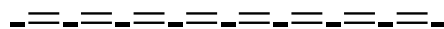




# **Midwest Geobiology Symposium 2024**

## **Meeting Program Booklet**



Hosted at Sukup Hall and Atrium  
Iowa State University, Ames, IA

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*Department of the Earth, Atmosphere, and Climate*  
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*Department of Ecology, Evolution, and Organismal Biology*  
*Department of Civil, Construction, and Environmental Engineering*  
*College of Liberal Arts & Sciences*

We are excited to welcome you to Ames for the 2024 Midwest Geobiology Symposium! To ensure a positive experience for all attendees, we hope to maintain a collegial, respectful, and kind atmosphere during this meeting. Any aggressive, disruptive, or egregiously unprofessional behavior may be grounds for removal from the symposium venue.

Iowa State University is located on the ancestral lands and territory of the Baxoje (bah-kho-dzhe), or Ioway Nation. The United States obtained the land from the Meskwaki and Sauk nations in the Treaty of 1842. We wish to recognize our obligations to this land and to the people who took care of it, as well as to the 17,000 Native people who live in Iowa today.

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# About Midwest Geobiology

The primary goals of the 12th Midwest Geobiology Symposium are

1. to facilitate scientific communication and networking among early-career (undergraduate, graduate, and postdoctoral) researchers at the intersection of the biological and Earth sciences,
2. to strengthen collaboration in geobiological research across disciplines, departments, and institutions throughout the Midwest, and
3. to foster an open, collegial environment where participants may practice communicating their research while engaging with, and learning from, other interdisciplinary researchers.

Similar to previous Geobiology symposiums, this meeting serves to promote engagement and collaboration between institutions across the Midwest while minimizing personal expenditures for participants. There are no abstract submission fees, and a sizable portion of funding is traditionally allocated to reimburse traveling expenses for students and trainees.

The first Midwest Geobiology (MWGB) symposium was organized and held at Washington University in St. Louis, MO on September 22, 2012 with 28 submitted abstracts, serving as a regional platform for cross-institutional collaboration and science communication. Over the ensuing decade, MWGB has grown substantially, with roughly 45-50 abstracts accepted per year on average. This number has continued to grow – the most recent MWGB meeting, which took place on September 23, 2023 in the Twin Cities, MN, published 56 total abstracts, 16 of which were for oral presentations. Since 2012, the meeting has facilitated regional collaboration and communication between research groups that would seldom establish contact at a larger, national conference. In particular, the meeting has provided a collegial, supportive environment for graduate students, postdocs, and many undergraduates to practice sharing their biological and Earth science research while learning from their colleagues. This early-career focus is also helpful to the meeting organizers themselves, who thereby gain valuable experience in organizing and hosting scientific meetings, in addition to providing incentives for career networking across the Midwest. This year's MWGB meeting will be the first to be held in the state of Iowa, providing a central location accessible to participants from across the Midwest and especially from the Great Plains region.

# Meeting Schedule

8:30 -9:00 am: Registration and Opening Remarks

## **9:00 - 10:00 am : Breakfast and Poster Session I**

**Poster Presenters:** Isabelle Rein, Maggie Hinkston, Margo Crothers, John Herring, Alexandra Grajales, Gabriela Rizzo, Yasaman Azizipour, Massie Jones, Ben Johnson, Christopher Greidanus, and Emily Apel

10:00 - 10:15 am : Break

## **10:15 - 11:30 am : Oral Presentation Session I**

10:15 - 10:30 am - Zachary Burton

10:30 - 10:45 am - Libby Chelsvig

10:45 - 11:00 am - Zirije Hasani

11:00 - 11:15 am - Alessandro Mauceri

11:15 - 11:30 am - Sam Schultz

11:30 - 11:45 am : Break

## **11:45 am - 1:00 pm : Oral Presentation Session II**

11:45 - 12:00 pm - Emily Hanson

12:00 - 12:15 pm - Justin Mackey

12:15 - 12:30 pm - Taylor Rosso

12:30 - 12:45 pm - Joshua Sackett

12:45 - 1:00 pm - Zackry Stevenson

1:00 - 2:00 pm : Lunch Break

## **2:00 - 3:00 pm : Poster Session II**

**Poster Presenters:** Benjamin Teerlinck, Christopher Hanson, Meera Shah, Jennifer Houghton, Michaela Hostetler, Julia Kassis, Madeline Taylor, Elza Dugamin, and Samuel Duncanson

3:00 - 3:15 pm : Break

## **3:15 - 4:15 pm : Oral Presentation Session III**

3:15 - 3:30 pm - Yogaraj Banerjee

3:30 - 3:45 pm - Thomas Getz

3:45 - 4:00 pm - Judy Malas

4:00 - 4:15 pm - Emily Millman

4:15 - 4:45 pm : Discussion and Closing Remarks

5:00 - 5:30 pm : Travel time to Alluvial

5:30 - 9:00 pm : [Alluvial Brewing](#)

# Sequence of Oral Presentations

## **Session 1: Biomarkers, Methods, and Applications in Geobiology**

Zachary Burton - *Investigating the Corrosion Outcomes of Complex Microbial Communities*

Libby Chelsvig - *Effect of stoichiometry on magnetite and maghemite redox behavior*

Zirije Hasani - *Implementation of real-time anomaly detection algorithm for Big IoT sensor data for smart agriculture*

Alessandro Maucci - *Leaf wax biomarkers uncover millennial- to orbital-scale drivers of hydroclimate change in the Northern Hemisphere Andes since 19,000 yr BP*

Sam Schultz - *Characterizing Indian Summer Monsoon hydroclimate over the last 3,000 years using leaf wax biomarkers in lacustrine sediments*

## **Session 2: Microbes, Metabolisms, and Geochemical Dynamics**

Emily Hanson - *Biofilm-dependent  $Fe^0$  oxidation by a model methanogen*

Justin Mackey - *Determining the Genes Involved in Thioclava electrotropha's Rock-Eating Metabolism*

Taylor Rosso - *Microbial Iron and Nitrate Reduction in Unsaturated Soil Following Rewetting*

Joshua Sackett - *Rock-EETing Microbes: Uncovering novel mechanisms of extracellular electron uptake in the mineral-oxidizing marine sediment bacterium, Thioclava electrotropha*

Zackry Stevenson – *Breaking the Mo Barrier: Nitrogen Fixation in Mo Scarce Deming Lake*

## **Session 3: Feedbacks between Life, Earth, Minerals, and Climate**

Yogaraj Banerjee - *Investigating the influence of Deccan volcanism on the K/Pg extinction event using a multi-proxy approach*

Judy Malas - *High-pressure incubations reveal polyextremotolerant microbial communities from Yellowstone National Park hydrothermal surface features*

Emily Millman - *Variations in Amino Acid Selectivity during Adsorption to Smectite and Serpentine Clays*

Thomas Getz - *It's a Small Boi: The Identification of a Small Scale Hypothermal in the Early Eocene*

## **Discussion/Closing Remarks**

# Oral Presentation Abstracts

## **Investigating the Corrosion Outcomes of Complex Microbial Communities**

Zachary Burton

Iowa State University (Civil, Construction, and Environmental Engineering Dept.)

Microbiologically influenced corrosion (MIC) and microbiologically influenced corrosion inhibition (MICI) are two types of corrosion outcomes that have been the subject of many recent studies on how biofilms affect corrosion outcomes. Regardless of these outcomes, most studies tend to look only at biofilms composed of only one environmental isolate, or on biofilms composed of pure culture isolates. With this in mind, we investigated the corrosion outcomes of environmentally derived biofilms on steel surfaces to study the role of complex bacterial communities in MIC and/or MICI outcomes. These biofilms were grown from microbial communities derived from soil and water samples on steel corrosion and then immersed in artificial seawater for 14 days. Thus far, we have observed that some of the environmentally derived complex microbial communities contributed to MIC outcomes, while others have contributed to MICI outcomes. We hypothesize that specific interactions within the bacterial community are key to differentiating MIC and MICI outcomes in complex microbial communities. To test this hypothesis, DNA samples from each unique environmentally derived biofilm were taken at different time points and microbial community sequencing is currently underway.

