3.5 Ga ago, and that associate methanogenic archaea (methanogens) with several cornerstone events in Earth's history. Molecular controls of methanogenesis at the level of gene regulation are key to identify the links between the physiology of methanogens and their environmental impact in both modern and ancient environments. However, the mechanisms by which methanogens regulate methanogenesis in response to environmental cues remain unknown. Here, we use laboratory evolution in the model methanogen Methanosarcina acetivorans to uncover an uncharacterized gene (MA2561) that encode for a putative regulator of methylotrophic methanogenesis. We used CRISPR-Cas9 genome editing to mutagenize MA2561, and conducted downstream transcriptomic and protein analyses to show that this regulator represses the expression of essential genes involved in methylotrophic growth. Furthermore, we have found functionally active homologs of this protein in diverse methanogens, suggesting a regulatory role that is widespread in the environment. Understanding how methanogens sense and respond to their environment via these regulators has cascading ramifications on the role of biological methanogenesis on Earth's geological record.

Arsenic in soil-plant-human continuum: exposure and risk assessment

Debasis Golui, Md. Basit Raza, Arkaprava Roy, Jajati Mandal, Achintya Bezbaruah

Department of Civil, Construction and Environmental Engineering, North Dakota State University, Fargo, USA

This article presents the regional-level health risks due to the consumption of arsenic contaminated rice in the three regions of Asia. Such macro-level study has not been reported so far, while there are micro-level reports for smaller geographic areas. The study also suggests a possible safe limit of bioavailable arsenic in soil for a smaller geographic area based on the solubility-free ion activity model. A discussion on risk assessment analyses for better appraisal of arsenic risks in soil-plant-human system is also included. It was found that adults in Asian countries are prone to a high risk of cancer due to the consumption of arsenic contaminated rice. South Asia (SA), South East Asia (SEA), and East Asia (EA) regions exceeded the USEPA-prescribed safe limit for cancer risk with ~100 times higher probability of cancer due to rice consumption. The hazard quotient for the ingestion of arsenic containing rice was found to be 4.526±5.118 for SA, 2.599±0.801 for SEA, and 2.954±2.088 for EA, which is much above the safe limit of HQ of 1. This study presents rice consumption related carcinogenic and non-carcinogenic risks to adults. A model was tested to calculate the safe limit of bioavailable arsenic in paddy soils. The methods and findings of this study are expected to be useful for regional level policy making and resource mobilization to alleviate the public health issues related to arsenic and the work can be expanded to arsenic present in drinking water.

Predicting pollutant removal in constructed wetlands by employing machine learning

Achintya N. Bezbaruah, Akhilendra Bhushan Gupta, Urmila Brighu

North Dakota State University, Fargo

This study is aimed to aid in the horizontal flow constructed wetland (HFCW) design by analyzing their treatment dynamics using secondary datasets (n = 1232). Prediction of effluent BOD, Chemical oxygen demand (COD), Ammonium-Nitrogen (NH4+-N), Total Nitrogen (TN), and Total phosphorous (TP) was carried out via machine learning algorithms - multiple linear regression and support vector regression (SVR). Out of the two models, SVR resulted in a better prediction of all the effluent parameters in mg/l as well as in g/m3-d. The prediction of NH4+-N and TN (g/m3-d) could be performed with the highest accuracy (R2 and root mean square error 0.847 and 0.44 %; and 0.947 and 0.18 % respectively). The classification of the dataset according to organic loading rate (OLR) enhanced the performance of SVR for BOD (high OLR), COD (low OLR), and TP (low OLR). The performance of all the trials was acceptable in the training and validation stages in 3-fold cross-validation which was helpful in reducing the mean square error value by 68.19 % and increasing the R2 value by up to 16.13 %. Areal removal rate (K, m/d) values computed by the reverse P-k-C* approach using the predicted effluent concentrations were found to be highly correlated with actual K values for BOD, COD, and TN (R2 0.954, 0.948, and 0.819, respectively). These K values can be used for the customized design of HFCWs for organics and nitrogen removal and might also help to achieve the targeted discharge standards in HFCWs.

Phosphate Removal from Aqueous medium with Agricultural Waste based Nanocellulose

Anand Gupta, Achintya Bezbaruah

Civil Construction and Environmental Engineering Department, North Dakota State University, Fargo, North Dakota

High concentration of phosphate in lakes, ponds, reservoirs and estuaries leads to eutrophication. Nanocellulose (NC) produced from agricultural wastes is a novel nanomaterial for aqueous pollutant removal. In our present study, NC was produced from barley straw (an agricultural waste) and activatd to get activated nanocellulose (ANC) and then functionalized with iron (FANC). The production efficiency for NC from raw barley straw was ~22% and that of ANC was ~4.3%. The size of the produced NC was in the range of 3–62 nm. The FTIR results indicated the presence of -OH functional groups in NC while -CH and -C-C groups dominated in the ANC. Batch studies were performed to examine the removal of phosphate from aqueous solution by the cellulose fibers. The results showed no removal of phosphate with raw barley straw and NC. While ANC (15 g/L) removed 19.33% phosphate while FANC (2 g/L) achieved 100% removal.

Iron Reduction in Unsaturated Soils Following Perturbations of Nitrate

Taylor Rosso, Karrie A. Weber

University of Nebraska-Lincoln

Oxygen minimum zones (OMZs) are layers in the water column that have low oxygen due to a combination of biological, chemical, and physical processes. Redox reactions involving iodine species can be used to track these processes in modern OMZs as well as ancient oceans where OMZs were more expansive than today. However, the mechanisms and oxygen thresholds driving iodine cycling are not well understood, thus limiting quantitative applications. To this end, we performed experiments in Shewanella oneidensis cultures to quantify the rate dependency of iodate reduction on O2 and the O2 threshold at which iodate reduction becomes favorable. Shewanella are metal-reducing bacteria commonly found in warm and temperate regions worldwide and are part of the marine environment microflora. Shewanella are also known reducers of iodate in anaerobic conditions, however, the exact oxygen saturation at which Shewanella begin to reduce iodate to iodide is unknown. In our experiments, cultures were maintained at 30 deg C using 20mmol/kg lactate, 40mmol/kg fumarate, and 250 μmol/kg iodate. We used an environmental hypoxia chamber which controls ambient levels of both CO2 and O2 using a 0-3000 ppmv CO2 and 0-1000 ppmv and 0.1-25% O2 analyzer. Preliminary results at ambient atmospheric CO2 levels and O2 at ranges <10% reveal O2 dependencies for iodate reduction at levels relevant to that known for both modern OMZs and inferred within seawater more broadly across key intervals of Earth history.

ABSTRACTS

POSTER PRESENTATIONS

Deciperhing primary mineralogy of the Mid-Proterozoic Freedom Formation, WI, USA

Farhan Ahmed Bhuiyan, Latisha Brengman, Esther Stewart

Earth and Environmental Sciences, University of Minnesota Duluth

Historic drill cores of the <1.71 - 1.47 Ga Freedom Formation near Baraboo, Wisconsin, USA offer new opportunities to reconstruct geochemical attributes of evolving Mid-Proterozoic surface environments. Here, we present new mineralogical and geochemical datasets of the Freedom Formation. The Freedom Formation is an iron-rich chemical sedimentary unit that conformably overlies the classic Baraboo quartzite and Seeley slate. Mineralogy changes up stratigraphy from a magnetite, quartz, siderite, chlorite-dominant assemblage with limited stilpnomelane, and chamosite, to an ankerite, Mn-rich carbonate, hematite-dominant assemblage that grades into dolomite. Accompanying this mineralogical change, we document decreasing clastic contamination up section (decreasing Al2O3 concentrations, lower Zr/Hf), minor influence of high temperature fluids at the base of the section (positive shale normalized Eu/Eu*SN anomalies), and anoxic signatures (positive shale-normalized cerium (Ce/Ce*SN) anomalies) that prevail throughout the lower units. The transition from reduced Fe2+ minerals to oxidized Fe3+ minerals mixed with Mn-carbonate and accompanying anoxic geochemical signatures may indicate transient changes in oxygen conditions during the formation of the mineral phases preserved in the Freedom Formation. Data presented here represent a preliminary characterization as a part of an ongoing effort to decipher primary redox signatures from diagenetic indicators of the Freedom Formation.

Preservation of protein molecular fossils in resin

Christopher Greidanus, Jacob Waldbauer

University of Chicago

Molecular fossils are one of the key tools for reconstructing ancient biodiversity and environmental processes. Two of the most well-studied classes of molecular fossils, lipid biomarkers and ancient DNA, have provided invaluable insights, yet both have significant limitations. For lipids, taxonomic resolution can be limited, leaving ambiguities about the connections between the environment and organisms. DNA has limited survival in geologic archives and is difficult to sequence when damaged. Proteins can preserve genetic information over geologic time, but the use of protein molecular fossils as environmental proxies has been less explored. There is an outstanding need in the field for methods to discriminate truly ancient proteins from subsequent or modern contamination. This discrimination relies on a clearer molecular-level understanding of protein diagenesis. The preservation of proteins might be maximized in certain especially durable geologic archives, such as amber (fossil tree resin), where they are isolated from microbial degradation. Previous work has successfully isolated amino acids from amber, suggesting that higher-molecular weight proteins may also survive. This project analyzes natural sub-fossil resin samples from Madagascar containing plant and insect material. Preliminary results indicate that proteins can be extracted and sequenced from fossil resins, suggesting that amber may preserve valuable molecular fossil records of past environments.