## Effect of stoichiometry on magnetite and maghemite redox behavior

Libby Chelsvig  
University of Iowa

Iron minerals are active participants in biogeochemical redox cycling in soils and sediments. Magnetite, a mixed valent iron mineral, can contain varying amounts of Fe(II) resulting in different stoichiometries ( $x = \text{Fe(II)}/\text{Fe(III)}$ ) ranging from  $x = 0.5$  (fully stoichiometric) to  $x = 0$  (maghemite). While there is some evidence that redox potentials ( $E_H$ ) vary with magnetite stoichiometry [1], it remains unclear how redox potentials change as a function of magnetite stoichiometry, Fe(II) concentration, and pH. Here, we measured open-circuit potentials of magnetite and maghemite over a range of magnetite stoichiometries, pH values, and dissolved Fe(II) concentrations.

As expected and consistent with previous work [2], we found magnetite redox potentials decreased as stoichiometry increased from  $x = 0.09$  to  $0.50$ . Over a pH range of  $5.5$  to  $9.0$ , the  $E_H$  vs.  $x$  slopes were linear and ranged from  $-260$  to  $-625$  mV with a general trend of steeper slopes with increasing pH values. We also observed a linear relationship between  $E_H$  vs. pH for all stoichiometries with slopes ranging from  $-91$  to  $-117$  mV. We further adjusted the stoichiometry of maghemite ( $x = 0$ ) and nonstoichiometric magnetite ( $x = 0.17$ ) by adding aqueous Fe(II) to the suspensions and observed more negative redox potentials as stoichiometry increased. Additional work is underway to develop an electrochemical model for predicting redox potentials of magnetite/maghemite suspensions over a range of pH, aqueous Fe(II) concentration, and stoichiometry conditions and to evaluate the potential for magnetite/maghemite recharge in environmental systems for contaminant reduction applications.

[1] Redox behavior of magnetite: Implications for contaminant reduction, Gorski, C.A., et al. (2010), *Environmental Science & Technology* 44(1), 55-60.

[2] Redox potentials of magnetite suspensions under reducing conditions, Robinson, T.C., et al. (2022), *Environmental Science & Technology* 56(23), 17454-17461.



# **Implementation of real-time anomaly detection algorithm for Big IoT sensor data for smart agriculture**

Zirije Hasani

Iowa State University- Engineering agriculture

IoT technology in agriculture has ushered in a new era of information-rich farming, where IoT sensors continue to generate valuable real-time data. However, to properly harness this information for smart agriculture, suitable algorithms for real-time anomaly detection are required. Our research is focused on the development and implementation of specialized anomaly detection algorithms. Our research is concentrated on the demarcation between data in modern agriculture and the detection of anomalies that can affect crop health, resource management, and overall farmer efficiency. We employ data processing techniques and intelligent machine learning, including real-time operational mechanisms, to provide support to farmers and interested parties. Through rigorous validation, this study highlights the importance of this algorithm in real-time anomaly identification, which is vital for informed decision-making in the agriculture sector. Considering issues such as plant diseases and resource shortages, the algorithm aids in enabling sustainable and efficient agricultural practices.

# Leaf wax biomarkers uncover millennial- to orbital-scale drivers of hydroclimate change in the Northern Hemisphere Andes since 19,000 yr BP

Alessandro Mauceri

Washington University in St. Louis

The isotopic and structural composition of leaf wax-derived biomarkers from lacustrine sediments can reveal details about past shifts in hydrology and ecology. Here, we present high-resolution leaf wax n-alkane records from Lake Tota (5.54 N, 72.92 W), Boyacá, Colombia. Tota is situated in the seasonal migration path of the Intertropical Convergence Zone (ITCZ) and experiences changes in the isotopic composition of precipitation ( $\delta_{\text{precip}}$ ) in response to variations in ITCZ mean latitude. We use these records—the first leaf wax records from the NH Andes—to assess hydroclimate and environmental changes over the past ~19,000 years. Specifically, we use the compound-specific  $\delta^2\text{H}$  and  $\delta^{13}\text{C}$  of long-chain n-alkanes to reconstruct precipitation  $\delta^2\text{H}$  ( $\delta^2\text{H}_{\text{precip}}$ ) and vegetation changes, respectively. Before 16 kyr BP,  $\delta^2\text{H}_{\text{precip}}$  oscillated by ~35‰, followed by a transition to lower variability (~20‰) during the early Holocene. Pronounced  $\delta^2\text{H}_{\text{precip}}$  excursions were also observed throughout the deglaciation, centered around ~16 kyr BP (-15‰), ~15.5 kyr BP (+25‰), and ~13 kyr BP (-10‰), which correspond to fluctuations in the strength of the Atlantic Meridional Overturning Circulation.  $\delta^2\text{H}_{\text{precip}}$  did not vary much during the Younger Dryas (12.9–11.7 kyr BP), but a rapid  $\delta^{13}\text{C}$  increase occurred (+2.5‰), indicating changes in vegetation composition.  $\delta^2\text{H}_{\text{precip}}$  and  $\delta^{13}\text{C}$  exhibited a consistent negative trend throughout the Holocene, with  $\delta^2\text{H}_{\text{precip}}$  notably in-phase with several other southern hemisphere Andean and lowland  $\delta_{\text{precip}}$  records from multiple paleoclimate archives and proxy types. The in-phase interhemispheric relationship between the  $\delta^2\text{H}_{\text{precip}}$  record and other Andean  $\delta_{\text{precip}}$  records suggests a regional coherence in both hemispheres due to ITCZ and South American Summer Monsoon dynamics.

## **Characterizing Indian Summer Monsoon hydroclimate over the last 3,000 years using leaf wax biomarkers in lacustrine sediments**

Sam Schultz

Washington University in St. Louis

The Indian Summer Monsoon (ISM) provides rainfall to billions of people on the Indian subcontinent. Understanding the evolution of ISM hydroclimate during recent geologic time is critical to evaluating its response to current and future global changes. Currently, there are few terrestrial paleoclimate records that exclusively capture past ISM variability without competing signals from the East Asian Summer Monsoon (EASM). Plant leaf waxes preserved in sediment cores recently collected from Loktak Lake, Manipur (24°N 93°W) provide valuable means to reconstruct past ISM changes without interference from the EASM. Here, we show the first results of a leaf wax n-alkane hydrogen ( $\delta^2\text{H}_{\text{wax}}$ ) and carbon ( $\delta^{13}\text{C}_{\text{wax}}$ ) isotope record extending back roughly 3,000 years at centennial-scale resolution. The  $\delta^2\text{H}_{\text{wax}}$  record primarily conveys changes in regional precipitation driven by ISM intensity. The  $\delta^{13}\text{C}_{\text{wax}}$  record is expected to capture changes in the surrounding vegetation community linked to shifts in regional effective moisture. Characteristics of n-alkanes, such as average chain length (ACL) accompany isotope data. These reveal changes in the source of n-alkanes preserved in Loktak Lake, which also reveal past hydroclimatic and environmental changes. The ISM is expected to respond significantly to global forcings occurring during the last 3,000 years, such as those during the Little Ice Age. Our leaf wax n-alkane records will augment previous speleothem and marine records in helping to better understand ISM dynamics.

## Biofilm-dependent Fe<sup>0</sup> oxidation by a model methanogen

Emily Hanson

University of Minnesota

In the environment, most microbes live in biofilms communities attached either to a surface or other cells. Biofilms can provide many fitness advantages, including access to resources and resistance to environmental stressors. When microbes colonize human-made steel alloys, metabolic activities within biofilms can accelerate their breakdown in a process known as microbiologically influenced corrosion. This can lead to costly infrastructure and environmental damage. An important group of microbes known to be involved in corrosion are the obligate anaerobes responsible for most of Earth's methane emissions known as methanogenic Archaea. This study focuses on the model methanogen *Methanococcus maripaludis*, which is capable of both biofilm formation and acceleration of iron oxidation. However, the molecular details supporting both of these phenotypes have yet to be determined. Using mutants lacking *aglB*, a gene necessary for surface colonization, we show that biofilm formation by *M. maripaludis* on a variety of steel substrates increases the rate of iron oxidation. Data also shows that the chemical properties of steel, such as corrosion-resistant additives and carbon content, also influences both colonization and iron oxidation by *M. maripaludis*. To investigate this further, we developed a transposon mutagenesis screen that can identify mutants defective in biofilm formation in a 96-well format. These mutants are revealing additional components contributing to the worldwide problem of corrosion facilitated by methanogenic Archaea.