Fate and transport of metals within Twin Cities stormwater catchment ponds using inductively coupled mass spectrometry

Christof Zweifel, Ben Janke, Jacques Finlay, Emilie Snell-Rood, and Cara Santelli

Earth and Environmental Science, University of Minnesota Twin Cities

Industrial emissions, legacies of leaded gasoline, and the breakdown of lead paint have created a high risk for lead contamination in urban environments. In the Twin Cities of Minneapolis and St. Paul there are multiple sources of lead emissions from the downtown garbage burner, small-craft airports, smelters, lead paint, and decades long accumulation from leaded gasoline. Sediments, runoff, and the direct input from industrial sources means stormwater catchment areas have the potential to capture lead and other metals. The concentration of dissolved lead in 10 stormwater ponds throughout the Twin Cities was quantified by inductively coupled plasma - mass spectrometry (ICP-MS). The concentration of dissolved lead ranged from 0 to 4.9 ppb. Environmental regulations focus on total lead, with drinking water capped at 15 ppb. Generally, samples from the hypolimnion had higher dissolved lead. Concentration varied across three sampling dates taken once per month in summer 2023. This may indicate that rain and other hydrologic events cause lead to flow into the pond from continuing emission sources. This work will continue with total lead concentrations using acid digestion and collecting sediment cores. Sediment cores are used to analyze porewater, total metals in the sediment, and metal speciation. Metal concentrations and speciation will offer insight into the types of sources, processes that affect lead fate and transport, and potential remobilization of metals in urban ponds.

Late Quaternary environmental changes in the Eastern Cordillera of the Colombian Andes: Preliminary assessment of sedimentary n-alkyl lipids from Lake Tota

Alessandro A. Mauceri, Bronwen L. Konecky, Jack A. Hutchings, Broxten Bird, Byron Steinman, Jaime Escobar, Alejandra Rodriguez-Abaunza, Alejandro Fernández, Mark Shapley

Department of Earth, Environmental, and Planetary Sciences, Washington University in St. Louis

Lake Tota (5.54ºN, 72.92ºW) is the largest lake in Colombia (60 m deep), located in the Department of Boyacá. A previous seismic survey of Tota identified an exceptionally thick (300 m) late Quaternary sedimentary record potentially extending back over ~1 Ma. In addition, Tota is situated in the migration path of the intertropical convergence zone (ITCZ), where mean annual precipitation (MAP) varies in response to shifts in its mean meridional position. As such, Tota is well-positioned to investigate Holocene changes in tropical Andean hydroclimate in response to ITCZ dynamics—holding tremendous potential as an archive of paleoenvironmental variability. Here, we present preliminary isotopic and structural data of n-alkyl lipids from a composite sediment sequence composed of two Kullenberg and surface cores from Tota. Though 14C and tephra age-depth control is pending, lithostratigraphic data suggest that the upper ~4.5 m of sediment likely spans the Holocene. Sediments contain sufficient concentrations of n-alkyl lipids from aquatic (C21–25) and higher (C29–35) plants to construct a dual C/H compound-specific isotope record. The C25, C27, and C29 alkanes are dominant in most samples. The δ13C and δD of long-chain n-alkanes may be used to reconstruct vegetation gradients responding to changes in MAP, controlled by ITCZ dynamics—allowing for an interhemispheric assessment of hydroclimate response to insolation forcing via comparison with Andean ice and speleothem δ18O records.

A new SIMS method to measure d34S and d18O in barite samples from modern methane seeps

J. Houghton, R. S. Wood, C. Jones, D. Fike

Earth and Planetary Sciences, Washington University in St. Louis

Stable isotope analyses of geologically stable minerals that record microbial activity is a commonly used proxy to try to interpret the history of Earth's environmental evolution. The d18O and d34S values of sulfate in marine porewaters are strongly influenced by microbially mediated sulfur redox chemistry, with sulfate-reduction pathways affecting d34S and reoxidation pathways primarily affecting d18O. The expectation based on pure culture studies is sulfate d34S and d18O values will be positively correlated with a slope that is low (<0.5) when the carbon is abundant and high as re-oxidation processes increase (Antler and Pellerin, 2018). In this study, we evaluate barite crust samples from several methane seep locations spanning a range in methane availability to test this hypothesis. We have developed a high-resolution SIMS method to evaluate co-located d34S and d18O in barite using <20 um spots. Our observations from all seep sites combined support the findings in the literature that methane seep sites have low slopes (~0.3). However, between sites the slope varies widely, and no single site records the full range of d34S and d18O seen in the combined dataset. Samples from sites with low methane concentrations but different advection rates do not exhibit linear trends and instead cluster along the overall 0.3 slope. In addition, samples from seeps with the lowest methane concentrations have vertical to slightly negative slopes, contrary to the predictions.

Snow algae responses to differing N:P ratios

Victoria Rebbeck, Pablo Almela, Trinity Hamilton

Plant and Microbial Biology, University of Minnesota Twin Cities

Snow algae are a specialized algae that live in cold conditions (around 0°C) predominantly on supraglacial and mountain snow. Snow algae contribute to biogeochemical cycling though altering the albedo or reflectiveness of a surface. When snow algae grow on the surface of snow, they reduce albedo and thus increase melt. Snow algae produce both chlorophyll and carotenoids including astaxanthin which make cells appear a red color (Hoham & Remias, 2020). Agricultural activity and urbanization deliver nitrogen and phosphorus to snow and these key nutrients support snow algae growth. While initial studies have shown blooms of algae occur with an N:P ratio from 11-20 on snow (Spijkerman et al., 2012), it is largely unknown how nitrogen and phosphorus inputs impact snow algae growth and thus their impact on albedo and melt. This experiment characterized the response of snow algae to a variety of N:P ratios. Snow algae species were grown in media in a variety of N:P ratios ranging from .025 to 40 in an effort to capture a wide range of possible N:P ratio conditions. The algae were grown at 5°C and 9°C in triplicate for 30 days. Cell concentrations were determined after 4, 8, 12, 16, 20 and 30 days after initial inoculation using a hemocytometer. And we observed that cell counts across the board were higher at 9°C than 5°C. We also observed that while increased N:P ratios tended to increase cell counts, differing snow algae species responded in various ways to N:P fertilization.

Investigating Deep Subsurface Microbial Communities in Gas-rich Rock-Hosted Aquifers: Relationship between microbial biomass and depth

Nicole Smith, Matthew Schrenk

Department of Microbiology & Molecular Genetics, Michigan State University

The deep subsurface biosphere is sometimes referred to as the "Dark Energy Biosphere", due to dependence of microbial communities on chemical energy to fuel their growth rather than light. High pressures and temperatures combined with low permeability and nutrient availability challenge subsurface microbes with extreme conditions deep within the Earth's crust, leading to questions concerning how deeply these organisms permeate into subsurface environments (Sahu 2021). In this study, drill cuttings from a hydrogen exploration well drilled to 11,000 feet in Nebraska were utilized to uncover the relationship between depth, geochemistry, and the abundance and biodiversity of microbial communities. Total genomic DNA was extracted and purified from 10g samples; the DNA extracts were quantified fluorometrically before being tested by PCR amplification using bacterial specific primers for Illumina Sequencing. Through the quantified DNA (ng of DNA per gram of sample), it was shown that as depth increases, there is a decrease in the abundance of biomass and microorganisms. These data are being used to identify correlations between the geochemical composition of the subsurface and microbial diversity and cell density. These data will also help to understand nutrient and gas utilization by subsurface microbes within the deepest levels of the biosphere.

Effects of seasonality on planetary habitability for complex life

Jonathan Jernigan, Emilie A. Lafleche, Stephanie L. Olson

Purdue University

Planetary obliquity and orbital eccentricity together modulate climate through their influence on the quantity and spatiotemporal distribution of incoming stellar radiation. The implications for planetary habitability in terms of the stability of liquid water have been thoroughly investigated. However, the effects of the extreme seasonality generated by high obliquity and/or eccentricity on the survival of complex organisms are not well understood. To address this gap, we use cGENIE-PlaSim, a 3D biogeochemical model coupled to an atmospheric general circulation model, to simulate the climates of Earth-like planets for various obliquity and eccentricity combinations. We then quantify the habitability of land and marine environments, both seasonally and annually. Finally, we discuss the implications of our results for the search for life on other worlds.

Influence of subsurface snow algae blooms on albedo reduction

Pablo Almela, Chris Hansen, Joe Giersch, Jim Elser, Scott Hotaling, Trinity Hamilton

Plant and Microbial Biology Department, University of Minnesota

Snow algae are characterized by their ability to produce pigments, such as chlorophyll and carotenoids, which give them their distinctive red, orange, or green coloration. These microorganisms thrive in cold environments and contribute to snow melt by darkening the surface, reducing its albedo (reflectivity), and absorbing more sunlight, accelerating the melting process. Nevertheless, the potential consequences of the presence of such communities on albedo reduction when located beneath the surface—such as after snowfall, avalanches, or sub-surface blooms—remain elusive. In this study, we unveil the outcomes of an experiment examining the impact of a sub-surface snow algae bloom on energy absorption. The results indicate energy absorption across all analyzed wavelength ranges when snow algae are covered by snow, and a correlation with both cell count and chlorophyll concentration. These findings suggest potential metabolic activity and increased melt rates even when snow algae blooms occur under the snow surface and are undetectable for remote sensing.

Biological Sulfate Treatment with Iron-based Immobilization

Katie Linderholm, Chan Lan Chun, Nicholas Eshleman, Nathan W. Johnson

Natural Resources Research Institute

Biological sulfate systems have flexible and cost-effective options to reduce the ecological impacts of anthropogenic loading (e.g. industrial and municipal wastewater) of sulfate (SO4-2) to freshwater environments where sulfate is often present in low concentrations. In our recent work, we have developed a pilot-scale two-stage biological treatment: sulfate-reducing bacteria (SRB) have the ability to convert sulfate into hydrogen sulfide (HS-). Iron-bearing minerals in the immobilization phase are reactive to sulfide, producing byproducts such as iron (II) sulfide (FeS) and elemental sulfur (So). While this information is known, there is not much known about the full potential of using SRB and the reactivity of iron materials to recover a stable solid form of sulfur. This study aims to examine the iron-bearing mineral media of sulfide immobilization to improve the longevity of the iron mineral media and enhance final solid forms of sulfur to So in the treatment system. The media before and after sulfide immobilization were characterized using Scanning Electron Microscopy with Energy Dispersive X-Ray analysis. Iron-to-sulfur ratios were dependent on iron mineral composition. Moreover, hydrogen peroxide was used to regenerate iron mineral media to harvest a solid form of sulfur as So. Preliminary results show optimal dosage of hydrogen peroxide will allow us to regenerate iron material multiple times, potentially reducing the cost of materials needed for the treatment.

Utilizing Oxford Nanopore Technology to Sequence the Genome of the Green Alga Trentepohlia

Hannah Hausman, Tami McDonald

Biology, St. Catherine University

The goal of this research is to sequence and assemble genomes of green algae in the genus Trentepohlia in partnership with the Joint Genome Institute at the Department of Energy to better understand carbon cycling in extreme habitats. The genus Trentepohlia contains many filamentous green algae that are common symbionts in lichens, symbiotic associations between algae and fungi. Unlike many of their aquatic relatives, these are desert green algae able to survive drying out and re-wetting cycles common to desert climates by exhibiting poikilohydry as a desiccation tolerance mechanism. Poikilohydry promotes survival in this extremely dry environment by slowing down diverse metabolic processes to put more energy toward protective functions. Lichenization may also protect against desiccation. Sequencing the genome of Trentepohlia will provide significant information regarding the transcriptomics behind desert green algal poikilohydry and what factors cause Trentepohlia to form lichen symbioses. We have begun sequencing the genome of Trentepohlia algae by establishing and maintaining pure cultures of Trentepohlia algae and building an efficient protocol for extracting pure high molecular weight (HMW) DNA necessary for Oxford Nanopore MinION sequencing. Currently, we have sequenced DNA from Trentepohlia aurea and Trentepohlia odorata. Future directions for this project include using the information from the assembled genomes to better understand the symbioses of lichens.

Uncovering the mechanism for synthesizing tooth-shaped magnetosomes in Desulfovibrio magneticus RS-1

Virginia V. Russell, Arash Komeili

University of California Berkeley

Magnetotactic Bacteria (MTB) are a diverse group of bacteria capable of navigating along the geomagnetic field in search of the optimal environment. To do this they synthesize magnetosomes, an organelle composed of magnetite or greigite usually enclosed in a lipid membrane. The mechanism for magnetosome formation is most well studied in two species of alpha-proteobacteria, which have cubooctohedral-shaped magnetite crystals surrounded by a lipid membrane. Little to nothing is known about the mechanism for synthesizing tooth-shaped magnetosomes, which are thought to be the ancestral form of magnetosomes. As such, this study can help uncover the evolution of the mechanism. I am using Desulfovibrio magneticus RS-1, a delta proteobacterium, as a model organism to understand the mechanisms of synthesizing tooth-shaped magnetosomes. To do this I will (1) identify the genes responsible for different steps of magnetosome synthesis in RS-1, and (2) uncover any mechanism that inhibits or regulates biomineralization. The results thus far show that the following genes: mad2, mad20, mad23, mad25, mad28, mad10, and mad26 when deleted or mutated show phenotypes for hindering different steps of magnetosome synthesis: controlling the size and shape of magnetosomes, and chain alignment. In addition, I have discovered that when RS-1 is grown in the presence of hydrogen it prevents magnetosome formation. Thus, hydrogen could be important for inhibiting or regulating the synthesis of magnetite.

Don’t Leaf It Alone: The Importance of Sample Size and Distribution on the Biosynthesis of Leaf Waxes

Valencia Ajeh, Jack Hutchings, Tyler Huth, Alessandro Mauceri, Bronwen L Konecky

Washington University in St. Louis

Plant leaf waxes act as biomarkers in paleoclimate and paleoenvironmental studies, as their hydrogen isotope composition reflects climate conditions like temperature and precipitation. Leaf wax properties such as chain length and carbon isotopes are influenced by plant characteristics. The hydrogen isotope composition also responds to growth environment and biosynthesis, contributing to differences from source water. Modern leaves aid understanding of these variables but extending to species level lacks a standard approach. We assessed sample size needed for species characterization. We studied 5 American sycamore trees (Planatus occidentalis) in an urban setting (Washington Uni.). Close in proximity and age, we collected 30 leaves from each tree and extracted leaf wax n-alkanes using solvent. After purification, gas chromatography analyzed n-alkane abundance and stable carbon (δ13C) isotopes. Dominant n-alkanes were C31, C33, and occasionally C25, causing up to 2-carbon variation in average chain length. C25's sporadic presence emphasizes sampling multiple individuals for reliable measurements. δ13C of major n-alkanes differed by 3-4 ‰ across compounds and ~1 ‰ among individuals. Initial data suggests 17-21 leaves for C31, C33 δ13C analysis, ensuring standard error falls below propagated errors of 0.19 ‰. Less leaves may suffice for less stringent confidence. Similar sampling requirements are expected for forthcoming δ2H data despite hydrogen’s larger analytical errors.

Innovative Removal of Methylene Blue Dye from Water Using Montmorillonite Clay-Modified Chitosan Beads

Aditya Goyal, Achintya N. Bezbaruah

North Dakota State University

Discharging methylene blue (MB) dye improperly poses environmental risks, affecting marine ecosystems, soil health, and human well-being. Our study focuses on a sustainable solution for efficient MB removal from water using Montmorillonite clay-modified chitosan beads. Recognizing the substantial impact of MB pollution on aquatic and terrestrial environments, our research focuses on advanced adsorption techniques. Montmorillonite clay modification of chitosan beads creates an effective adsorbent, capable of targeting and extracting MB molecules. This approach highlights our commitment to sustainability and our responsibility to mitigate anthropogenic consequences on ecosystems. Our methodology involves synthesizing Montmorillonite Clay-Modified Chitosan Beads and evaluating their efficacy in methylene blue removal. UV-VIS spectroscopy characterizes the adsorbent, revealing significant reductions in MB concentrations. Our research offers an eco-conscious strategy for water bodies. By utilizing sustainable materials and innovative design, we aim for a healthier ecosystem. Our study emphasizes the urgency of addressing dye pollution and promotes interdisciplinary cooperation for effective environmental solutions.In conclusion, our study successfully develops Montmorillonite Clay-Modified Chitosan Beads as a viable MB adsorbent. Encouraging UV-VIS spectroscopy results warrant further exploration of this sustainable approach to alleviate water pollution.

IGenetic evidence that multiple cytochrome nanowires are necessary for Fe(III) oxide reduction in Geobacter sulfurreducens

Madeline Ammend, Chi Ho Chan, Daniel R. Bond

BioTechnology Institute, University of Minnesota

Geobacter sulfurreducens is a dissimilatory metal-reducing microorganism capable of utilizing insoluble acceptors via extracellular electron transfer. While many multiheme c-type cytochromes expressed by G. sulfurreducens are implicated in linking its cytoplasmic respiratory chain to extracellular substrates, whether these proteins have specific roles in reduction or recognition of metals is unknown. Comprised of either OmcS, OmcE, or OmcZ, these nanowires are long polymers of protein subunits with a core of closely spaced hemes. We utilized a markerless deletion approach to construct single, double, and triple-deletion strains in an isogenic background to investigate possible roles of OmcS, OmcE, and OmcZ. When soluble Fe(III) or the organic acceptor fumarate were electron acceptors, no defects were observed in any mutant. When freshly precipitated Fe(III) oxide was tested as an electron acceptor, mutants lacking omcE were strongly affected, reducing Fe(III) approximately half as fast. No other single mutant (ΔomcS or ΔomcZ) showed a defect. Double mutants containing only omcE (ΔomcSZ) also showed a defect, suggesting other proteins could be required in addition to OmcE. The double mutants containing only omcS (ΔomcEZ) and the triple mutant containing none of the three major nanowires (ΔomcESZ) were completely unable to reduce Fe(III) oxide. Taken together, this indicates that genes for two separate nanowires are necessary to completely reduce this form of Fe(III) oxide.