## Determining the Genes Involved in *Thioclava electrotropha*'s Rock-Eating Metabolism

Justin Mackey  
University of Cincinnati

Lithoautotrophic metabolisms – those microbial metabolisms that derive energy from the oxidation of inorganic substrates and obtain reduced carbon via CO<sub>2</sub> fixation – are important in biogeochemical cycling and the microbial ecology of marine sediments. Some lithoautotrophic organisms obtain energy from the oxidation of solid-phase minerals via a process called extracellular electron transfer (EET). EET is the process where electrons are moved across cell membrane(s) into or out of a microbial cell from solid substrates, such as sulfur, iron, or manganese-bearing minerals or electrodes. Mechanisms of EET are well characterized in model iron-reducing and iron-oxidizing bacteria; however, less is known about the mechanisms of EET in sulfur-oxidizing bacteria. Our research investigates *Thioclava electrotropha*, an EET-capable sulfur-oxidizing chemolithoautotrophic bacterium isolated from marine sediments. *T. electrotropha*'s genome lacks homologs to canonical EET proteins, such as those that make up the well-known Mtr pathway, and lacks putative multiheme outer membrane cytochromes altogether. Our goal is to uncover the genes involved in EET in *Thioclava electrotropha*. To gain insight into this novel metabolism, we developed a genetic system in *T. electrotropha* and are leveraging previous whole-genome mutagenesis screens and transcriptomics analysis to generate and test gene deletion mutants to identify genes that are indispensable for extracellular electron uptake. This presentation will report on our efforts to construct and test gene deletion mutants in *T. electrotropha* to gain insight into the mechanism and ecological implications of extracellular electron uptake in marine sediments.

## **Microbial Iron and Nitrate Reduction in Unsaturated Soils Following Rewetting**

Taylor Rosso

University of Nebraska-Lincoln

Microbial iron (Fe) and nitrogen cycling has been well studied in saturated systems. Few studies have investigated these processes in unsaturated systems, such as agricultural soils impacted by nitrogen fertilization. To assess their role in unsaturated systems, soil was collected from an agricultural field and served as the inoculum in a series of anoxic batch reactors with Fe(III) oxide, or reactors with no Fe(III) oxide amendment. The soils were preincubated prior to nitrate amendment (0 mM, 0.25 mM, or 2 mM). No significant Fe(III) reduction was observed during the preincubation. Following nitrate amendment, Fe(III) reduction was observed in all treatments with concomitant nitrate reduction. Transient accumulation of nitrite and nitrous oxide occurred resulting in the production of dinitrogen gas.

Investigation of the soils revealed that microorganisms capable of respiratory ( $9.2 \times 10^3$  cells/g) and fermentative ( $8.3 \times 10^5$  cells/g) Fe(III) reduction, as well as respiratory ( $9.2 \times 10^7$  cells/g) and fermentative nitrate reducers ( $7.5 \times 10^8$  cells/g), were abundant. Simultaneous nitrate and Fe(III) reduction was unexpected as nitrate has been demonstrated to inhibit Fe(III) reduction. Given the abundance of fermentative microorganisms, another experiment was conducted with an electron transport chain inhibitor, sodium azide. Omission of azide resulted in concurrent nitrate and Fe(III) reduction. Whereas azide amendment inhibited nitrate reduction while Fe(III) reduction continued, although diminished relative to the treatments without azide. Together these data suggest that fermentative iron reduction could play a significant role in the reduction of Fe(III) in unsaturated soils, influencing Fe cycling following periods of precipitation or irrigation.

**Rock-EETing Microbes: Uncovering novel mechanisms of extracellular electron uptake in the mineral-oxidizing marine sediment bacterium,**

*Thioclava electrotropha*

Joshua Sackett

University of Cincinnati

Extracellular electron transfer (EET) is the process by which some microorganisms transfer electrons across their insulating cellular envelope to/from solid-phase materials, such as mineral surfaces or electrodes. While much of our knowledge of EET mechanisms has been gleaned from physiologic investigations of iron-oxidizing and iron-reducing bacteria, considerably less is known about the mechanisms and ecological implications of EET in mineral-oxidizing organisms, especially those that do not interface with iron. To better elucidate the mechanisms and ecology of EET in oxidative processes, we are investigating EET in the mineral-oxidizing marine sediment bacterium, *Thioclava electrotropha*. *T. electrotropha* is metabolically versatile and capable of chemoorganoheterotrophic growth or chemolithautotrophic growth with hydrogen or reduced sulfur species as electron donors. *T. electrotropha* is also capable of cathode oxidation – a proxy for mineral oxidation – despite the genome lacking homologs to known EET pathways, such as the outer-membrane multi-heme cytochromes responsible for EET in organisms such as *Shewanella*, *Geobacter*, and some *Gallionellaceae*. Previous electrochemical investigations have shown that this electron uptake phenotype is interfacial (Karbelkar et al., 2019) and we have recently shown that EET is independent of the Sox sulfur oxidation system. Collectively, these data point to a novel EET mechanism. To gain insight into this novel EET mechanism, we conducted a suite of ‘omics’ screens, molecular genetics experiments, and bioelectrochemical assays that have given us a foothold into the EET pathway. In this presentation, I will discuss the results of these experiments and will share our ‘foothold’ into the novel EET pathway of *T. electrotropha*.

## **Breaking the Mo Barrier: Nitrogen Fixation in Mo Scarce Deming Lake**

Zackry Stevenson  
Iowa State University

During the Archean and Proterozoic eras, diazotrophic organisms used the molybdenum- requiring nitrogenase enzyme to fix nitrogen to support early primary productivity, despite low availability of molybdenum before widespread oxygenation. However, Earth's early primary producers, the Cyanobacteria, are Mo-limited in culture conditions with Mo 1 nM. We document nitrogen fixation at < 0.4 nM in cyanobacteria-dominated Deming Lake, Minnesota, U.S.A., a ferruginous and meromictic lake with some chemical analogy to Archean oceans. Nitrogen fixation occurred in the oxygenated epilimnion under nitrate depletion and above the anoxic metalimnion, where ammonium from remineralization was abundant, and Mo additions did not increase rates. The most abundant organism was a *Synechococcus* sp., verified by 16S rRNA amplicon sequencing and fluorescent cell counts. Only Mo-nitrogenase was detected in metagenomes of this organism and all other diazotrophs. Diazotrophs did not contain ModABC cassettes, which encode for a high-affinity Mo-transport system required for Mo-nitrogenase activity. We suspect that diazotrophs employ alternative strategies to cope with low Mo availability, which will be investigated through metatranscriptomics analyses. These results suggest that limited Mo bioavailability may not have constrained nitrogen fixation by early diazotrophs, and reconcile evidence for the activity of Mo-requiring nitrogenase in the Archean.



## **Investigating the influence of Deccan volcanism on the K/Pg extinction event using a multi-proxy approach**

Yogaraj Banerjee  
Central Michigan University

The Deccan traps represent a major continental flood basalt volcanism covering ~2 million km<sup>2</sup> area – the longest lava flows on Earth. Biogeochemical changes generated by these gigantic volcanic eruptions and their potential link to the K/Pg extinction event are still debated. During my talk, I will present new results based on data collected from continental and marine carbonate archives from India using conventional stable and carbonate-clumped isotopes. We recently analyzed an intertrappean lacustrine sedimentary horizon comprised of microbial carbonates from the Amba Dongar carbonatite complex of the Deccan volcanic province. Our stable isotope investigation shows evidence of gradual eutrophication of the lake system as Deccan volcanism reaches its terminal phase. In another study, the late Cretaceous seasonality was deciphered using carbonate-clumped isotopes on mollusk shells. A higher amplitude of seasonality and intensified winter-time precipitation was inferred for the late Cretaceous 30S latitude. I will also briefly discuss our ongoing work related to the analysis of redox-sensitive trace element systematics (concentration & isotope ratio) of promising geological sections from India that will certainly provide us with new insights into the Deccan-associated biogeochemical perturbation.