Nanotechnology for Agriculture and Food Systems: Nano-enabled Phosphorous platforms for increasing Phosphorous use efficiency

Shirsa Mazumdar, Achintya Bezbaruah, Mohiuddin Quadir

North Dakota State University

The current global population exceeds 7.6 billion and is projected to reach 9.5-10 billion in 2050. Global food production, therefore, must be significantly increased in order to meet the challenge of feeding nearly 10 billion people. Of the 14 possible nutrients required by crops, phosphorus (P) (along with N) and potassium (K) is one of the most important for optimum crop production. The use of P by crops is also characterized by low efficiency. Over 70% of applied P is lost due to fixation in soil or run-off into surface or underground waters. Increasing plant P use efficiency is vital, given that it is a non-renewable mined resource. The goal of my work is to facilitate the use of nanotechnology for sustainable agriculture through nutrient delivery to plants, particularly phosphorus, thereby improving nutrient uptake (fortification) and use efficiency in agriculture. This can be achieved by developing novel nano-based fertilizers for effective and sustainable phosphorus (P) delivery to agricultural crops causing reduction of P loss in soil and the enhancement of P uptake and plant performance, as compared to conventional P fertilizers, and minimizing the negative footprint of chemical fertilizers and resource wastage.

Investigating biogeochemical interactions between ktedonobacter racemifer and Ca2+-, Mg2+-bearing primary silicate minerals

Benjamin Teerlinck

Earth and Environmental Sciences, University of Minnesota

Mechanisms of soil formation are largely understudied in a geomicrobiological context. Microbial activities in soils provide varying controls on the dissolution and reprecipitation of silicate minerals, thus regulating their weathering rates and the mobilization of bioavailable cations. Studying the effects of specific microbial taxa on primary mineral dissolution can help elucidate their roles in the fertilization of nascent soils. Members of the bacterial class Ktedonobacteria hold high relative abundance in nascent soils and keystone positions in more mature soil communities, suggesting a role in nascent soil colonization and development. Here, I propose research to help define the relationship between the class's type strain, Ktedonobacter racemifer SOSP1-21, and the primary silicate minerals anorthite, diopside, and forsterite, which exhibit distinct rates of dissolution in ambient conditions and yield the highly bioavailable cations Ca2+ and Mg2+. When grown on these mineral surfaces, K. racemifer's ability to adsorb to and dissolve these minerals will be characterized by biofilm surface coverage, localization of pH gradients, and intracellular accumulation of Ca2+ and Mg2+. Monomineral soil columns will be used to quantify the changes in dissolution rates effected by K. racemifer. Finally, K. racemifer's genetic responses to mineral-adsorbed growth will be determined via transcriptome sequencing and identification of differentially-expressed genes.

Hot Genes, Hot Springs: Impact of Fluctuating Temperatures on the Microbial Community

Teresa Mccarrell, Trinity Hamilton

Department of Plant and Microbial Biology, University of Minnesota

Yellowstone National Park is home to numerous geothermal features, including hot springs and geysers. The periodic eruptions of a geyser are due to subterranean flash boiling events in confined underground water channels; these eruptions result in significant fluctuations in water flow and temperature in hot springs outflows fed by geysers. Despite their significance, geysing springs have received limited attention in the study of temperature's role in microbial adaptation and evolution. While the microbial communities in non-geysing hot spring outflows (hot spring outflows not associated with a geyser) have been extensively characterized, further research is required to understand the diversity and physiology of microbes in geysing hot spring outflows. In this study, we sequenced 16S rRNA amplicon sequences and metatranscriptomes from microbial mats in both geysing and nongeysing hot springs. While it is challenging to disentangle the differences in 16S diversity between geysing and non-geysing springs due to natural variations between springs, we did observe potential patterns in transcriptomic variations between the two spring types of springs. Furthermore, intriguingly, within a geysing cycle, during which water flow and temperature change over time, the community transcriptome remains largely unaffected. In summary, geysing hot springs represent a crucial but understudied environment for investigating the influence of temperature on microbial diversity and physiology.

Nitrogen Cycling Networks of Lake Superior Sediments

Hailey Sauer, Cody Sheik, Trinity Hamilton

Plant and Microbial Biology, University of Minnesota Twin Cities

Lake Superior is a valuable natural and cultural resource: it holds 10% of the world's freshwater and is the headwaters for the Laurentian Great Lakes. Over the last century, Lake Superior's nitrate concentration has increased ~0.2 μM/year leading to an extreme stoichiometric imbalance relative to phosphorus (N:P +10,000). In Lake Superior sediments, nitrate production depends on the proximity to shore but could account for nearly 50% of the annual accumulation of nitrate in the water column. To date little is known of the microorganisms that drive the cycling of nitrogen in these sediments. Here we assess the potential and active transformation of nitrogen species by individual organisms, through metagenomics and metatranscriptomics, in order to reconstruct hypothetical nitrogen cycling networks. We uncovered novel organizational structures for nitrogen recycling across both spatial and biochemical gradients. We find that regardless of oxygen penetration, there's potential for nitrate reduction and that taxonomic diversity for nitrate reducers doesn't correlate with oxygen concentration (e.g., sites with deeper penetration have greater diversity). Ultimately, our findings provide insight into the uniqueness of nitrogen cycling networks across a single system and provide further evidence of anaerobic processes in aerobic environments.

Promoted Molybdenum and Iron-containing Mineral Dissolutions by Microbially Produced Siderophores

Dongyi Guo, Yizhi Sheng, Jack Verbrugge, Hailiang Dong

Department of Geology and Environmental Earth Science, Miami University

Siderophores play a crucial role in the dissolution of metal-bearing minerals to increase metal bioavailability for microbial uptake. Previous studies have extensively investigated mineral dissolutions (mainly Fe minerals) by the model hydroxamate siderophore deferoxamine-B (DFOB). However, the interactions between other microbial siderophores and natural Mo-bearing minerals have not been explored. In this study, catecholate protochelin and hydroxamate DFOB, were utilized to examine their effects on the dissolutions of Mo-containing mineral molybdenite and Fe-bearing minerals (olivine, goethite, and nontronite) at near-neutral pH. The results demonstrated that both siderophores stimulated the dissolutions of various iron minerals, and the surface-controlled dissolution processes are controlled by siderophore absorptions and metal-binding affinities. Most importantly, protochelin enhanced molybdenite dissolution with the formation of molybdenum oxide (MoO3) on the mineral surface. The dissolution of molybdenite increased with higher concentrations of protochelin, and a redox-driven dissolution mechanism was proposed for this process. Conversely, the addition of DFOB resulted in the depression of molybdenite dissolution. These findings shed light on the dissolution mechanisms of natural metal-bearing minerals promoted by siderophores. Specifically, it contributes to a deeper understanding of the biological molybdenum uptakes from solid sources.

Long-term, repeated measures reveal fungal and bacterial succession dynamics during wood decomposition in a boreal forest.

Yanmei Zhang, Zewei Song, Jonathan Schilling

Plant and Microbial Biology, University of Minnesota

Deadwood decomposition plays a significant role in carbon and nutrient cycling in forest ecosystems and is a major challenge in climate modeling. Wood decomposition can vary in rates and fates for carbon release, depending on the successional development of microorganisms. Factors controlling community assembly and succession, however, are poorly explained by environment or wood traits. We sampled 80 individual logs over 5 years (repeated measures; annually), to track decomposing red pine (Pinus resinosa) and paper birch (Betula papyrifera) by fungal and bacterial communities using amplicon sequencing among four treatments manipulating microclimate conditions in wood (abiotic) and accessibility for colonizers (biotic) external to the logs (ground vs. aboveground contact; bark on vs. bark off). Treatments had significant effects on fungal community structure, but lignin-deficient white rot-type woody residues prevailed in all treatments, which resulted in familiar patterns of diversity loss (Shannon index), despite an increase in taxa richness. White rot taxa dominating at any given time were present at least in low abundance as endophytes. Bacterial communities, however, did not show comparable treatment effects, and their structure remained similar across decaying process. This supports the assertion that fungi determine bacterial presence more than vice versa, and that fungal specialists support bacterial generalists over the course of deadwood decomposition.

Protein Catalyzed Biomineralization of Magnetite as the Key to Magnetofossil Identification

Michaela Hostetler

The Ohio State University, School of Earth Sciences

Magnetotactic bacteria (MTB) are incredibly resilient organisms that can be found in extreme environments such as arsenic-rich hot springs and Antarctic lakes. Due to the diverse array of environments these organisms can survive in, hypotheses have been raised regarding whether they could have survived in extraterrestrial environments, such as early Mars. Magnetite nanoparticles have even been recovered from carbonate globules in Martian samples, such as the 1996 ALH84001 meteorite, but their origin is still a topic of much debate. To test these hypotheses, there must be a baseline understanding of magnetofossil identification, including morphological and chemical characteristics. MTB provide a window to Earth's present and past chemical and biological systems, and possibly other planetary conditions. Biogenic magnetite has high chemical purity in comparison to abiogenic magnetite, as well as specific physical configurations (e.g., unique bullet, prismatic, or octahedral shape). Analysis of the individual proteins MTB utilize in the biomineralization process and understanding not only how each protein functions, but how it is preserved, creates the potential for these proteins to act as biomarkers for MTB, aiding in identification of biomagnetite vs abiotic magnetite on Earth, and perhaps even Mars.

Stable isotope analysis of fossilized plants gives insight into C cycling and soil N availability during the Phanerozoic

Alexandra M Grajales, Benjamin W Johnson

Iowa State University

On Earth today, plants comprise the vast majority of fixed carbon in biomass. It is likely that they did in the past as well. Further, plant growth may be limited by bioavailable N. Thus, studying the evolution of the terrestrial C cycle depends on understanding how plants fixed C and the availability of N in their environments. The relationship between C and N may reflect a combination of atmospheric pCO2 and soil N availability. Here, we use stable isotope analysis of N and C in 49 fossilized C3 plan tissues from the Phanerozoic ranging from 400.5 Ma to 19.5 Ma to potentially quantify pCO2 fluctuations and analyze nutrient availability within soils recorded in plant material. Within this time range the values ranged from -32.8 to -22.8‰ and values varied between -5.9 to 8.65‰. The C/N ratio of the analyzed plant tissues ranged from 7 to 129. The results show no discernible change within the values with time. The and the C/N ratio show large fluctuations in the amount of carbon and nitrogen that is available for plant uptake. With further analysis of this data, the nitrogen and carbon concentrations can potentially be used as an indicator of soil nutrient availability changes through the Phanerozoic in a particular environment, since paleosol analyses are restricted to their limited availability. We suggest that stable isotope analysis of fossilized plant material can be a possible archive for another proxy record for pCO2 through the Phanerozoic.

Field experiment assessing the effect of nitrogen and salt addition on freshwater phytoplankton abundance and diversity.

Amanda H. Rodgers, Micah Jay Strike, Beatriz Baselga Cervera

Biology (EEB), University of Minnesota Twin Cities

Phytoplankton are key primary producers in freshwater ecosystems; therefore, it is essential to understand how they respond to human disturbances. Salinization and eutrophication of freshwater bodies enhance growth of some phytoplankton species and influence community composition. In this study, 21 independent populations were established simultaneously from water samples of Cedar Bog Lake, MN. Populations were suspended at the surface of the lake in transparent flasks for a three-week period, allowing for natural fluctuations in environmental conditions. Populations were grown in either deionized water (control), 0 mM NaNO3 BG11 media (-N), 9 mM NaNO3 BG11 media, or standard 17.6 mM NaNO3 media with either 0 mM or 10 mM NaCl. Results indicate that nitrogen, but not salinity, affected growth. While biovolume generally increased with nitrogen concentration, there was no difference between the 9 mM and 17.6 mM NaNO3 treatments. Total protein density at 9mM was significantly different from the control and the -N treatment, but the 17.6 mM treatment was not. Simpson's and Shannon's diversity indices varied by population, but there were no statistically significant differences. While further research is needed to develop a comprehensive understanding of the relationships between nitrogen, salinity, and phytoplankton diversity, this study provides unique insights in the context of a controlled field study.

Iodine content in methane-derived authigenic carbonates and their implications for marine methane flux dynamics

Sajjad Akam, Dalton Hardisty, Xudong Wang, Dong Feng, Mohammed Hashim, Janet Burke, Elizabeth Swanner, Antoine Crémière, Jörn Peckmann

Geological and Atmospheric Sciences, Iowa State University

Iodine (I) exists as two inorganic species in seawater - iodate (IO3-) and iodide (I-). Only the oxidized form (IO3-) is incorporated into carbonate minerals, enabling the utility of I/(Ca+Mg) in carbonates as a paleo proxy to track dissolved oxygen in the water column. Methane-derived authigenic carbonates (MDAC) are a globally relevant carbonate factory and are commonly distributed in sediments settings with subsurface methane transport. This study evaluated I/(Ca+Mg) records of MDAC from methane/hydrocarbon seep settings. We analyzed (I/Ca+Mg) and Rare Earth Elements (REE) distribution of MDAC samples from globally distributed seep sites. Our preliminary results identified I/(Ca+Mg) ratios from 0.25 to 5.33 µmol/mol in 70% of samples with a negative Ce anomaly. These findings suggest that changes in flux intensity and/or increased oxygen penetration in sediments would expose the MDAC to intermittent oxic conditions and subsequent incorporation of IO3-, reflected in high I/(Ca+Mg) ratios and negative Ce anomalies. Samples with negative Ce anomaly and close to zero I/(Ca+Mg) suggest an additional mechanism, enhanced AOM-induced alkalinity in the presence of organic matter, that can also generate a negative Ce anomaly. The results expand the utility of the I/(Ca+Mg) proxy in reconstructing variations in seepage conditions and demonstrate the effectiveness of pairing I/(Ca+Mg) with Ce (and REE) data for such efforts.

De Novo evolution of morphological diversity in the cyanobacterium *Anabaena variabilis*

Beatriz Baselga Cervera, Michael Travisano

University of Minnesota

Cyanobacteria reached their maximum morphological complexity in terms of cell types, modes of multicellularity and size, early in earth history (~2 Ga) and reminded morphologically static as “living fossils”. Given the widespread distribution and ecological relevance of cyanobacteria, experimentally exploring the evolutionary possibilities and constraints within this lineage can inform possible geobiology interactions. Utilizing experimental evolution, we show that morphological diversity can rapidly evolve in the filamentous cyanobacteria Anabaena variabilis (syn. Trichornus variabilis). We subjected multiple populations of the A. variabilis to a selection regime for larger size, given the relationship between size and organismal complexity. As a result, after 45 cycles of selection, we observed an increase in size of more than 30-fold compared to the ancestral size. We also observed the emergence of morphological diversity. Two distinguishable morphological elaborations, Tangle (long, tangled filaments) and Cluster (clusters of short filaments) morphologies were identified in all the selected populations. These results open unprecedented opportunities to address ascribed constraints to the evolutionary stasis, opportunities for palaeontology and the exploration of interactions between the physical environment.

New family of enzymes produces ethylene in *Rhodopseudomonas palustris*

Nicole L. Márquez Reyes, Kathryn R. Fixen

University of Minnesota - Twin Cities

The nitrogenase superfamily evolutionarily points out to the existence of nitrogen fixation-like sequences with unknown functions that produce interesting by-products. A group of nitrogenase-like enzymes, methyl-thio alkane reductases (Mar enzymes), are capable of reducing volatile organic sulfur compounds like methyl-thio ethanol (MT-EtOH) to produce ethylene gas. Ethylene as a by-product is a precursor to plastics and an important phytohormone. Ethylene production by Mar enzymes has been observed in Rhodopseudomonas palustris under sulfate limiting conditions, however, R. palustris Mar enzymes are not characterized. The goal of this project is understanding and characterizing R. palustris' Mar isozymes and their contribution to ethylene production in the bacterium. To define R. palustris' Mar isozymes, we will test individual and double mutants in the different Mar-like enzymes and test their role in ethylene production and their requirement to grow on a range of different organosulfur compounds. Mar isozymes, similar to nitrogenases, contain a metal cofactor in their active site, but what metals are in their cofactors is unknown. To characterize the Mar isozyme's cofactors, we will test the individual and double mutants requirement to grow in different metal limiting conditions. This will help us gain greater understanding of the role of these nitrogenase-like enzymes in the production of by-products and their biological activity.

Nitrogen isotopes suggest local oxygenated waters during Neoproterozoic glaciation: insights from the Pahrump Group, near Death Valley, California

Samuel Duncanson, Benjamin Johnson

Department of Geological and Atmospheric Sciences, Iowa State University

Nitrogen (N) in marine environments is mediated by microbial activity and water column oxygenation. Deciphering ancient N-cycling dynamics informs our understanding of Earth's habitability through time. This includes the Neoproterozoic, an era containing global glaciations and rapid developments in biologic evolution. However, N-cycling remains poorly constrained during this time. To address this, we present δ15N values from sediments of the Neoproterozoic Pahrump Group. Sixty-one samples of mud to gravel-size sediment were collected from the ~ 787 Ma Horse Thief Springs (HTS) and ~720 Ma Kingston Peak (KP) formations. Sediments in the HTS had an average δ15N of 6.7‰ and 357 ppm [N], with minimal N isotopic or concentration variability across stratigraphy. In contrast, the mean δ15N of KP sediments increased up section in two sites, increasing from 4.6 to 6.2‰. Average [N] at the former site decreased across this transition from 612 to 262 ppm, while increasing from 111 to 356 ppm at the latter site. Previous interpretations of the KP sedimentary facies consider the lower and upper members as forming in pre-glacial and glacially influenced environments, respectively. As such, increasing δ15N in the upper KP suggests a decrease in oxygenated waters as glaciation proceeded. Broadly, initial δ15N values from the HTS and KP suggest aerobic N cycling during sedimentation. Additional geochemical analyses will further inform interpretations of the HTS and KP paleoenvironments.