## **High-pressure incubations reveal polyextremotolerant microbial communities from Yellowstone National Park hydrothermal surface features**

Judy Malas

University of Illinois at Chicago

Life in the continental subsurface is subject to multiple extreme conditions, including increasing temperature and pressure with depth, as well as oligotrophic, hypersaline, or hyperalkaline conditions, depending on the environment. Hydrothermal features such as hot springs and pools conveniently deliver material from the subsurface to the surface. Hot springs are interface environments with inputs both from the surface and the subsurface. Thermophiles, acidophiles, and alkaliphiles are commonly described from the over 10,000 hydrothermal features at Yellowstone National Park (YNP). Given that a subset of the organisms found in hot springs were likely inhabitants of the continental subsurface, some of the extremophiles within hot springs may also be adapted to high-pressure conditions. Here, metagenomic sequencing was conducted to understand changes to YNP enrichments after high-pressure treatments of 30 MPa and 150 MPa. We find that both acidophiles and thermophiles are tolerant to high pressure, indicating a wider than expected habitable range for these organisms.

## **It's a Small Boi: The Identification of a Small Scale Hypothermal in the Early Eocene**

Thomas Getz  
Iowa State University

Within the Early Eocene (50 to 56 mya), there are several instances of negative carbon isotope excursions (CIE). These CIE's have been found with both marine and terrestrial formations on a global scale and represent periods in Earth's history with elevated levels of CO<sub>2</sub> within the Earth's atmosphere. The Willwood formation of the Bighorn Basin, Wyoming is one of the most well-preserved instances of these early Eocene aged CIE's, containing several of them. The largest and most well studied of these CIE's is the Paleocene Eocene Thermal Maximum (PETM). The Willwood also preserves the CIE's of the Eocene Thermal Maximum (ETM-2), H2, I1, and I2 events. These CIE's have been linked to changes to the climate on a global scale.

The Willwood preserves a record of higher mean annual temperature, changes to mean annual precipitation, and mass immigration of new species to the basin with minimal extinction of existing species. These changes to the climate of the Bighorn Basin have been observed within all the CIE's that have been identified within the Bighorn Basin. I used established techniques and isotopic archives to locate a small-scale CIE, of 10/00, located at the Sand Coulee 133 (SC-133) locality. This Lower intensity CIE, that is located at SC-133, provides the opportunity to further understand the impacts and relationships CIE's and their intensities have on the paleoclimate. All of which act as a natural experiment for the increasingly high amount of CO<sub>2</sub> within the Earth's present day atmosphere.

## **Variations in Amino Acid Selectivity during Adsorption to Smectite and Serpentine Clays**

Emily Millman

Washington University in St. Louis

The concentration of simple organic molecules, such as amino acids, onto mineral surfaces via adsorption may have aided the condensation reactions necessary for the formation of more complex bio-macromolecules on the early Earth. Prior work has established a relationship between the structural charge of a clay mineral and amino acid adsorption, suggesting that interactions between these biomolecules and diverse clays present on the early Earth would differ. This study evaluates the adsorption behavior of amino acids to smectites and serpentines, which are clays expected to be found in early submarine hydrothermal systems and subaerial shallow water basins. The pH of the fluid was controlled to reflect various environments: pH 5 (e.g., basalt-hosted hydrothermal systems), pH 7 (e.g., seawater), and pH 10 (e.g., alkaline lakes). Under equivalent conditions, montmorillonite (a smectite) showed greater amino acid adsorption than lizardite (a serpentine). Amino acids with basic sidechains (e.g., L-arginine and L-lysine) were selectively adsorbed to montmorillonite through a cation exchange mechanism into the mineral interlayer. However, adsorption of L-arginine decreased substantially at pH 10 due to a much smaller proportion of the cationic species in solution that can undergo cation exchange. L-arginine also showed the greatest adsorption to lizardite at pH 7 and 10 but at much lower adsorbed quantities than seen for montmorillonite. However, unlike montmorillonite, adsorption to lizardite increased as the pH increased, likely due to ligand exchange to edge sites. This pH dependent behavior highlights the differences in amino acid selectivity via clay binding, which is strongly controlled by rock composition.

# Poster Presentation Abstracts

## **Theme 1: *Life's Past on Earth and Beyond***

### **1a) Deep Geobiology: Origins, History, and Signatures of Past Life and Earth**

#### **Re-evaluating the “true” magnitude of the carbon isotope excursion at the Paleocene-Eocene Thermal Maximum in the SW Atlantic**

Emily Apel  
Purdue University

The Paleocene Eocene thermal maximum (PETM, ca. 56 Ma) was a period of intense warming and is characterized by a global negative carbon isotope excursion (CIE). The CIE has been attributed to a large, rapid release of isotopically light carbon to the atmosphere, the source of which is heavily debated. A key path towards determining the source involves accurately constraining the magnitude of the excursion. Though the CIE has been detected globally across various depositional settings, ocean basins, and sample types, its “true” magnitude is unclear. Different records show variable excursions ranging from 2‰-8‰ depending on the proxy, setting, and sample material. Various mechanisms could have artificially lowered the magnitude of the CIE in the marine record, including post-depositional processes on the seafloor. There has recently been a more concerted effort to determine how much of an effect diagenesis has had on our conventional marine carbon cycle proxies, e.g., bulk carbonate  $\delta^{13}\text{C}$ . Here, we outline a plan to use secondary ion mass spectrometry (SIMS) to measure in situ  $\delta^{13}\text{C}$  in the planktic foraminifera *Morozovella* spp. from ODP Sites 1262 and 1263 at Walvis Ridge in the southwest Atlantic Ocean. This work will enable primary, biogenic  $\delta^{13}\text{C}$  values to be distinguished from secondary, diagenetically altered  $\delta^{13}\text{C}$ . Thus, the “true” magnitude of the CIE in the mixed layer of the southwest Atlantic will be constrained for the first time.

## **A Comparison of Bulk and Microscale Isotopic Analyses on Late Cambrian Sedimentary Marine Pyrites and Carbonates**

Margo Crothers

Washington University in St. Louis

The Steptoean Positive Isotopic Carbon Excursion (SPICE) event in the late Cambrian period preserves a positive shift (approximately +4-6‰) in carbonate and organic carbon isotopic compositions ( $\delta^{13}\text{C}$ ) in parallel with a sulfur isotope ( $\delta^{34}\text{S}$ ) excursion (approximately +40-60‰, with magnitude varying between localities) in both oxidized (sulfate) and reduced (pyrite) S-bearing phases. Paired excursions in C and S suggest a coupled disruption to global ocean carbon and sulfur cycles. Here, we utilize microscale techniques to contextualize this parallel phenomenon— multiple factors influence  $\delta^{34}\text{S}_{\text{pyrite}}$ , but these converging signals are often not differentiable in bulk mass spectrometry. Secondary Ion Mass Spectrometry (SIMS) collects isotopic compositions from individual mineral grains or regions of interest (ROI) on a micron scale. SIMS analyses coupled with Scanning Electron Microscopy (SEM) mapping allow integration of mineral morphology and isotopic compositions. Observed variation between pyrite grain size, morphology, and associated surrounding sediments as observed on a microscale suggests local processes influence  $\delta^{34}\text{S}_{\text{pyrite}}$  during the SPICE event, superimposed over any signals from global perturbations.

# **Revisiting Ediacaran-Cambrian environmental change in western Laurentia and its impacts on animal life**

Isabelle Rein  
Purdue University

Planetary-scale environmental changes have been suggested to have influenced the evolution of advanced life on Earth. For example, the seemingly stark transition between Ediacaran and Cambrian Faunas is accompanied by geochemical evidence for ocean redox and carbon cycle upheaval. However, there is limited consensus on the nature of these environmental changes and their association with biotic turnover.

Carbonate-associated sulfate sulfur isotopes ( $\delta^{34}\text{S-CAS}$ ) have been measured in Ediacaran-Cambrian boundary sections to reconstruct global ocean redox evolution. One prior study observed high stratigraphic  $\delta^{34}\text{S-CAS}$  variability, which they interpreted to reflect low coeval ocean sulfate concentrations. However, more recent advancements suggest that  $\delta^{34}\text{S-CAS}$  can be altered during early diagenesis, and that these diagenetic effects require deconvolution from primary water column  $\delta^{34}\text{S}$  signals.

To address this issue, we will collect new geochemical data from a continuous carbonate sequence from the western Great Basin across the Ediacaran-Cambrian boundary, for which  $\delta^{13}\text{C-carb}$ ,  $\delta^{18}\text{O}$ , and  $\delta^{44/40}\text{Ca}$  data already exist. This research will analyze (1)  $\delta^{34}\text{S-CAS}$  to constrain global redox changes in the late Ediacaran-early Cambrian ocean and (2)  $^{87}\text{Sr}/^{86}\text{Sr}$  to provide high resolution relative age constraints. These data will be filtered using facies analysis and  $\delta^{44/40}\text{Ca}$  to construct a faithful and time-calibrated record of Ediacaran-Cambrian seawater  $\delta^{34}\text{S}$  values, as context for contemporaneous faunal turnover.

## Stable Isotope Analysis of Fossilized Plants for C Cycling and N Soil Availability During the Phanerozoic

Alexandra M Grajales Perez  
Iowa State University

Plants play a crucial role in Earth's geochemical cycling. Plant growth is dependent on their ability to absorb and fix atmospheric carbon dioxide ( $\text{CO}_2$ ) and obtain nitrogen (N) from soils. The combined reliance on C and N directly affects plant development and may reflect environmental and atmospheric conditions. Carbon and N in plants can have specific isotopic signatures that depend on nutrient source, which are recorded inside the plants cell tissue throughout maturity, death, and fossilization. One such signature is a correlation between the discrimination factor ( $\Delta^{13}\text{C} = \text{atmospheric } \delta^{13}\text{C}_{\text{CO}_2} - \delta^{13}\text{C} \text{ in leaf tissue}$ ) and leaf N content. Since N is necessary for building proteins involved in photosynthesis, low concentrations of N lead to a decreased photosynthetic rate causing a negative correlation between  $\Delta^{13}\text{C}$  and N concentrations in leaf tissue [1]. Therefore, analyses of fossilized plant C and N composition may provide valuable constraints on the evolution of atmospheric  $\delta^{13}\text{C}_{\text{CO}_2}$  and soil N availability through time. By knowing atmospheric  $\delta^{13}\text{C}_{\text{CO}_2}$  and its relationship with N soil availability, further studies can be performed to understand the diverse plant lineages through time, as well as provide deeper insight into the evolutionary process behind the development of plant metabolic pathways. We completed isotopic and concentration measurements for C and N on 56 fossilized plants. All  $\delta^{13}\text{C}$  values from fossil material are within the range for modern C3 photosynthetic plants (-21.7 to -36.8‰) and show a decreasing trend through time. Values of  $\Delta^{13}\text{C}$  were then obtained using observed relationships between  $\Delta^{13}\text{C}$  and N concentrations per area in modern trees. The  $\delta^{13}\text{C}_{\text{CO}_2}$  of the atmosphere was determined from these calculations and results are consistent with existing records for evolving atmospheric  $\delta^{13}\text{C}_{\text{CO}_2}$ , where  $\delta^{13}\text{C}_{\text{CO}_2}$  has been slowly decreasing towards the present. These preliminary results indicate that fossilized plant tissue is a potential proxy for atmospheric  $\delta^{13}\text{C}_{\text{CO}_2}$  during the Phanerozoic, that can help fill the gaps in existing proxy records.

[1] Sparks & Ehleringer (1997), *Oecologia*, 109



## **Experimental Diagenesis of Proteins Fossilizing in Tree Resin**

Christopher Greidanus

University of Chicago

Amber (fossil tree resin), is an archive that preserves fossils from different environments than those commonly found in sedimentary rocks. However, paleobiological information from amber has been limited to those organisms that we can identify visually, which excludes most microbes. While sequenceable DNA is unlikely to be preserved in amber for long time periods, the preservation of proteins might be better due to isolation from many kinds of diagenetic alteration. Like DNA, proteins can preserve taxonomic and metabolic information, but proteins are more durable over geologic time in a variety of depositional contexts. However, the use of protein molecular fossils as recorders of microbial evolution and as environmental proxies is in its infancy. There is an outstanding need in the field for methods to discriminate truly ancient proteins from modern contamination, which hinges on a clearer molecular-level understanding of protein diagenesis in a wider array of preservational settings. In this project, we performed diagenetic experiments with microbial biomass in tree resin to develop protein isolation and sequencing methods and understand protein diagenesis in fossil resins. Preliminary results indicate that proteins can be extracted and sequenced from fossil resins, suggesting that amber may preserve valuable molecular fossil records of ancient microbial taxa and past environments. In diagenetic experiments, the total number of identified peptides decreases over time, while average length does not change. This suggests that diagenetic covalent modifications to the peptide structures could be making them unidentifiable, or cross-linking peptides to the resin matrix and inhibiting extraction.

## **EarthN<sub>2</sub>O: Reconstructing the History of Atmospheric and Marine Nitrogen Trace Gases Across Geologic Time**

John Herring  
Iowa State University

Nitrous oxide (N<sub>2</sub>O), a trace gas produced as a biogeochemical byproduct and as technological waste, is a potent greenhouse gas (GHG) which may have sustained metabolic pathways ancestral to eukaryotic aerobic respiration. As such, N<sub>2</sub>O and other nitrogen trace gases (NH<sub>3</sub> and NO<sub>x</sub>) could have influenced Earth's past climate and played an important role in the evolution of the earliest metabolisms. However, no continuous reconstruction of atmospheric or oceanic N<sub>2</sub>O abundances over Earth history is yet available prior to 800 ka. To address this knowledge gap, we are developing a planetary N-cycle box model (EarthN<sub>2</sub>O) to reconstruct the dynamics and abundances of N<sub>2</sub>O, NH<sub>3</sub>, and NO<sub>x</sub> across deep time. EarthN<sub>2</sub>O tracks the marine, geologic, and terrestrial N and P cycles, the steady-state production and consumption of N trace gases, the atmospheric chemistry and lifetime of N<sub>2</sub>O, and its contribution to climate warming. Independent paleoclimatic and paleogeographic forcings are applied to constrain the sensitive and dynamic processes controlling N<sub>2</sub>O abundances in the ocean and atmosphere. Preliminary results suggest that 1) N<sub>2</sub>O was a significant GHG from the Neoproterozoic through the Mesozoic, 2) deep marine [N<sub>2</sub>O] was high in the Proterozoic, potentially driving the metabolic evolution of early eukaryotes, and 3) the effects of N<sub>2</sub>O on Proterozoic climate warming, while likely minor, could vary strongly with atmospheric pO<sub>2</sub> and marine productivity. After model validation, EarthN<sub>2</sub>O will be applied to study both the Earth's past N-cycle and its future under varying scenarios of anthropogenic perturbation.

## **Genetic and Molecular Complexity of Lipid Biomarkers**

Maggie Hinkston

Washington University in Saint Louis

Fossilized lipid biomarkers provide important evidence for reconstructing the history of life on Earth. But the interpretation and quantification of lipid biomarker information is commonly ambiguous, due to uncertainty regarding the production and diagenesis of fossilized lipids. Biomarkers carry information through their chemical structure and isotope ratios. We here describe structure in terms of chemical complexity, which is the number of unique units required to describe a molecule. A lipid's topological complexity gives insight into its biological functions. The structure represents an imperfect record of the DNA sequences that encoded enzymes responsible for lipid biosynthesis. We compare the topological complexity to the genetic complexity, which is the average number of unique enzymes involved in its biosynthesis.

We have applied this approach to analyze the chemical and genetic complexity of samples from a field site at Lago Strobel, a Martian analog in Patagonia. Information complexity across the lake will be spatially mapped to better understand its variation in this environment. This is the first step towards quantifying the distribution of interpretable biological information in an environment. Quantifying these information channels will help address how to approach uncertain biomarker information on Earth or elsewhere. Our framework can be broadly applied to many kinds of biomarkers – including those of life “not as we know it.”

## **1b) Astrobiology: Models and Analogues for Life Beyond Earth**

### **Sulfur Metabolism Across Worlds: Yellowstone's Hydrothermal Systems and Europa's Icy Oceans**

Yasaman Azizpour  
University of Illinois at Chicago

Sulfate reduction is prevalent in many of Earth's anaerobic environments, from the wetlands to the deep subsurface, offering varying degrees of energy depending on the ecosystems' environmental conditions. Our metagenomic analysis challenges the long-held belief that sulfur metabolism yields limited energy in the hot springs of Yellowstone National Park (Shock et al., 2010), revealing a widespread presence of sulfate-reducing bacteria and archaea in a variety of types of springs. Key functional genes, including *sat*, *apr*, and *dsr*, were detected, supporting the feasibility of sulfate reduction across diverse hydrothermal environments. These findings align with earlier studies (Swingley et al., 2012; Fishbain et al., 2003), emphasizing sulfur metabolism's ecological importance in extreme settings. Sulfate reduction, a critical pathway in Earth's sulfur biogeochemical cycles, has far-reaching astrobiological implications. Enzymes like dissimilatory sulfite reductase (DsrAB) are pivotal in this process and may also function in environments beyond Earth, particularly Europa's subsurface oceans (Zolotov and Shock, 2003; Weber et al., 2023). While debates about sulfate abundance on Europa continue (Vance et al., 2022), its confirmed presence invites further exploration of sulfate-reducing microorganisms (SRM) as potential biosignatures in extraterrestrial hydrothermal systems.