Relating chaotic continent-biosphere feedbacks to the convergent evolution of increasing geobiological complexity and stability

John Herring, Benjamin W. Johnson

Department of Geological and Atmospheric Sciences, Iowa State University

While many aspects of geobiological evolution have been well described, unpredictable nonlinear behavior characterizes some key drivers of macroscale geobiological change (such as deep-Earth cooling dynamics, continental emergence, and biosphere evolution), necessitating their formalized description and inclusion in existing models. However, subtle positive feedbacks between these Earth system processes may drive quasi-predictable trends that help sustain stable and persistent geobiological networks on Earth and Earth-like planets elsewhere. We present a qualitative overview of these feedbacks, focusing on two aspects of continental growth and emergence: a coupling between continental emergence and deep-Earth thermal and structural complexity and coupling between increased continentality and increased geobiological complexity (and stability) over time. We suggest that quasi-logistic growth of geobiological complexity and stability can transform into quasi-exponential growth in response to increases in environmental heterogeneities associated with strong continent-biosphere couplings. Further work is needed to refine quantitative models of these geobiological feedbacks and to evaluate whether Earth-like continent-biosphere couplings across the cosmos may evolve convergently as “stable attractor” configurations, whose relative persistence may be a source of observational bias in future life-detection efforts.

Investigating Lead Resistance and Sequestration in the Soil Bacterium *Bacillus megaterium*

Jamison M. Ward

Department of Earth and Environmental Sciences, University of Minnesota-Twin Cities

Lead (Pb) is a priority pollutant whose environmental occurrence has increased since human industrialization with deleterious consequences for both human and natural ecosystem health. The application of Pb-resistant microorganisms for bioremediation has received considerable attention for its advantages over physiochemical remediation strategies. The soil bacterium, Bacillus megaterium, has been previously observed to harbor Pb resistance and accumulate Pb intracellularly; however, the mechanism for Pb storage was not entirely elucidated. One possibility is Pb sequestration in microbial polyphosphate (polyP) granules—nanometer-scale inclusions of phosphate polymers used as phosphorus storage and cellular energy reserve. PolyP also contains metal atoms as counterions, and Pb has been observed associated with polyP in bacteria grown in Pb-rich environments. This project will employ a suite of analytical methods to investigate the magnitude and mechanism of Pb resistance in B. megaterium with Pb storage in polyP as the working hypothesis. The bacterium will be cultured in media of varying Pb concentrations to establish Pb tolerance, and Pb uptake from the medium will be measured using ICP-MS. Harvested cells stained with DAPI and tetracycline will be observed via epifluorescence microscopy to probe the spatial distribution of Pb and polyP within cells. Additionally, specimens will be imaged via STEM-EDS to further investigate cellular morphology and elemental distribution.

A Novel Predator-Prey System: Ciliates and Cyanotoxins

Jordan Sivigny, Beatriz Baselga-Cervera, Michael Travisano

University of Minnesota

Harmful algae blooms (HABs) pose a serious threat to aquatic ecosystems through their production of toxic compounds such as cyanotoxins. While the damaging impacts of cyanotoxins are known, the specific environmental factors that may instigate their production have yet to be sufficiently explored. It is proposed that production of these compounds evolved as a defense against predation. However, studies have found mixed results of how these compounds impact predation and none have explored how predation impacts the rate of cyanotoxin production. In order to explore how toxin-production impacts and is impacted by predator-prey dynamics, a series of Co-Cultures between five Microcystis strains that produce different quantities of microcystin, a prevalent cyanotoxin, and the common aquatic predator Tetrahymena thermophila were tracked over time. From these experiments it was found that, despite cyanotoxin production impacting predator growth and active grazing by the predators, strains that produce greater quantities of cyanotoxin don't have significantly different rates of predation. Given this finding, further exploration of the environmental factors that instigate toxin production in algae are needed to elucidate their ecological and evolutionary role.

Elucidating the distinct diagenetic pathways of discrete steroidal hydrocarbons

Kelsey Doiron, Peter Bijl, Thomas Wagner, Jens O. Herrle, Simon Brassell

Earh & Atmospheric Sciences, Indiana University

Steroidal hydrocarbons are prominent aliphatic hydrocarbons in Paleocene to Campanian sediments (~63-74 Ma) recovered from the Transkei Basin (Hole U1581B), offshore South Africa, during IODP Expedition 392. The dominant compounds are C27 to C29 sterenes and steradienes with subordinate amounts of diasterenes, partially rearranged sterenes, and steranes. The predominance of C28 steradienes in the upper Campanian reflects major phytoplankton contributions of their C28 sterol precursor. The proportion of C28 steradienes (>60%) far exceeds that for sterenes & steranes (~10-30%), confirming origins from discrete sterol precursors. The composition of steroidal hydrocarbons changes systematically with depth matching the succession of proven diagenetic transformations. Increasing amounts of partially rearranged sterenes and diasterenes in middle Campanian samples are accompanied by a concomitant decrease in the proportions of sterenes and steradienes. The prevalence of C28 diasterenes in these samples (~40-55%) suggests an affinity with steradienes. Thus, carbon number distributions for specific series of steroidal hydrocarbons suggest a preferential pathway for diagenetic conversion of steradienes to diasterenes, while the sedimentary fate of sterenes involves reduction to steranes. Yet evidence for distinct diagenetic pathways for discrete sterols is progressively lost as later-stage products reflect convergence toward an aggregate distribution of all precursors.

Impact of sulfide concentration and illumination on Anoxygenic photosystems of Leptolyngbya sp. strain hensonii

Reda A.I. Abou-Shanab, Eric Kees, Trinity Hamilton

Plant and Microbial Biology, College of Biological Sciences, University of Minnesota

Oxygenic photosynthesis is often cited as the most important microbial innovation. The emergence of oxygen-evolving photosynthesis, aided by geologic events, is credited with tipping the scale from a reducing early Earth to an oxygenated world that eventually led to complex life. The first phototrophs were likely anoxygenic—anoxygenic phototrophs employ a single reaction center to harvest light and generate energy and reducing power through the oxidation of reduced inorganic or organic compounds. In contrast, oxygenic phototrophs use two reaction centers, Photosystem II and Photosystem I, for light-driven oxidation of H2O to fuel primary productivity. Reaction centers, including Photosystem I and II, share a single common ancestor. Gene duplication and divergence events from this common ancestor have given rise to reaction centers in anoxygenic phototrophs (AP) that are distinct from one another and from Photosystem I and II in oxygenic phototrophs (OP). Despite this shared ancestry, outstanding questions remain in the evolution of photosynthesis, primarily what was the physiology of the first phototroph, what was the nature of the first reaction center (which reaction center came first), and how did oxygenic phototrophs evolve to use two reaction centers in concert to split water, producing O2 as a by-product and fueling primary productivity. These questions are a key to understanding the role of biology in planetary evolution.

Deciphering the Diagenetic History of the Avon Park Formation through a Trace Metal Perspective

Andrew McGallian, Maria Luiza C. Ferreira, Jordan P. Todes, Roger Bryant, Clara Blättler

Department of the Geophysical Sciences, The University of Chicago

Shallow marine carbonates can reveal past seawater chemistry and environments. However, they are highly prone to diagenetic changes, which impact past seawater reconstructions. To assess these processes, we present trace element concentrations along with isotopic analyses from the mid-Eocene Avon Park Formation in Florida. Trace metals abundances offer some insights into biogeochemical reactions, redox shifts, and biotic components within the sediment. Early marine diagenesis led to partial dolomitization of these shallow-water carbonates, impacting their observed geochemistry and providing a chance to explore diverse diagenetic controls. Low Mn/Sr ratios in these diagenetically altered samples challenge the use of Mn/Sr thresholds as indicators of alteration. Increased levels of Mn and redox-sensitive elements (e.g., V, Cr, U) correspond with a decrease in δ13C values within a dolomite-rich section. In the same interval, reductions in Sr/Ca ratios followed by elevated δ44/40Ca ratios possibly show a shift from aragonite to calcite as the initial primary mineralogy. At greater depths, increased vanadium content correlates with fossil-rich facies, indicating a potential role of biogenic material in influencing trace metal behavior. In tandem with stable isotopic tools, trace metal analyses can contribute to unraveling the paleodepositional and diagenetic contexts for early marine carbonate sediments.

XAFS study of Ce adsorption by different phases of iron and manganese oxides and its effect on stable Ce isotope fractionation

Weiming Ding, Wei Ren, Tingying Xu, Xin-Yuan Zheng

Department of Earth and Environmental Sciences, University of Minnesota, Twin Cities

Iron (Fe) and manganese (Mn) oxides are ubiquitous in surface environments, and they exert substantial controls on the fate of many trace metals considering their capacity of adsorption, structural incorporation, or mediation of redox reactions. Among rare earth elements (REEs), cerium (Ce) can be preferentially enriched in natural Fe and Mn oxides through the oxidative scavenging of aqueous Ce(III) to insoluble Ce(IV). Recent data show the large fractionation of stable Ce isotopes (142Ce/140Ce) during Ce oxidative adsorption onto δ-MnO2, indicating the potential application to trace the Earth's Mn cycle. However, the mechanism for the observed Ce isotope differences among different phases of minerals is not fully understood. Therefore, we propose to study Ce speciation associated with different phases of experimental Fe and Mn oxides, and its influence on the stable Ce isotope fractionation. In the laboratory, a series of controlled experiments were conducted to study potentially oxidative adsorption of Ce(III) by various phases of Mn oxides and Fe oxides as well as one fungal species. XANES for Ce and XANES + EXAFS for Mn and Fe were conducted to explore the speciation variations after adsorption processes. Stable Ce isotopes of solid and aqueous phases were measured to acquire the influence of mineral phases on the isotopic fractionation. This work will provide a fundamental basis for the application of stable Ce isotope to the paleoenvironment reconstruction.