Our research suggests that understanding sulfur metabolism and microbial interactions on Earth, particularly in Yellowstone's hydrothermal systems, provides crucial insights into potential life-sustaining processes on ocean worlds like Europa. Enzymes such as DsrAB could be analyzed as biomarkers for sulfate reduction in these environments.

Future studies will explore how these enzymes behave under pressures similar to those in Europa's oceans, revealing potential changes in structure, function, and activity, further advancing our understanding of sulfur metabolism in extreme extraterrestrial environments.

## **Nitrogen recycling efficiency at subduction zones could influence planetary biosphere size**

Ben Johnson

Iowa State University

Nitrogen is an important nutrient. It is abundant in the atmosphere today, but the crust and mantle also contain appreciable N. After biological processes transform atmospheric  $N_2$  into  $NH_4$ , N as  $NH_4$  can be incorporated in sediments and altered crust, where it can be subducted. Depending on the redox state and temperature of a subduction zone, such subducted N can either return to the atmosphere or be retained in the solid Earth. N in the solid Earth is not available for life, and if substantial N is sequestered, the biosphere may become N limited. In this poster, I explore potential outcomes of this using an Earth system N model, and apply to different planetary evolutionary pathways.

## **Exploring the limits of Psychromonas under high pressure and low temperature**

Massie Jones

University of Illinois Chicago

This project investigates the optimal and upper limits of pressure and temperature that allow for the growth of psychrophilic (cold-loving) and piezophilic (pressure-loving) microorganisms. Specifically, I focus on seven understudied species of Psychromonas bacteria, and subject them to experimental conditions mimicking the environments found in icy ocean worlds like Titan and Europa. By identifying the growth conditions that support extremophiles, we can gain valuable insights into the potential for life and its resilience in the harsh conditions of outer space.

Extremophilic microbes were the first agents of life on Earth and have demonstrated remarkable adaptability to some of the most extreme environments on our planet. From highly alkaline hot springs to metal-rich waters and the crushing depths of the ocean floor, extremeophiles not only survive but grow and reproduce. In Earth's deepest ocean trenches, pressures can reach up to 110 MPa, with temperatures averaging around 4°C (Mitchell 2016). The microorganisms that survive and thrive in these cold, high-pressure environments hold clues to understanding the conditions that supported early life on Earth and offer a model for life on icy moons where similar environmental extremes are present.

Titan and Europa exhibit oceanic pressures that range from ~40 MPa to ~930 MPa, with temperatures ranging from -22°C to 30°C (Pikuta 2007). This spectrum of conditions overlaps with some of the most extreme environments on Earth. By studying the growth and survival of piezophilic and psychrophilic bacteria under simulated high-pressure, low-temperature conditions, we can build predictive models that help assess the potential for life to exist and persist. Understanding how life can adapt to extremes not only informs the evolution of life on early Earth but also our search for life in the cosmos (Thombre et al. 2020).

This project aims to quantify the pressure and temperature conditions that allow survival of Psychromonas and what are their optimum growth condition to better understand if the possibility of microbial life exists on other planetary bodies with similar environmental conditions.

## **Methanogenesis in Martian Regolith Simulant Containing Calcium Carbonate**

Gabriella Rizzo

University of Nebraska Lincoln

Methanogenic archaea are a diverse group of anaerobic microorganisms capable of metabolically converting organic or inorganic carbon to methane for energy generation. Due to their anaerobic nature and metabolic ability, methanogens have been considered candidates for microbial life on Mars. Remote detection of methane in the Martian atmosphere further supports the use of methanogens to study the potential for Martian life. Here, we present the results of a set of experiments investigating the influence of a Martian regolith simulant (MMS-1) on methane production by a methanogenic enrichment culture containing *Methanobacterium* sp. ACI-7 with calcium carbonate that serves as the sole source of inorganic carbon. Batch cultures inoculated with live cells of the enrichment culture containing *Methanobacterium* sp. produced methane when gaseous and solid-phase carbon dioxide sources, CO<sub>2</sub> and CaCO<sub>3</sub> respectively, were amended into culture medium containing regolith simulant. In addition, preliminary characterization of *Methanobacterium* sp. ACI-7 was performed to determine optimal growth conditions including salt tolerance and temperature. In pure culture, the organism tolerated NaCl concentrations ranging from 0 to 10% with 0-1% NaCl yielding optimal growth. ACI-7 grew optimally at 40°C and grew across a range of 23-45°C. The growth of this novel *Methanobacterium* sp. in Mars regolith analog strengthens the potential for methanogenic archaea or physiologically similar organisms to exist in environmental niches on Mars and generate methane.

## **Theme 2: *Geobiology and Society***

### **2a) Microbiogeochemistry: Microbes, Element Cycles, and Minerals**

#### **Identifying Iron Mineral Sinks for Phosphorus in a Eutrophic Lake**

Mariela Alfaro Garcia

Iowa State University

There is a concern when there is excess phosphorus in lakes due to it causing harmful cyanobacterial blooms. There is a way that phosphorus can be removed from the lake and into lake sediments; which is with an iron oxide mineral. Although the phosphorus can be moved to lake sediments, the oxides in the sediments can also oxidize and release the phosphorus if the lake is seasonally anoxic. Little Comfort Lake in Minnesota is seasonally stratified and anoxic with abundant iron and phosphorus. With these conditions, vivianite ( $\text{Fe}^{2+}_3(\text{PO}_4)_2 \cdot 8\text{H}_2\text{O}$ ), an iron phosphate mineral, can be formed. Once buried in sediments, vivianite does not usually remobilize or dissolve again. This leads to the question, “Can vivianite be used as a permanent burial sink for phosphorus in Little Comfort Lake?”. Over several seasons, courses collected chemical measurements on Little Comfort Lake and chemical extractions of sediments. We used optical and electron microscopy to identify vivianite in sediments. Then, calculations of the saturation of vivianite minerals were conducted. We can conclude that phosphorus is being naturally removed from Little Comfort Lake through a pathway that is overlooked.



## **A Polar-izing Methane Source: Spatiotemporal Production, Oxidation, and Resources Beneath the Greenland Ice Sheet**

Christopher Hansen

University of Minnesota, Plant and Microbial Biology

Despite their barren appearance, ice sheets host a diverse microbiome that actively cycles nutrients in response to seasonal water flow. Beneath glacier ice, methane ( $\text{CH}_4$ ) producers, methanogens, can supersaturate meltwater with  $\text{CH}_4$ , a potent greenhouse gas, under low-flow conditions. During summer, the downstream export of this  $\text{CH}_4$  can be substantial, resembling major world rivers. However, the contribution of subglacial methanogens to the global  $\text{CH}_4$  budget remains uncertain due to limited flux studies and variability in  $\text{CH}_4$  concentrations driven by local flow rates, microbial activity, and resource availability. Using naled ice, ice preserving an over-wintering record of subglacial ecosystems, we investigated seasonal shifts in biogeochemical conditions beneath the Greenland Ice Sheet (GrIS), targeting forces that may regulate  $\text{CH}_4$  cycling communities and – in turn –  $\text{CH}_4$  pools. By collecting naled ice and proglacial water samples from two GrIS glacier catchments during winter, spring, and fall campaigns, we aimed to (i) track microbial community composition, geochemistry, and dissolved organic matter (DOM) metrics over space and time, (ii) assess metabolic potential using metagenomics and qPCR, and (iii) identify co-relationships between environmental gradients, community traits, and  $\text{CH}_4$ -cycling gene abundance. Here, our initial analysis of 16S rRNA amplicon data and DOM metrics reveals spatiotemporal differences in community structure, dissolved organic carbon concentrations, and DOM bioavailability. Together, these findings take first steps toward understanding the controls on biological  $\text{CH}_4$  cycling beneath the GrIS while, eventually, improving our predictions of ice sheet  $\text{CH}_4$  release today and as Arctic warming continues.

## Imaging pyrite sulfur isotopes using the 7f-GEO SIMS

Jennifer Houghton

Washington University in St. Louis

Much of our understanding of the Earth's global sulfur cycle is based on the  $\delta^{34}\text{S}$  record in sedimentary pyrite. The  $\delta^{34}\text{S}_{\text{pyr}}$  bulk composition is a function of two major variables: (1) ambient  $\delta^{34}\text{S}_{\text{H}_2\text{S}}$ , affected by changes in microbial fractionation during microbial sulfate reduction and/or distillation within porewaters, and (2) the fraction of this sulfide that gets preserved as pyrite, potentially forming intermittently over time in marine sediments during multiple intervals of early diagenetic pyrite precipitation. The history of these complex processes has been evaluated in a subset of samples using a combination of petrographic (SEM) and isotopic analysis of individual pyrite grains using secondary ion mass spectrometry (SIMS). Samples deposited in shallow shelf settings display the greatest complexity, with multiple pyrite textures and subpopulations in  $\delta^{34}\text{S}_{\text{pyr}}$ . All samples analyzed from the Valle di Manche section, regardless of bulk  $\delta^{34}\text{S}_{\text{pyr}}$  (ranging from -44 to +7‰) and depositional setting (outer to inner shelf) contain a significant population of  $^{34}\text{S}$ -depleted pyrite (<-40‰, always exhibiting framboidal textures) with minima from -55 to -50‰, suggesting near-equilibrium microbial fractionation ( $\epsilon \sim 70\text{‰}$ ) is ubiquitous. In addition, the average  $\delta^{34}\text{S}_{\text{pyr}}$  of the population of framboidal grains correlates strongly with the sediment accumulation rate moderated by the %TOC, suggesting these environmental variables primarily control the extent of distillation during early diagenesis. Deviations in bulk  $\delta^{34}\text{S}_{\text{pyr}}$  from these minimal values result from varying contributions of texturally distinct later-stage sedimentary pyrites, which are confined to particular stratigraphic intervals and are possibly associated with episodes of pulsed sedimentation.

## **Tar-iffic Microbes and the Biodegradation of Oil in Paradox Basin, Utah**

Meera Shah

Northwestern University

Microorganisms are known to degrade petroleum, cycling carbon within fossil fuel reservoirs and forming bitumen deposits. The rate of oil biodegradation is influenced by microbial communities and reservoir conditions, including temperature, availability of electron donors, salinity, and fluid flow. In this study, we compare the extent of biodegradation between two sites: (1) Rainbow Rocks from the Jurassic Entrada Sandstone (RR) and (2) Tar Sands Triangle in the Permian White Rim Sandstone (WRSS). The extent of biodegradation is measured by analyzing the aliphatic and aromatic biomarkers of oil across sample transects. RR is an exposed bitumen-bearing outcrop displaying moderate levels of biodegradation. The reservoir lacks n-alkanes and exhibits signs of alkylbenzene, phenanthrene, and sterane depletion. Additionally, the top and bottom of the reservoir are more biodegraded than the middle sections. WRSS is still buried and undergoing slower rates of biodegradation, indicated by the higher abundance of n-alkanes. The extent of biodegradation increases with depth, with the bottom being more degraded than the top. The varying extent of oil biodegradation within reservoirs may indicate changes in permeability along the transect, which influences water and nutrient circulation. Differences in degradation across reservoirs may be influenced by temperatures and oxygen availability. The deeply buried WRSS may have higher temperatures and lower oxygen influx, thus limiting microbial activity. In contrast, shallowly buried reservoirs like RR are at lower temperatures and have higher oxidant availability, promoting microbial activity. While genetic evidence hydrocarbon degrading microbes are currently active within the basin, this study illustrates the role of environmental conditions and paleohydrology in influencing the levels of degradation by a reservoir.

## **The potential role of Ktedonobacter in igneous mineral dissolution**

Benjamin Teerlinck

University of Minnesota - Twin Cities

Members of the bacterial phylum Chloroflexota have widely varied metabolic functions, habitats, and organic synthesis capabilities. Among these bacteria, those belonging to the class Ktedonobacteria are frequently classified as mesophilic, soil-dwelling heterotrophs, but they otherwise remain poorly understood. However, their distribution and abundance in different soil environments suggest that they may play a role in the early stages of soil formation. The dissolution and reprecipitation of minerals in nascent soils directly influences soil pore water chemistry, which in turn influences secondary mineral formation, microbial community composition, and soil fertility. Thus, studying how Ktedonobacteria impact soil mineral dissolution can shed light on their potential role in soil formation. The type strain of class Ktedonobacteria, *Ktedonobacter racemifer* SOSP1-21T, was cultured alongside igneous rock samples from northern Minnesota's Duluth Complex. The rock's surface was previously determined to host a high relative abundance of unclassified Ktedonobacteria and was analyzed by X-ray diffraction to determine its mineralogy. In triplicate, fine sand-size fractions of the crushed rock were incubated in 10% R2A liquid medium with either no inoculant, killed biomass from *K. racemifer* cultures, or live *K. racemifer* cells. Over the course of several weeks, the liquid medium was periodically sampled for pH measurements and total concentrations of dissolved mineral products (Ca, Mg, Al, Si, Na), as determined by inductively coupled plasma optical emission spectroscopy. Although these measurements are still being collected and analyzed, these data may provide a preliminary view into how *K. racemifer* may alter the rate of mineral dissolution in nascent soils.

## **2b) Geobiology Applied: The Shared Future of Human and Environmental Health**

### **Lithium geochemistry in brines: origin and enrichment mechanisms**

Elza Dugamin

Central Michigan University

Lithium is currently playing a key role in reducing carbon emissions and contributing to energy sustainability with lithium-ion rechargeable batteries. Most lithium resources are found in pegmatites type deposits, salt lake (brine) deposits, and sedimentary (clay type) deposits.

However, environmental effects of lithium mining may affect lithium future production (water pollution, human health effects, soil and marine contaminations) (Balaram et al., 2024). The identification of alternative metal resources like "liquid ores", particularly the brines in sedimentary basin, could contribute to meeting global demand.

Throughout my Ph.D. project, I have translated in-depth studies into peer-reviewed publications: (1) the estimation of lithium resources (Scientific Report, Dugamin et al., 2021), (2) a model that shows the favorable or unfavorable conditions for lithium enrichment in formation waters from sedimentary basins (Chemical Geology, Dugamin et al., 2023) and (3) a model of metal transfers (mainly lithium) related to fluid-rock interactions in a case study of the Rhine Graben, on the example of the Soultz-Sous-Forêts geothermal system (Lithos, Dugamin et al., 2024).

My current project is an exciting post-doctoral research focused on the molecular characteristics of critical metals, with a particular emphasis on lithium. This involves integrating concentration measurements, isotope signatures, and geochemical modeling. Here, I provide insights into my research on lithium geochemistry in groundwater and the geological settings of sedimentary basins from laboratory to basin scale utilizing experimental and numerical modeling methods.

## **Magnetosome Associated Protein Functions and Magnetite Applications in Drug Delivery Nanotechnology**

Michaela Hostetler  
Ohio State University

Magnetotactic bacteria (MTB) are diverse prokaryotes that biomineralize magnetic nanoparticles within a unique organelle, called a magnetosome, which organizes in a chain and allows the cell to act as a motile compass needle, aligning the MTB to Earth's magnetic field lines. With the rising popularity of nanotechnology research and use, scientists are turning to MTB for targeted therapy and drug delivery purposes. By conjugating necessary drugs to the magnetosome surface, not only are these organisms a reservoir for drug transport through the human body, but MTB also become a specialized nanorobot controlled by changing magnetic fields. The use of MTB as drug delivery nanorobots is incredibly promising, but one must understand the organism itself to create the optimal nanorobot. Using biogeochemical and morphological measurements, one can understand the functions of the magnetosome associated proteins (MAPs) located in the magnetosome membrane and how they affect magnetite synthesis and morphology. These MAPs can be analyzed through 1.) investigating specific amino acids' relationship to the individual proteins involved in the biomineralization process and their interactions with magnetite, 2.) observing key steps in magnetite biomineralization in real-time to create a mechanistic schematic of the biomineralization process, and 3.) conducting chemical and morphological analysis of magnetite to establish the optimal morphology for drug delivery purposes. This work will allow for gene manipulation to delete, reduce, or amplify certain MAPs to create the optimal magnetite morphology for drug delivery purposes, and thus advance the flourishing field of pharmaceutical nanotechnology.