Leveraging Machine Learning Approaches to Characterize Organic Matter Abundance in Mars-Analog Hypersaline Sediments

Floyd Nichols, Alexandra Pontefract, Andrew Masterson, Mia Thompson, Christopher Carr, Hannah Dion-Kirschner, Maggie Osburn

Northwestern University

Modern technology has led to a growth in advanced laboratory techniques producing large and complex datasets for the geosciences. These datasets more closely reflect the true complexity of environmental settings. To more quantitatively extract key information from these datasets, we refined machine learning (ML) techniques to predict the abundance of organic matter (OM) in dynamic Mars-analogue hypersaline lakes from elemental abundance data. ML is historically underutilized in organic geochemistry and astrobiology due to the typical small datasets compared to other fields,but can be extremely effective at revealing structure and patterns in complex data. We trained a suite of classification models including random forest, k-nearest neighbor, support vector machine, and logistic regression on these Mars analogue sediments, and overall, our trained models were successful at predicting the abundance of OM with 78% to 87% accuracy. Overall, our results show the potential for applying ML to these datasets for both data curation and sample selection for more time intensive approaches, such as lipid extraction and analysis. ML offers agnostic insight into complex data, ultimately creating a more efficient search for biosignatures. Additionally, our results highlight the potential for ML models to be trained using data available on Earth and transferring that knowledge (transfer learning) to astrobiological targets such as current life detection missions on Mars.

Varying oxygen saturation in vitro to determine oxygen threshold of iodate reduction in *Shewanella oneidensis*

Ian Carley, Keyi Cheng, Dr. Matthew Schrenk, Dr. Michaela TerAvest, Dr. Dalton Hardisty

Earth and Environmental Sciences, Michigan State University

Oxygen minimum zones (OMZs) are layers in the water column that have low oxygen due to a combination of biological, chemical, and physical processes. Redox reactions involving iodine species can be used to track these processes in modern OMZs as well as ancient oceans where OMZs were more expansive than today. However, the mechanisms and oxygen thresholds driving iodine cycling are not well understood, thus limiting quantitative applications. To this end, we performed experiments in Shewanella oneidensis cultures to quantify the rate dependency of iodate reduction on O2 and the O2 threshold at which iodate reduction becomes favorable. Shewanella are metal-reducing bacteria commonly found in warm and temperate regions worldwide and are part of the marine environment microflora. Shewanella are also known reducers of iodate in anaerobic conditions, however, the exact oxygen saturation at which Shewanella begin to reduce iodate to iodide is unknown. In our experiments, cultures were maintained at 30 deg C using 20mmol/kg lactate, 40mmol/kg fumarate, and 250 µmol/kg iodate. We used an environmental hypoxia chamber which controls ambient levels of both CO2 and O2 using a 0-3000 ppmv CO2 and 0-1000 ppmv and 0.1-25% O2 analyzer. Preliminary results at ambient atmospheric CO2 levels and O2 at ranges <10% reveal O2 dependencies for iodate reduction at levels relevant to that known for both modern OMZs and inferred within seawater more broadly across key intervals of Earth history.

Rates and Pathways of Euphotic Iodine Redox Transformations Across the Atlantic Meridional Transect (AMT-30)

Kirsten Fentzke, Alexi Schnur, Andy Rees, Sune Nielsen, Dalton Hardisty

Michigan State University

The oxidized iodine species, iodate, is the most pervasive in well-oxygenated marine waters and can be tracked in carbonates as a paleo-redox proxy. Despite well-known spatial concentration variations in the ocean today and temporal gradients across Earth history, the rates and mechanisms of iodate formation remain poorly understood. To quantify rates and mechanisms of iodine cycling, we performed ship-board tracer experiments across a latitudinal transect of euphotic waters with known gradients in iodine speciation. Specifically, The AMT (Atlantic Meridional Transect) cruise provides the opportunity to collect these data across a range of ocean conditions transecting the Atlantic (45°S to 37°N). We collected samples for incubations and accompanying depth profiles (5-500 meters) from 11 stations along the transect. All incubation sets were spiked with radioactive 129I- (t1/2 ~15.7 My) and were performed at four depths transecting the surface to the deep chlorophyll maximum. Because of low natural abundance of iodine-129 relative to the only stable iodine isotope, iodine-127, in seawater (129I/127I ~10-12), the radioactive spike acts as a tracer throughout the oxidation and reduction processes. Specific iodine species iodate and iodide were separated via ion chromatography and iodine isotope ratios were analyzed using a sparge-based MC-ICP-MS technique. Preliminary results reveal that rates of iodine oxidation and reduction varied at both individual depths and across stations.

A survey of lake sediments reveals diatom-derived highly branched isoprenoids display unexpected structural diversity and correlations with salinity.

Watts L. Dietrich, Aaron F. Diefendorf, Thomas V. Lowell, Megan C. Corcoran, Hans H. Naake

Department of Earth and Environmental Sciences, Michigan State University

Geochemical biomarkers can aid investigation of environmental and ecological change in the past. Highly branched isoprenoids (HBIs) are diatom biomarkers documented in sediments around the world. However, most prior investigations of these compounds have been carried out in marine environments. HBIs in lacustrine settings remain poorly understood in comparison and may harbor untapped potential as paleoenvironmental proxies. To address this knowledge gap, sediment was collected from twenty-four lakes in the Midwestern U.S. The abundance and structures of HBIs in sediment were compared with water chemistry measurements to assess environmental controls on HBIs. HBIs appeared in higher abundance and more diverse forms than previously anticipated for lacustrine settings. Fifteen different HBIs with varied chain lengths and degrees of unsaturation were detected, including a variety of C25 HBIs, which are scarcely documented in lakes. All twenty-four lakes also contained unusual C21 HBIs previously reported only at two coastal marine sites. This previously unrecognized wealth of HBIs in lakes may represent a neglected record of diatoms, water chemistry, and environmental change. The data also indicate that salinity exerts control on the composition of HBIs in lake sediments. The relative abundance of two C25 HBI dienes appears to depend on lake salinity, as does the abundance of C20 HBIs, suggesting these biomarkers hold potential as indicators of lake salinity in the past.

Chemostratigraphic Investigation of an End-Ordovician Shallow Marine Sequence, Indiana, USA

Brooke Vander Pas, William Gilhooly, Ben Dattilo

IUPUI

The Ordovician period was a pivotal era characterized by significant climatic, geologic, and evolutionary transformations. The transition from an Early Ordovician "hot-house" to Late Ordovician "ice-house" climate, marked by glaciation and cooling, led to major environmental changes, increased biodiversity (GOBE), and a mass extinction. In addition, the first appearance of land plants may have had extensive consequences on terrestrial and marine ecosystems including shifts in atm CO2 and O2 levels and periods of increased Corg burial rates, and subsequent anoxia, evident in two Late Ordovician global positive carbon isotope excursions (GICE and HICE). The evolution of land plants, particularly their role in enhanced silicate weathering, including Late Ordovician extensive shallow-water phosphate deposits, has been proposed as an important contributor for decreased atm CO2 and subsequent cooling. Our study focuses on an end Ordovician shallow-water sequence collected from the IMI Pendleton Quarry in Indiana, comprised of interbedded dolostones, limestones, and shales. By analyzing these samples, we aim to unravel the climatic complexities of the end Ordovician, with a specific focus on the Hirnantian glaciation and the associated mass extinction event. We will investigate paleoclimatic, paleoceanographic, and redox cycle changes that occurred during this time, shedding light on the factors contributing to global cooling and marine extinctions.

Meeting Attendees

Name	Email	Institution/Affiliation
Hailey Sauer	breis014@umn.edu	Plant and Microbial Biology, University of Minnesota Twin Cities
Cara Santelli	santelli@umn.edu	Earth and Environmental Sciences, UMN
Moses Jatta	Mjatta@iupui.edu	Earth Science Indiana University Purdue University Indianapolis
Jeff Gralnick	gralnick@umn.edu	BioTechnology Institute / UMN
Madeline Taylor	tayl2383@umn.edu	Earth Sciences, University of Minnesota
Chris Crosby	crosb118@umn.edu	Oakton College
Amelia Olsen	olse0397@umn.edu	Earth & Environmental Sciences, UMN
Therra Wilbrandt	thewilbr@iu.edu	Earth Science, IUPUI
Trinity Hamilton	trinityh@umn.edu	Plant and Microbial Biology, University of Minnesota
Katie Fixen	kfixen@umn.edu	Plant and Microbial Biology, University of Minnesota
Nicole Smith	smit3363@msu.edu	Department of Microbiology & Molecular Genetics, Michigan State University
Dongyi Guo	guod9@miamioh.edu	Department of Geology and Environmental Earth Science, Miami University
Daniel Stanton	stan0477@umn.edu	Ecology, Evolution and Behavior, University of Minnesota-Twin Cities
Bruce witthuhn	Witth004@umn.edu	University of Minnesota
Mai Beauclaire	vuxxx231@umn.edu	Biochemistry, Molecular Biology, and Biophysics, University of Minnesota
Yanmei Zhang	zhan4170@umn.edu	Plant and Microbial Biology
Maowei Liang	mwliang@umn.edu	Cedar Creek Ecosystem Science Reserve, University of Minnesota
Adity Biswas	biswa112@umn.edu	Plant and Microbial Biology, University of Minnesota
Michaela Hostetler	hostetler.157@osu.edu	The Ohio State University, School of Earth Sciences
Emma MacNeil	macne029@d.umn.edu	LLO, UMD
Cory Sauer	Cdsauer@mmm.com	3M Company
Andrew Wood	wood0795@d.umn.edu	Large Lakes Observatory, University of Minnesota Duluth
Johann Verbrugge	verbrujd@miamioh.edu	Geology & Environmental Earth Science, Miami University
Viktor J. Radermacher	rader089@umn.edu	Department of Earth & Environmental Sciences, University of Minnesota
Amanda Rodgers	rodge278@umn.edu	Biology (EEB), University of Minnesota Twin Cities
Sajjad Akam	sajjad@iastate.edu	Geological and Atmospheric Sciences, Iowa State University
Ave Bisesi	bises004@umn.edu	EEB, UMN TC
Beatriz Baselga Cervera	bbaselga@umn.edu	University of Minnesota
Beverly Flood	beflood@umn.edu	University of Minnesota
Jake Bailey	baileyj@umn.edu	University of Minnesota
Nicole Márquez	mrque001@umn.edu	University of Minnesota - Twin Cities
Sam Duncanson	sdunc@iastate.edu	Department of Geological and Atmospheric Sciences, Iowa State University
John Herring	herring3@iastate.edu	Department of Geological and Atmospheric Sciences, Iowa State University
Hallie Wirth	hwirth@uiowa.edu	Earth and Environmental Science Department, University of Iowa
Jamison Ward	ward0975@umn.edu	Department of Earth and Environmental Sciences, UMN
Clara Blättler	cblattler@uchicago.edu	Geophysical Sciences, University of Chicago
Catherine Polik	polik020@umn.edu	Ecology, Evolution, and Behavior, University of Minnesota
Judy Yang	judyyang@umn.edu	Civil, Environmental, and Geo-Engineering
Jordan Sivigny	sivig005@d.umn.edu	University of Minnesota
Jeff Havig	jhavig@umn.edu	Plant and Microbial Biology, Earth, and Environmental Sciences, UMN
Simon Brassell	simon@iu.edu	Earh & Atmospheric Sciences, Indiana University
Nicole Fiore	nfiore@huskers.unl.edu	University of Nebraska-Lincoln
Reda Abou-Shanab	rabousha@umn.edu	Plant and Microbial Biology, College of Biological Sciences, UMN
Weiming Ding	ding0304@umn.edu	Department of Earth and Environmental Sciences, UMN
Valencia Ajeh	a.valencia@wustl.edu	Washington University in St. Louis
Christos Robertson	robe0833@umn.edu	University of Minnesota
Athena Eyster	aeyster@wisc.edu	University of Wisconsin-Madison/Tufts University

Name	Email	Institution/Affiliation
Brooke Vander Pas	vanderpb@iu.edu	IUPUI
Ella Milliken	ellamilli00@gmail.com	Junior Scientist, Alkali Earth
Celine Smith	celine.ng.smith@gmail.co	Genetics and Cell Development, University of Minnesota
Amanda Patsis	patsi005@umn.edu	Earth and Environmental Sciences, University of Minnesota
Malu C Ferreira	malucferreira@uchicago.edu	University of Chicago
Kirsten Fentzke	fentzkek@msu.edu	Michigan State University
Sarah Jarozewski	jaroz001@d.umn.edu	Earth and Environmental Sciences, University of Minnesota Duluth
Latisha Brengman	lbrengma@d.umn.edu	Earth and Environmental Sciences, University of Minnesota Duluth
Eric Rego	rego@uchicago.edu	The University of Chicago
Ian Carley	carleyia@msu.edu	Earth and Environmental Sciences, Michigan State University
Mari Leland	mleland@smm.org	St. Croix Watershed Research Station, Science Museum of Minnesota
Lienne Sethna	lsethna@smm.org	Science Museum of Minnesota - St. Croix Watershed Research Station
Taylor Rosso	trosso2@huskers.unl.edu	University of Nebraska-Lincoln
Madelyn Banks	banks264@d.umn.edu	Earth and Environmental Sciences, University of Minnesota Duluth
Farhan Ahmed Bhuiyan	bhuiy017@d.umn.edu	Earth and Environmental Sciences, University of Minnesota Duluth
Ari Pouchak	apouchak@smm.org	SCWRS, Science Museum of Minnesota
Émilie Laflèche	elaflech@purdue.edu	Purdue University
Chris Greidanus	cgreidanus@uchicago.edu	University of Chicago
Bill Gilhooly	wgilhool@iupui.edu	Earth Sciences, IUPUI
Christopher Schuler	schu4222@umn.edu	Department of Earth & Environmental Sciences, UMN
Jonathan Jernigan	jjernig@purdue	Purdue University
Kly Suquino	klysuquino@uchicago.edu	University of Chicago
Pablo Almela	almel006@umn.edu	Plant and Microbial Biology
Matt Schrenk	schrenkm@msu.edu	Dept. of Earth & Environmental Sciences, Michigan State University
Katie Linderholm	linde939@d.umn.edu	Natural Resources Research Institute
Hannah Bladow	hcbladow426@stkate.edu	Biology, St. Catherine University
Hannah Hausman	hehausman931@stkate.edu	Biology, St. Catherine University
Virginia Russell	vrussell@berkeley.edu	University of California Berkeley
Maggie Hinkston	hinkston.m@wustl.edu	Earth and Planetary Sciences, Washington University in Saint Louis
Amelia Wilson-Jackson	awilson-jackson@smm.org	St. Croix Watershed Research Station
Joe Rabaey	rabae005@umn.edu	University of Minnesota Duluth, Large Lakes Observatory
Saurabh Singh	Saurabh.singh@ndsu.edu	North Dakota State University, Fargo
Aditya Goyal	aditya.goyal@ndus.edu	North Dakota State University
Madeline Ammend	ammen011@umn.edu	BioTechnology Institute, University of Minnesota
Shirsa Mazumdar	shirsa.mazumdar@ndus.edu	North Dakota State University
Benjamin Teerlinck	teerl003@umn.edu	Earth and Environmental Sciences, University of Minnesota
Teresa Mccarrell	mcca1048@umn.edu	Department of Plant and Microbial Biology, University of Minnesota
Allison Lochen	loche021@umn.edu	Earth Sciences, University of Minnesota
Amanda Borowski	Borow084@umn.edu	PMB, UMN
Nahui Medina Chavez	nmedinac@umn.edu	College of Biological Sciences, UMN
Haleigh Brown	brow2467@purdue.edu	Purdue University
Dalton Hardisty	hardist1@msu.edu	Michigan State University
Andrea Halling	Andrea.Halling@colorado.edu	University of Colorado Boulder
Will Daniels	dani0357@d.umn.edu	University of Minnesota Duluth
Cole Barre		University of Minnesota Duluth

Name	Email	Institution/Affiliation
Meera Shah	meerashah2026@u.northwestern.edu	EPS, Northwestern University
Alexandra Maria Grajales	grajales@iastate.edu	Iowa State University
Evelyn Strombom	evelyn.strombom@gmail.com	EEB, UMN
Mahsa Tashakor	mahsa.tashakor@cmich.edu	Central Michigan University
Floyd Nichols	floydnichols2025@u.northwestern.edu	Northwestern University
Watts Dietrich	dietr108@msu.edu	Department of Earth and Environmental Sciences, Michigan State University
Ashika Capirala	acapiral@purdue.edu	Department of Earth, Atmospheric, and Planetary Sciences, Purdue University
Christof Zweifel	zweif017@umn.edu	Earth and Environmental Science, University of Minnesota Twin Cities
Jen Houghton	jhoughton@wustl.edu	Earth and Planetary Sciences, Washington University in St. Louis
Victoria Rebbeck	rebbe002@umn.edu	Plant and Microbial Biology, University of Minnesota Twin Cities
Michelle Chamberlain	mchamber@iastate.edu	Department of Geological and Atmospheric Sciences, Iowa State University
Fernando Medina Ferrer	medinaferrer@berkeley.edu	Molecular and Cell Biology, University of California, Berkeley
Andrew McGallian	amcgallian@uchicago.edu	Department of the Geophysical Sciences, The University of Chicago
Marcelo Prianti	marcelotesser19@gmail.com	Department of Earth And Atmospheric Sciences, Central Michigan University
Seyed Mohammad Javad Abdolah Saberi	abdol031@umn.edu	Ecology, Evolution and Behavior, University of Minnesota
Jack Hutchings	jackh@wustl.edu	Earth, Environmental, and Planetary Sciences, Washington University in St. Louis
Alessandro Mauceri	a.a.mauceri@wustl.edu	Department of Earth, Environmental, and Planetary Sciences, Washington, University in St. Louis
Debasis Golui	debasis.golui@ndsu.edu	Department of Civil, Construction and Environmental Engineering, North Dakota State University, Fargo, USA
Anand Gupta	anand.gupta@ndsu.edu	Civil Construction and Environmental Engineering Department, North Dakota State University, Fargo, North Dakota