## **Testing mechanisms for sulfide tolerance in eelgrass to predict the future stability of seagrass ecosystems in the face of anthropogenic climate change**

Julia Kassis  
Purdue University

Seagrasses are a carbon sink in shallow marine environments worldwide. One remarkable feature of these plants is their ability to tolerate hydrogen sulfide, which diffuses into their rhizomes at night. However, some dieback of seagrasses has been observed in recent times, leading to fears that these ecosystems could collapse. Here, we seek to identify the mechanisms for sulfide tolerance in a common species, *Zostera marina* (eelgrass) to begin to predict the future stability of these ecosystems. Earlier studies have suggested that eelgrass and its microbiome can store hydrogen sulfide or convert it into less toxic forms of sulfur. To test these ideas, we use X-Ray Absorption Spectroscopy (XAS) to track the spatial abundance and speciation of sulfur in cryosectioned eelgrass tissues (e.g., rhizome nodes and internodes). Our hypothesis is that ‘tolerance’ of eelgrass of sulfide will be expressed as an anomalous (e.g., in concentration, and valence) accumulation of sulfur in tissues.

We have observed increased abundances of sulfur: 1) in the epidermises of rhizome internodes; 2) surrounding the aerenchyma of rhizome nodes; and 3) in cortical vascular bundles. Sulfur speciation varies spatially, as follows: thiols dominate the central stele, sulfate the parenchyma/cortex, and disulfide the epidermis. We also observe numerous ‘hotspots’ of reduced sulfur throughout all tissues, which we speculate could be locations of sulfur transformation. This work suggests that XAS can be used to understand mechanisms of sulfide tolerance in seagrasses, to begin to predict their future stability.

## **Microbiome sequencing provides insights into microbially-mediated lead (Pb) transformations in urban soils**

Madeline Taylor  
University of Minnesota

Urban green spaces are potential hotspots for lead (Pb) exposure as soil Pb accumulates through industrial materials, legacy gasoline, atmospheric deposition, and runoff. Rhizosphere microbes can transform Pb species and influence Pb toxicity and bioavailability through processes like biosorption, chelation, and biomethylation. Deciphering soil-plant-microbe interactions in contaminated environments can help decrease Pb-related illnesses, however, microbial genes that facilitate Pb transformations are not well understood. Through targeted gene and shotgun metagenome sequencing, we aim to examine microbial communities adapted to elevated Pb environments and seek functional genes associated with soil Pb transformations. Here, we used a portable X-ray fluorescence spectrometer (pXRF) to measure Pb concentrations in the rhizosphere soils of six plant species and the bulk soil at urban and suburban sites in Minneapolis, MN. The urban samples had significantly higher Pb content (avg=106.4 ppm) than the suburban samples (avg=16.6 ppm). We extracted microbial DNA from 42 samples across both sites and used 16S rRNA gene amplicon sequencing targeting the V4 region to determine relative abundance and taxonomy. While all samples shared three dominant phyla (Proteobacteria, Acidobacteriota, and Actinomyceota), there were distinct communities between the two sites with notably more Nitrososphaeria in the urban samples, suggesting that organisms from the Nitrososphaeria class may be adapted to higher pollution environments. We will use shotgun metagenome sequencing to look for genes in the urban microbes that encode similar proteins and enzymes as those used in known heavy metal detoxification pathways, as these may indicate required functions for Pb transformations.



# Attendance

<b>Name</b>	<b>Email</b>	<b>Institution/Affiliation</b>
Mehdi Alibaglouei	mehdi.alibaglouei@luminultra.com	University of Cincinnati
Emily Apel	eapel@purdue.edu	Purdue University
Elena Ayala	ayala119@umn.edu	University of Minnesota
Yasaman Azizpour	yazizp2@uic.edu	University of Illinois at Chicago
Yogaraj Banerjee	ybanerjee15@gmail.com	Central Michigan University
Farhan Bhuiyan	bfarhan@iastate.edu	Iowa State University
Clara Blättler	cblattler@uchicago.edu	University of Chicago
Thomas Brinson	tbrison2@unl.edu	University of Nebraska Lincoln
Roger Bryant	rnbyrant@purdue.edu	Purdue University
Zachary Burton	zburton@iastate.edu	Iowa State University
Michelle Chamberlain	mchamber@iastate.edu	Iowa State University
Libby Chelsvig	caroline-chelsvig@uiowa.edu	University of Iowa
Ann Clarisse Siababa	asiababa@iastate.edu	Iowa State University
Chris Crosby	ccrosby@oakton.edu	Oakton College
Margo Crothers	c.margo@wustl.edu	Washington University in St. Louis
Supantha Dey	supantha@iastate.edu	Iowa State University
Elza Dugamin	dugamin1e@cmich.edu	Central Michigan University
Samuel Duncanson	sdunc@iastate.edu	Iowa State University
David Fike	dfike@levee.wustl.edu	Washington University in St. Louis
Gwen Froehlich	gfro03@iastate.edu	Iowa State University
Mariela Alfaro Garcia	mariela@iastate.edu	Iowa State University
Thomas Getz	tagetz@iastate.edu	Iowa State University
Alexandra M Grajales	grajales@iastate.edu	Iowa State University
Christopher Greidanus	cgreidanus@uchicago.edu	University of Chicago
Trinity Hamilton	trinityh@umn.edu	University of Minnesota
Christopher Hansen	hans7454@umn.edu	University of Minnesota, Plant and Microbial Biology
Emily Hanson	hans5969@umn.edu	University of Minnesota
Zirije Hasani	zirije.hasani@uni-prizren.com	Iowa State University-Engineering Agriculture
Paige Havener	havener@wustl.edu	Washington University in St. Louis
John Herring	herring3@iastate.edu	Iowa State University
Maggie Hinkston	hinkston.m@wustl.edu	Washington University in Saint Louis
Michaela Hostetler	hostetler.157@osu.edu	Ohio State University
Jennifer Houghton	jhoughton@wustl.edu	Washington University in St. Louis

Ursula Humayun	ulhumayun@hotmail.com	University of Minnesota
Jack Hutchings	jackh@wustl.edu	Washington University in St. Louis
Ben Johnson	bwj@iastate.edu	Iowa State University
Massie Jones	mjone46@uic.edu	University of Illinois Chicago
Tyler Karp	atkarp@uchicago.edu	University of Chicago
Julia Kassis	jkassis@purdue.edu	Purdue University
Anjali Khisty	khisty@iastate.edu	Iowa State University
Esmée Kuiper	esmee@u.northwestern.edu	Northwestern University
Justin Mackey	mackeys@mail.uc.edu	University of Cincinnati
Judy Malas	jmalas2@uic.edu	University of Illinois at Chicago
Alessandro Mauceri	a.a.mauceri@wustl.edu	Washington University in St. Louis
Jennifer Melara-Valle	j.a.melara-valle@wustl.edu	Washington University in St. Louis
D'Arcy Meyer-Dombard	drmd@uic.edu	University of Illinois Chicago
Emily Millman	emillman@wustl.edu	Washington University in St. Louis
Anurup Mohanty	anurupmohanty2028@u.northwestern.edu	Northwestern University
Amelia Olsen	olse0397@umn.edu	University of Minnesota - Twin Cities
Faith Rahic-Seggerman	fms@iastate.edu	Iowa State University - Animal Science Department
Isabelle Rein	irein@purdue.edu	Purdue University
Gabriella Rizzo	grizzo3@huskers.unl.edu	University of Nebraska Lincoln
Taylor Rosso	trosso2@huskers.unl.edu	University of Nebraska-Lincoln
Joshua Sackett	joshua.sackett@uc.edu	University of Cincinnati
Sam Schultz	s.t.schultz@wustl.edu	Washington University in St. Louis
Meera Shah	meerashah2026@u.northwestern.edu	Northwestern University
Zackry Stevenson	zackrys@iastate.edu	Iowa State University
Jessica Strathman	jessica5@iastate.edu	Iowa State University
Kly Suquino	klysuquino@uchicago.edu	University of Chicago
Betsy Swanner	eswanner@iastate.edu	Iowa State University
Madeline Taylor	tayl2383@umn.edu	University of Minnesota
Benjamin Teerlinck	teerl003@umn.edu	University of Minnesota - Twin Cities